
E v o l D i r

May 1, 2010

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

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.

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Conferences

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AMNH NewYork Conservation Nov3-5

Please share this announcement with students and colleagues.

The 2010 Student Conference on Conservation Science (SCCS-NY) American Museum of Natural History New York City 3-5 November 2010

If you are currently pursuing or considering a career in conservation science, the American Museum of Natural

History invites you to take part in the 2010 Student Conference on Conservation Science-New York (SCCS-NY), a conference exclusively for graduate students and recent post-doctoral fellows. Be part of the next generation of conservation professionals meeting in New York to exchange ideas with established leaders in conservation science, policy, and management during three days of presentations, workshops, networking events, and more.

Those wishing to attend 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 ones application as well as its relevance to conservation.

Applications will be accepted through Monday, 10 May 2010. To apply, please go to <http://-symposia.cbc.amnh.org/scsny/> . A list of plenary speakers and workshop topics will be posted in the coming weeks.

We hope to welcome you in November!

Fiona Brady Outreach Program Coordinator Center for Biodiversity and Conservation American Museum of Natural History Central Park West at 79th Street New York, NY 10024 USA brady@amnh.org <http://-cbc.amnh.org/> Fiona Brady <brady@AMNH.ORG>

Baltimore AnimalGenomics Sep23-25

Dear Colleagues,

We are writing to inform you that registration is now open for the “5th International Conference: Advances in Canine and Feline Genomics and Hereditary Disease” which will be held September 23-25, 2010 in Baltimore, Maryland. Online registration is now available at the website <http://caninefelinegenomicsconference.org/-index.html> for both the conference and the conference hotel, the Baltimore Marriot Waterfront. The hotel is offering conference attendees special discounted rates, which are less expensive than comparable downtown hotels. The conference is based on past successful conferences focused on genomic advances and genetic characterization of hereditary disease and interesting phenotypes in cats and dogs supported by Nestlé Purina PetCare Company. This year the conference is co-sponsored by the American Genetics Association. With the continued advances of genomic resources in both the cat and dog, this is an exciting time for cat and dog geneticists. Some specific areas we plan to discuss include molecular characterization of hereditary disease, genome wide association studies and selective sweep mapping. Keynote speakers represent the canid, felid and human genetics community. All meals (breakfasts, breaks, lunches, dinners and conference dinner at the Baltimore National Aquarium) will be included in the registration fee. We encourage you to attend and participate in this conference and to pass along this information to colleagues, coworkers and others. We look forward to sharing this unique scientific and

social experience with you. Yours sincerely,

Conference organizers: Dr. Stephen J. O’Brien, Marilyn Menotti-Raymond, National Cancer Institute-Frederick Dr. Steven Hannah, Nestlé Purina PetCare Company Dr. Elaine Ostrander: National Human Genome Research Institute

warjohns@mail.nih.gov

Beijing PlantSystematics Jul7-9 2

International Conference

New Frontiers in Plant Systematics and Evolution (NF-PSE) Beijing, China July 7-9, 2010

SECOND ANNOUNCEMENT

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

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

Conference Venue The conference will be held at the Xiangshan Jinyuan Hotel. This five-star hotel is located in the southeast foot of the Fragrant Hill (Xiangshan), one of Beijings most famous scenic and historical sites. It stands near the precious royal garden with 800 years of history, beautiful landscapes, and elegant environ-

ment. The hotel is within walking distance to the Beijing Botanical Garden and the Institute of Botany, the Chinese Academy of Sciences.

Academic Committee Chair De-yuan Hong (President, Botanical Society of China)

Members Jin Chen (Xishuangbanna Botanical Garden, CAS, Xishuangbanna, China) Hong-ya Gu (Peking University, Beijing, China) Bin Han (Beijing Institute of Genomics, Beijing, China) Hong-wen Huang (South China Botanical Garden, CAS, Guangzhou, China) De-zhu Li (Kunming Institute of Botany, CAS, Kunming, China) Jia-yang Li (Institute of Genetics and Developmental Biology, CAS, Beijing, China) Shao-hua Li (Wuhan Botanical Garden, CAS, Wuhan, China) Ke-ping Ma (Institute of Botany, CAS, China) Hong Ma (Fudan University, Shanghai, China)

Organizing Committee: Chairs Song Ge (Institute of Botany, CAS, China) Tao Sang (Michigan State University, USA) Jun Wen (Smithsonian Institution, USA)

Members Jing-hua Cao (Bureau of International Cooperation of CAS) Zhi-duan Chen (Institute of Botany, CAS, Beijing, China) Cheng-xin Fu (Zhejiang University, Hangzhou, China) Shuang-quan Huang (Wuhan University, China) Yong Li (Fairy Lake Botanical Garden, Shenzhen, China) Jian-quan Liu (Lanzhou University, Lanzhou, China) Guang-yuan Rao (Peking University, Beijing, China) Su-hua Shi (Zhongshan University, Guangzhou, China) Hang Sun (Kunming Institute of Botany, CAS, Kunming, China) Xiao-quan Wang (Institute of Botany, CAS, Beijing, China) Da-yong Zhang (Beijing Normal University, Beijing, China) Yang Zhong (Tibet/Fudan University, Lhasa/Shanghai, China)

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

University, USA) Libin Zhang (Missouri Botanical Garden, USA)

Domestic speakers (tentative): Zhi-duan Chen (Institute of Botany, CAS, Beijing, China) Cheng-xin Fu (Zhejiang University, Hangzhou, China) Song Ge (Institute of Botany, CAS, Beijing, China) Hong-ya Gu (Peking University, Beijing, China) Bin Han (Beijing Institute of Genomics, Beijing, China) Shuang-quan Huang (Wuhan University, Wuhan, China) Hong-zhi Kong (Institute of Botany, CAS, Beijing, China) De-zhu Li (Kunming Institute of Botany, CAS, Kunming, China) Ke-ping Ma (Institute of Botany, CAS, China)

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Berlin Biosystematics Feb21-27

Biosystematics: Berlin, 21 à 27 February 2011

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

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

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

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

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

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

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

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

Organizing Committee Prof. Dr. Thomas Borsch (IOSEB President, BGBM) Dr. Regine Jahn (GfBS President, IOSEB Secretary General, BGBM) Prof. Dr. Dirk Albach (Section Biodiversity and Evolutionary Biology of DBG, Speaker) Dr. Peter Gieré (GfBS Council, MfN) Prof. Dr. Werner Greuter (IOSEB Council, BGBM) Dr. Christoph Häuser (MfN) Jana Hoffmann (GfBS Council, MfN) Dr. Cornelia Löhne (BGBM) Dr. Diana Mutz (Dahlem Centre of Plant Sciences, DCPS) Dr. Michael Ohl (GfBS Secretary General, MfN) Congress Office and Contact Birgit Nordt, berlin2011@bgbm.org Mailing address: Botanic Garden and Botanical Museum Berlin-Dahlem, Freie Uni-

versität Berlin Königin-Luise-Str. 6-8, 14195 Berlin, Germany Phone: ++49/30/838 50 383, Fax: ++49/30/841 729 52

Chris Cameron <ccameron@bms.bc.ca>

Braga Portugal DNABarcoding Jun2-4 DeadlineExtended

Dear Colleagues

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

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

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

We are very pleased to announce our confirmed invited speakers:

Bob Ward (CSIRO, Australia)

Paul Hebert (University of Guelph, Canada)

Pete Hollingsworth (Royal Botanical Gardens, Edinburgh)

Peter Bonants (Wageningen University, The Netherlands)

Mehrdad Hajibabaei (University of Guelph, Canada)

Simon Creer (Bangor University, UK)

Stuart Pimm (Duke University, USA)

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

Filipe Costa

ECBOL2 Chair

Mónica Landi <mlandi@bio.uminho.pt>

Brittany SocialEvolution Oct11-15

Dear colleagues,

We organize a conference on “Social systems: demographic and genetic issues” next October (11-15th) 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 15th.

Organization and registration details including a list of confirmed invited speakers 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)

2 Department of Ecology and Evolution at the University of Lausanne (University of Lausanne, Switzerland)

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

nelly.menard@univ-rennes1.fr

CarnegieMellonU GigaPan Apr12 ProposalDeadline

Fine GigaPan International Conference on Gigapixel

Imaging for Science

Carnegie Mellon University Pittsburgh, Pennsylvania, USA November 11-13, 2010

<http://www.cs.cmu.edu/~fofs> The CREATE Lab, Carnegie Mellon University with The Fine Foundation, is pleased to announce the first Fine International Conference on Gigapixel Imaging for Science to be held November 11-13, 2010 on the campus of Carnegie Mellon University in Pittsburgh, PA. The conference aims to explore innovative use of gigapixel in the classroom, the field and the laboratory by leading scientists. The main purpose of the event is to bring together students, researchers, scientists, teachers and practitioners to present and discuss their latest techniques, ideas, applications and research findings related to various aspects of gigapixel imaging for science. The conference program will consist of keynote speakers, tutorials, workshops, technical presentations, poster presentations, lightning talks, birds of a feather sessions and a juried exhibition of GigaPan prints.

Open Registration: Coming soon

Important Dates

April 12, 2010 Workshop proposal deadline
May 10, 2010 Gallery submission deadline
June 14, 2010 Paper submission deadline
August 6, 2010 Paper, workshop and gallery show acceptance notification
August 23, 2010 Revised paper upload deadline
September 13, 2010 Early registration deadline

– M. Alex Smith PhD Assistant Professor Biodiversity Institute of Ontario & Integrative Biology University of Guelph 50 Stone Road East Guelph, Ontario, Canada N1G 2W1 phone - 519-824-4120 ex 52007 fax - 519-824-5703 www.biodiversity.ca www.barcodinglife.org www.uoguelph.ca/~salex/ salex@uoguelph.ca

Copenhagen AncientDNA Sep7-11

Dear Friends and Colleagues,

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

versity of Copenhagen and will be held at the Geocenter in central Copenhagen.

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

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

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

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

The ISBA4 committee

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

Copenhagen AncientDNA Sep7-11 AbstractDeadline

Dear Friends and Colleagues,

This is just a brief reminder that the deadline for abstract submissions for ISBA4 is coming up at the end of the week, Saturday 1 May. The symposium is being hosted by the Center for GeoGenetics of the University of Copenhagen and will be held at the Geocenter in central Copenhagen between 7-11 September, 2010.

To submit your abstract please follow this link to our website, download the abstract template, and submit it no later than 1 May. We welcome submissions on all aspects of research on ancient biomolecules, including recent applications of biomolecular techniques to archaeological questions, as well as papers dealing with recent technological advances and the use of newly emerging technologies in biomolecular archaeology.

To register for the symposium, please go to our website at www.isba4.net and follow the links to registration. Once you have registered online you will receive an email, containing the payment details. The registration fee is 130 Euros, if you register before 1 June 2010. Thereafter, the registration fee will increase to 150 Euros. This includes a symposium pack, lunch, free wireless access, and a buffet reception at the Carlsberg Academy.

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

The ISBA4 committee

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

Copenhagen SocialEvolution Aug8-14

Dear Evoldir readers,

We still have some slots available in our symposium "The social evolution of fusion and exclusion" at the IUSSI meeting in Copenhagen (8-14 August 2010, <http://www.iussi.org/iussi2010/>). The symposium will bring together researchers working on the evolution of fusion or exclusion at different hierarchical levels of biological organization, ranging from single cells to social parasitism in social insects. Invited speakers are Rick Grosberg and Joan Strassmann. Below you find the description of our symposium. The deadline for abstract submission is 1 May 2010.

The social evolution of fusion and exclusion The potential for fusion or mixing between different biological units is widespread, ranging from single cells forming multicellular structures, via modular multicellular organisms such as fungi forming larger individuals, to colonies of social insects forming super colonies. However, successful integration is usually restricted to close relatives regulated by precise kin recognition systems. Such conditional integration is consistent with kin-selection theory, because the potential inclusive fitness cost and the potential for cheating decrease with increasing relatedness. However, if recognition is based on genetic cues, in the short term, allorecognition alleles are under positive-frequency dependent selection, which removes the required polymorphism (Crozier, 1986). Several possible solutions have recently been proposed for this paradox, but these largely remain to be tested. In this symposium, the social biology of fusion and mixing in general, and the maintenance of genetic kin recognition regulating integration in particular, will be covered. The symposium will bring together researchers working on different hierarchical levels of biological organization, at which mixing occurs, ranging from single cells to social parasitism in social insects.

Names and contact information of the organizers: Duur K. Aanen, assistant professor in evolutionary biology Department of Plant Sciences Laboratory of Genetics Wageningen University and Research Center Droevendaalsesteeg 1, 6708PB Wageningen, The Netherlands Email: duur.aanen@wur.nl

David Queller Dept. of Ecology and Evolution, MS-170 Rice University P.O. Box 1892 Houston, Texas 77251-1892 U.S.A. phone: 713-348-5220 fax: 713-348-5232 email: Queller@rice.edu

“Aanen, Duur” <duur.aanen@wur.nl>

Copenhagen SocialInsectEvolution Aug8-14

A reminder that the deadline for abstract submission for the XVI International Congress of the IUSSI (IUSSI2010) is 1 May 2010

The international congress of the International Union for the Study of Social Insects is held every fourth year, and is the leading forum for the presentation and discussion of research on the evolution of social systems and sociality in all organisms, not only insects.

The XVI congress will be held in Copenhagen, Denmark from 8-14 August 2010.

Confirmed plenary speakers for the congress are

* Gene Robinson University of Illinois at Urbana-Champaign, USA * Andrew Bourke University of East Anglia, UK * Iain Couzin Princeton University, USA * Kevin Foster Harvard University, USA * Deborah Gordon Stanford University, USA * Christina Grozinger Pennsylvania State University, USA * Hanna Kokko University of Helsinki, Finland * Kenji Matsuura Okayama University, Japan

Full details of the Congress, including on-line registration and abstract submission, can be found on the congress web site: <http://www.iussi.org/iussi2010/> We look forward to seeing you in Wonderful Copenhagen in August.

David Nash IUSSI2010 Organizing Committee
IUSSI2010@bio.ku.dk

IUSSI2010 <IUSSI2010@bio.ku.dk>

Hawaii PacificSympBiocomputing Jan4-7

CALL FOR PAPERS

Genome-wide association mapping and rare alleles: from population genomics to personalized medicine

A session of the Pacific Symposium on Biocomputing 2011 January 4-7, 2011 Big Island, Hawaii, USA

Genome-wide associations studies (GWAS) have been very successful in identifying common genetic variation associated to numerous complex diseases. However, most of the identified common genetic variants appear to confer modest risk and few causal alleles have been identified. Furthermore, these associations account for a small portion of the total heritability of inherited disease variation. This has led to the reexamination of the contribution of environment, gene-gene and gene-environment interactions, and rare genetic variants in complex diseases. There is strong evidence that rare variants play an important role in complex disease etiology and may have larger genetic effects than common variants. Currently, much of what we know regarding the contribution of rare genetic variants to disease risk is based on a limited number of phenotypes and candidate genes. However, rapid advancement of second generation sequencing technologies will invariably lead to

widespread association studies comparing whole exome and eventually whole genome sequencing of cases and controls. A tremendous challenge for enabling these “next generation” medical genomic studies is developing statistical approaches for correlating rare genetic variants with disease outcome.

The analysis of rare variants is challenging since methods used for common variants are woefully underpowered (e.g., accurately estimating allele frequencies in cases vs. controls requires ~10 observations of the minor allele; however, many of the functional rare alleles may be present only once in the resequence data). Therefore, methods that can deal with genetic heterogeneity at the trait-associated locus and that can be applied to both in cases vs. controls and quantitative trait studies are needed. Currently, these approaches are in their infancy and very basic criteria (such as functional annotation, sequence conservation, or biological pathway classification) are used. There is tremendous opportunity to apply data mining methods outside of the standard statistical toolkit to this problem. Additionally, deep sequencing will reveal many variants that are not causal, and in order to reduce the problems of misclassification, i.e. inclusion of non-causal variants and exclusion of causal variants in the analysis, it is beneficial to predict their potential functionality. Thus, methods to classify and annotate rare variants for subsequent analysis are necessary.

The session of PSB 2011 would focus on distilling current knowledge in assessing rare variant functionality and their correlation with complex traits, and more importantly bring forth methodological questions that need to be addressed for successful analysis of rare variants. “GWAS by sequencing” presents many new challenges and proposed solutions for interpreting sequencing data from clinical case/control cohorts will be of particular interest to a diverse audience. The session will similarly consider application-specific algorithms, analysis methods, or study planning and design tools with emphasis in the leveraging rare genetic variation in complex trait/disease correlation.

CALL FOR PAPERS AND POSTERS We encourage academic, government, and industrial scientists to submit manuscripts with original work in the subject area. PSB will publish accepted full papers in an archival proceedings indexed in Medline. All contributed papers will be rigorously peer-reviewed by at least two referees. A limited number of papers will be selected for oral presentation to the full assembled conference. Posters and computer demonstrations are also requested to complement the session, and require the submission of a one-page abstract. Accepted poster abstracts will be distributed at the conference separately from the archival

Proceedings. In addition of the oral presentation of the full papers, and the poster session, an invited panel discussion devised to encourage discussion of the challenges facing the field will be also held. **POSSIBLE SUBMISSION TOPICS**

* Population genetics of rare genetic variation * Strategies for GWAS design and analysis considering rare variants * Analysis of rare variant from second-generation sequencing data * Identification of functional rare genetic variation * Applications of findings of rare variants in personalized medicine

KEY DATES Deadline for full paper submission: July 12, 2010 Full paper author notification: September 10, 2010 Deadline for poster abstracts: November 1, 2010

CONFERENCE INFORMATION The Pacific Symposium on Biocomputing (PSB 2011) is an international, multidisciplinary conference for the presentation and discussion of current research in the theory and application

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Hilo Hawaii Conservation Genomics Jul26-28

The American Genetic Association (owner of the Journal of Heredity) 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.

The full speaker list is being completed. Currently, it includes:

* Fred Allendorf, Univ of Montana * Brian Bowen, Hawaii Inst of Marine Biology * Sheila Conant, Univ of Hawaii, Honolulu * Scott Edwards, Harvard Univ * David Foote, Volcanoes Natl Park * Rosie Gillespie,

Univ of California, Berkeley * David Haussler, Univ of California, Santa Cruz * Hopi Hoekstra, Harvard Univ * Stephen O'Brien, Laboratory of Genomic Diversity, MD * Patrick O'Grady, Univ of California, Berkeley * Steve Palumbi, Stanford Univ * Don Price, Univ of Hawaii, Hilo * Jennifer Schultz, Hawaii Inst of Marine Biology * Mark Schwartz, Univ of California, Davis * Brad Shaffer, Univ of California, Davis * Elizabeth Stacy, Univ of Hawaii, Hilo

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 will be available, on a competitive basis, to help defray costs of student attendance.

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 and Oliver Ryder

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

KansasCity ArthropodGenomics Jun10-13 AbstractDeadline

Arthropod Genomics: New Approaches and Outcomes
4th ANNUAL ARTHROPOD GENOMICS SYMPOSIUM June 10 - 13, 2010, in Kansas City, USA Symposium Website: www.k-state.edu/agc/symp2010

We welcome your participation in the 4th Annual Arthropod Genomics Symposium!

We have added two new features to the Symposium website: 1) A list of registered participants, and 2) Roommate matching.

You still have time to register and make arrangements to attend!!!

Deadlines:

Wed., May 19 Poster Abstract Submissions: Six platform presentations will be chosen from submitted

poster abstracts.

Please follow GUIDELINES < <http://www.k-state.edu/agc/abstracts/AbstractGuidelines.pdf> > posted to symposium website.

Wed., May 19 Hotel Reservations at the KC Marriott on the Plaza

Wed., May 19 Registration: Registration will continue to be accepted after May 19, if space is available.

REGISTRATION: The registration fee is \$395 (\$225 for graduate and undergraduate students) on or before Wednesday, May 19, and will include a welcome reception Thursday evening, breakfast and lunch on Friday and Saturday, and breakfast on Sunday.

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

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

FUNDING AGENCY PRESENTATIONS:

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

Alan Christensen, NSF Adriana Costero, NIAID, NIH Mary F. Purcell-Miramontes, USDA, NIFA

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

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

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

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

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

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

Keynote Speaker: Nora J. Besansky University of Notre Dame Population genomics of adaptation and speciation in malaria's vector

Featured Speakers: *Michael Akam, University of Cambridge, United Kingdom The genome of the Geophilomorph centipede, *Strigamia maritima*

*Scott J. Emrich, University of Notre Dame Opportunities and challenges of non-model transcriptome sequencing: From corn to wild butterflies and moths

*Matthew Hudson, University of Illinois at Urbana-Champaign Exploring the evolution of social behavior using genome sequencing and analysis

*Anthony A. James, University of California Message in a bottle, using whole genome expression analyses to fight vector-borne diseases

*Michael R. Kanost, Kansas State University Functional genomics of cuticle sclerotization in *Tribolium castaneum*

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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>

Lyon SMBE2010 Domestication Genomics Call Abstracts

This is a call for abstracts submission for the symposium "The Genomics of Domestication" at the SMBE2010 meeting in Lyon, France, 4-8 July 2010. See details at <http://smbe2010.univ-lyon1.fr/en/pages/-smbe2010-the-genomics-of-domestication>. Abstracts should be submitted by April 23rd through the conference website: <http://smbe2010.univ-lyon1.fr>. The Genomics of Domestication

Organizers: Adam R Boyko (Stanford Univ, USA) and Carlos D Bustamante (Stanford Univ, USA)

The exemplary role of domesticated organisms in elucidating evolutionary mechanisms has been appreciated ever since Darwin first present the theory of evolution in *Origin of Species*. Extreme and rapid changes in morphology, behavior and ecology have accompanied the process of domestication in dozens of animal and plant species. With the application of next-generation genotyping and sequencing technologies to a diverse set of domesticated species, we are now poised to develop a comprehensive understanding of the genomic impact of domestication. This symposium will focus on both in-depth genomic analysis from specific domestic plant and animal lineages as well as comparative research into general demographic patterns and selective processes affecting domesticated species.

Key words: Artificial selection, Selective sweep, Population structure, Genetic architecture, Introgression

Invited speakers: Michael Puruggannan (New York University, USA) Population genomics of plant domestication: Lessons from rice

Stephen O'Brien (National Institutes of Health, USA) The cat's out of the bag: the domestic feline genome project and its implication for domestication genomics

Adam R Boyko (Stanford University School of Medicine, USA) Village dog population genomics reveals complex history of domestic dogs

Adam R Boyko 327A Alway Hall Department of Genetics Stanford University School of Medicine Stanford, CA 94305 +1-650-723-2353 aboyko@stanford.edu

Adam Boyko <arboyko@gmail.com>

**Lyon SMBE2010
Eukaryotic Lateral Transfer
Call Abstracts**

CALL FOR ABSTRACTS

Symposium “Horizontal Transfer in Eukaryotic Genome Evolution” <http://smbe2010.univ-lyon1.fr/en/pages/smbe2010-horizontal-transfer-in-eukaryotic-genome-evolution> SMBE meeting, Lyon, France, 4-8 July 2010

Submit abstracts until April 23rd through the conference website: <http://smbe2010.univ-lyon1.fr> Organizers: Cedric Feschotte (University of Texas at Arlington, USA) Irina Arkhipova (Marine Biological Laboratory, USA)

Abstract: Recent advances in sequence analysis of eukaryotic genomes bring to the forefront their potential to be shaped by horizontal transfer (HT), which has long been recognized as a major force in prokaryotic genome evolution, but was under-appreciated in eukaryotes. This symposium will provide a unique opportunity to bring together researchers exploring the pathways and complexities of HT in a wide range of eukaryotes, including protists, plants, fungi and animals. Topics include, but are not limited to, mechanisms and consequences of HT, diversity of donors and recipients, role of biological interactions (e.g. endosymbiosis, parasitism) in facilitating HT, relative contribution of ecological, behavioral, and genomic factors to HT, and the ways by which various genetic elements, non-mobile as well as intrinsically mobile, can cross germline barriers, adapt to new genomic environments, shape genomic landscapes, and bring about evolutionary changes. Invited talks will be focused on gene transfer in microbial eukaryotes, possible mechanisms and environmental factors involved in massive HT in bdelloid rotifers, and the role played by viruses and parasites in lateral transmission of transposable elements across a wide range of animal taxa, including insects and vertebrates.

Key words: Lateral transfer, reticulate evolution, transposable elements

Invited speakers:

Jan Andersson (Uppsala University, Sweden) Lateral gene transfer and adaptation in microbial eukaryotes

Ellen Pritham (University of Texas at Arlington, USA)
The role of viruses and parasites in horizontal transposon transfer across eukaryotes

Irina Arkhipova (Marine Biological Laboratory, USA)
How do foreign genes make their way into the genomes of bdelloid rotifers?

We hope to select one or two abstracts as contributed talks. Others abstracts will be considered for poster session.

Best regards,

Cedric Feschotte, Ph.D Associate Professor Department of Biology UT Arlington Box 19498 - TX 76019
Phone: 817 272-2426 <http://www3.uta.edu/faculty/-cedric> cedric@uta.edu

**Lyon SMBE2010
Evolution Health Medicine
Call Abstracts**

This is a call for abstracts submission for the symposium “Evolution in Health and Medicine” at the SMBE2010 meeting in Lyon, France, 4-8 July 2010. See details at:

<http://smbe2010.univ-lyon1.fr/en/pages/smbe2010-host-population-genetics-natural-selection-and-immunity> Abstracts should be submitted by April 23rd through the conference website: <http://smbe2010.univ-lyon1.fr> . Evolutionary biology in health and medicine Organizers Joel Dudley (Stanford University School of Medicine, USA) Atul Butte (Stanford University School of Medicine, USA) Sudhir Kumar (Center for Evolutionary Medicine & Informatics, Biodesign Institute, USA)

Abstract Evolutionary biologists have long been interested in deciphering the role of evolution in the understanding of molecular processes underlying human disease. However, the application of evolutionary knowledge in medicine has only just recently begun to gain prominence among medical educators and practitioners. In the emerging post-genomic era, there is a proliferation of novel applications of evolutionary tools, theory and methods towards a unifying evolutionary perspective linking this basic science to medical knowledge. Today, molecular evolution is playing a pivotal role in understanding the molecular and demographical phenomena giving rise to deleterious mutations underlying monogenic and complex human diseases, offer-

ing insights into novel neurological and metabolic traits in humans and their associated disorders, and reshaping our understanding of the human immune system as an emergent evolutionary system. As the medical community begins its dialog and efforts towards the incorporation of evolutionary biology into medicine, the evolution community has an opportunity to contribute towards this integration in order to facilitate advances in the diagnosis, prognosis and treatment of human disease. Through this symposium, we seek to build on the gaining momentum at the nexus of evolutionary biology and medicine, and to further establish the central importance of evolutionary biology into the mainstream of medical discovery, practice and education.

Key words Disease, Health, Medicine, Translational, Bioinformatics

Invited Speakers

Joel Dudley (Stanford University School of Medicine, USA) Evolution as a Catalyst for Genomic Medicine

Shamil Sunyaev (Harvard Medical School, USA) TBA

James Sikela (University of Colorado Denver School of Medicine, USA) DUF1220 domains: linking cognitive disease and human brain evolution

jdudley@stanford.edu

Lyon SMBE2010 HostPopGenetics CallAbstracts

This is a call for abstracts submission for the symposium “Host Population Genetics: Natural Selection and Immunity” at the SMBE2010 meeting in Lyon, France, 4-8 July 2010. See details at <http://smbe2010.univ-lyon1.fr/en/pages/smbe2010-host-population-genetics-natural-selection-and-immunity> Abstracts should be submitted by April 23rd through the conference website: <http://smbe2010.univ-lyon1.fr> . Host Population Genetics: Natural Selection and Immunity

Organizers Brian Lazzaro (Cornell University, USA)
Lluis Quintana-Murci (Institut Pasteur, FRANCE)

The evolutionary dynamics of host-pathogen interactions lead to constant selection for adaptation and counter-adaptation in the two competing species. Throughout evolution, animals and plants have developed complex immune defence mechanisms to combat microbial infections. The past few years have seen an explosion of studies aiming to understand the effects

of natural selection in the genomes of different organisms. This interest has been particularly bolstered by the advent of genome-wide surveys of genetic variation based on genotyping or resequencing data from different populations and species, the expanding repertoire of complete genome sequences from several species, and the development of theoretical models in population genetics. In the context of infection, identifying the extent and type of natural selection acting upon genes involved in immunity and host-pathogen interactions can provide insights into the mechanisms of host defense mediated by them as well as delineate those genes being essential in host defenses with respect to those exhibiting higher immunological redundancy. This symposium aims to cover the latest findings in this field, to put together population genetics research coming from different species (from plants to insects and mammals), and to promote discussion on whether the way natural selection targets the different players of immune systems (receptors, adaptors, effectors, etc) is shared, or not, between species.

Key words host-pathogen interactions, adaptation, immune system, parasites, polymorphism

Invited Speakers Peter Parham (Stanford University, USA) Co-evolution of MHC Class I and Killer-cell Immunoglobulin-like Receptors in Simian Primates

Darren Obbard (University of Edinburgh, UK) Patterns of adaptive substitution in Drosophila: the role of parasites and pathogens

Luis Barreiro (University of Chicago, USA) Phenotypic Evolution of Innate Immune Responses in Humans and Non-human Primates

Lluis QUINTANA-MURCI UP Human Evolutionary Genetics, CNRS URA3012 Institut Pasteur 25, rue du Dr. Roux 75724 Paris Cedex 15 France

Tel: +33 1 40 61 34 43 Fax: +33 1 45 68 86 39 e-mail: quintana@pasteur.fr

Lluis QUINTANA-MURCI <quintana@pasteur.fr>

Lyon SMBE2010 IntegrativePhylogenomics CallAbstracts

Dear all,

This is a call for abstracts submission to the symposium on “Integrative phylogenomics: from genes to organis-

mal history” at the SMBE2010 meeting which takes place this summer in Lyon, France, 4-8 July 2010.

Abstracts are to be submitted until April 23rd through the conference website:<http://smbe2010.univ-lyon1.fr>. see details at <http://smbe2010.univ-lyon1.fr/en/pages/smbe2010-integrative-phylogenomics-from-genes-to-organismal-history> Integrative phylogenomics: from genes to organismal history

Organizers ***Vincent Daubin*** (Université Lyon1, FRANCE) ***Bastien Boussau*** (UC Berkeley, USA)

Abstract The traditional approach to studying genomes, starting from raw sequences, goes through largely independent steps: annotation and inference of sequence homology based on similarity, alignment of homologous genes or genome segments, single gene phylogeny and extrapolation to the underlying phylogeny of organisms, examination of selective pressure acting on genes, inference of correlations between life history traits, etc... However, all these levels of analysis depend on each other and the failure to model this dependence can result in the accumulation of errors. For instance, phylogenies are generally either inferred independently from single genes, or inferred from the concatenation of several genes. None of these approaches takes into account the fact that, for several biological reasons, gene histories are both unique and correlated with each other. The development of new statistical approaches coupling inferences at different levels of analysis and using whole genomes, allows explicit modeling of the influence of several evolutionary processes on the structure of data. The symposium will attempt to cover recent developments in this area, such as the simultaneous inference of gene trees and alignments, the concomitant reconstruction of gene trees and organism trees under models of coalescence, gene duplication and loss, or lateral gene transfers, and the joint reconstruction of sequence evolution and life history traits.

Key words Integrative Phylogenomic approaches, models of gene and genome evolution, simultaneous inference of gene trees and species trees, tree reconciliation.

Invited Speakers

Noah Rosenberg (U. of Michigan, USA) Genome-scale properties of species tree inference algorithms under the multispecies coalescent

Jens Lagergren (KTH Stockholm, Sweden) Estimation of gene trees under duplication/transfer model

Nicolas Lartillot (U. de Montréal, Canada) Molecular evolution, divergence dates, and the evolution of phenotypic and life-history traits.

Vincent Daubin Bioinformatique et Génomique Evolutive | Bioinformatics and Evolutionary Genomics Laboratoire Biométrie et Biologie Evolutive | Biometry and Evolutionary Biology Dept. 43 Bld du 11 Novembre 1918 69622 Villeurbanne cedex FRANCE

Phone: 33+ 4.26.23.44.74 Fax: 33+ 4.72.43.13.88

Vincent Daubin <daubin@biomserv.univ-lyon1.fr>

Lyon SMBE2010 Jul4-8 AwardsDeadline

Dear all,

The deadline for applying to the SMBE awards (undergraduate mentoring program, travel awards and the Fitch prize) is approaching (April 10th).

If you are interested, visit the SMBE 2010 website for more details (see the Awards section) and submit your application through the registration platform: <http://smbe2010.univ-lyon1.fr/en> With best regards,

Gabriel Marais & Manolo Gouy, On behalf of the SMBE 2010 Organizing Committee

Dr Gabriel Marais

Bioinformatics and Evolutionary Genomics Biometry and Evolutionary Biology Dpt. (UMR 5558) University of Lyon 1 Mendel's building, 16 rue Raphael Dubois 69622 Villeurbanne cedex France

Tel: (+33) (0) 4 72 43 29 09 Fax: (+33) (0) 4 72 43 13 88

Email: marais@biomserv.univ-lyon1.fr Web site: <http://lbbe.univ-lyon1.fr/> Gabriel Marais <gabmarais@gmail.com>

Lyon SMBE2010 Jul4-8 EvolvabilitySymposium

Dear Evoldir readers,

We invite submissions of abstracts for the “Evolvability and the Origin of Novelty” symposium at the SMBE2010 Conference July 4-8 in Lyon. A description of the symposium follows. Abstracts will be accepted

through April 23 at the conference web site:

<http://smbe2010.univ-lyon1.fr/en> Organizers Joanna Masel (University of Arizona, USA) Susan Rosenberg (Baylor College of Medicine, USA) Mark Siegal (New York University, USA)

Invited Speakers Lilach Hadany (Tel Aviv University, Israel) Christophe Herman (Baylor College of Medicine, USA) Andreas Wagner (University of Zürich, Switzerland)

Abstract A remarkable aspect of evolution is that it works at all. “Mutations” to single characters in a computer program essentially never improve its function, but a small but still significant proportion of mutations to DNA do. Many features have been proposed to explain the high evolvability of biological systems, including robustness, modularity, sex and recombination, and a wide variety of molecular mechanisms, including many that create correlations between the quantity of available variation and the degree of stress. This symposium will bring together researchers exploring each of these putatively general explanations for evolvability, as well as those investigating case studies of innovation.

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

212-998-7908 mark.siegal@nyu.edu <http://homepages.nyu.edu/~ms4131> mark.siegal@nyu.edu

Lyon SMBE2010 Jul4-8 Recombination

Dear Evoldir readers,

We invite submissions of abstracts for the “Recombination and genome evolution” symposium at the SMBE2010 Conference July 4-8 in Lyon. A description of the symposium follows. Abstracts for oral presentations will be accepted through April 23 at the conference web site:

<http://smbe2010.univ-lyon1.fr/en> Organizers: Laurent Duret (CNRS, Université de Lyon 1, France)

Matt Webster (University of Uppsala, Sweden)

In sexual eukaryotes, homologous chromosomes exchange genetic information through recombination during meiosis. Meiotic recombination is considered to be

a fundamental process for two reasons: first, in many taxa crossovers are required for the proper segregation of chromosomes during meiosis; second, crossovers create new combinations of alleles, and hence contribute to increase the genetic diversity on which selection can act. Moreover, there is evidence that recombination can strongly affect genome evolution via non-adaptive processes (mutation or biased gene conversion). Besides, it is known that recombination rates vary at different scales - across genomes, between sexes and between taxa. However, the determinants of the evolution of recombination are still poorly understood. The purpose of our symposium is to provide a forum for recent work on the impact of recombination on genome evolution (via selective or non-adaptive processes) and on the evolution of recombination. We propose to bring scientists together from both theoretical and data analysis lines of research.

Invited Speakers: Molly Przeworski (University of Chicago, USA)

Nicolas Galtier (CNRS, Université de Montpellier, France)

Simon Myers (University of Oxford, UK)

Matt Webster <matthew.webster@imbim.uu.se>

Lyon SMBE2010 Metapopulation- DemographySelection

Dear Evoldir members,

This is a call for abstracts to be submitted to the symposium on “Demography and selection in metapopulations” at the SMBE meetings this summer in Lyon, France, 4-8 July 2010.

Abstracts are to be submitted until April 23rd through the conference website: <http://smbe2010.univ-lyon1.fr> For the description of the symposium (<http://smbe2010.univ-lyon1.fr/en/pages/smbe2010-demography-and-selection-in-metapopulations>):

Invited speakers:

Laurent Excoffier (University of Bern, Switzerland) “Detecting selection in subdivided populations”

Stephen Wright (University of Toronto, Canada) “Demographic history and directional selection associated with the evolution of selfing in *Capsella*”

Aurélien Tellier (Ludwig-Maximilians University, Mu-

nich) “Demography vs selection: Evolutionary history of wild tomatoes”

Abstract Most, if not all, species are characterized by a spatial population structure, i.e. demes connected by migration. Spatial structuring is a prerequisite for local adaptation to exist. On the other hand, metapopulation structure and past demographic events are known to affect the ability to detect signatures of selection in genomic data. It is therefore important to analyze the signature of neutral processes depending on the metapopulation structure and demography before attempting to detect local adaptation. This symposium will be dedicated to novel theoretical and empirical studies aiming to infer the metapopulation structure and past demography of natural populations. The symposium will also focus on presenting new methodological developments to infer local adaptation from genomic data and presents successful case studies. We plan to discuss how to quantify local adaptation at candidate genes, and the level of purifying selection at the population level. Contributions from animal and plant systems will be welcome.

Key words Spatially structured populations, selective sweeps, balancing selection, purifying selection

Best regards,

Aurelien TELLIER and Wolfgang STEPHAN University of Munich LMU, Germany

Dr Aurelien TELLIER LMU University of Munich LMU Biocenter Grosshaderner Strasse 2 82152 Planegg-Martinsried Germany

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tellier@zi.biologie.uni-muenchen.de

Lyon SMBE2010 Symposium ProkEvolGenomics CallAbstracts

Dear Evoldir members,

This is a call for abstracts to be submitted to the symposium on “Evolutionary genomics of prokaryotes” at the SMBE meetings this summer in Lyon, France, 4-8 July 2010.

Abstracts are to be submitted until April 23rd through the conference website: <http://smbe2010.univ-lyon1.fr> . For the description of the symposium (<http://smbe2010.univ-lyon1.fr/en/pages/smbe2010->

evolutionary-genomics-of-prokaryotes):

Invited speakers: Julian Parkhill (Wellcome Trust Sanger Institute, UK) High-throughput sequencing of microbial populations.

Angus Buckling (University of Oxford, UK) Coevolution between bacteria and phages

Balasz Papp, Hungarian Academy of Sciences, Hungary Evolutionary systems biology of microbial metabolic networks

The now routine generation of genomic sequence datasets has transformed our understanding of the dynamics of molecular evolution in prokaryotes, and is providing ever more detailed insights into the emergence, spatial structuring, specialisations and interactions between different bacterial lineages in nature. We are now beginning to understand the trade-offs involved in determining bacterial lifestyle choices: To be a specialist or a generalist? A pathogen or a commensal? To cooperate or to cheat? This symposium captures the continuing erosion of the barriers between comparative genomics, population genetics, biogeography, metagenomics and experimental evolution to explore how bacteria adapt in the face of shifting selective landscapes. Four different threads are combined: i) Comparative genomics overview on how molecular processes (e.g. gene transfer) impact on ecological adaptation, ii) how ecology in turn impacts on sequence evolution iii) detecting the adaptive basis underlying bacterial diversity using metagenomics, and iv) identifying the molecular basis of adaptation in experimental systems. The symposium is deliberately broad, as the synthesis of these threads into a single symposium will provide an opportunity to explore fundamental aspects of bacterial micro-evolutionary dynamics at the intersection between ecological and molecular processes. A comparative genomics overview at the start of the session will highlight the role of horizontal transfer in the exploitation of new niches. The role of stochastic forces, in particular relating to the effective population size and selective sweeps, will also be considered in the context of ecological specialisation and host adaptation. The inclusion of experimental evolution will add the basic question of trade-offs between cooperation and competition between populations and cells, how these trade-offs can be studied at the molecular level.

Best regards,

Eduardo Rocha (erocha@pasteur.fr) Edward Feil (bssef@bath.ac.uk)

eduardo.rocha@pasteur.fr

Lyon SMBE2010 SystemsBiology CallAbstracts

CALL FOR ABSTRACTS

Symposium on “Systems biology and the evolution of genotype-phenotype maps”.

SMBE meetings, Lyon, France, 4-8 July 2010.

Submit abstracts until April 23rd through the conference website:

<http://smbe2010.univ-lyon1.fr> . Organizers Scott Rifkin (University of California, San Diego, USA) Christian Landry (Université Laval, Québec, Canada)

Invited Speakers Mark Siegal (New York University, USA) Itay Tirosh (Weizmann Institute of Science, Israel) Olivier Tenaillon (Université Paris 7, France)

Abstract Evolution proceeds in two phases: variation is generated and then sorted into the next generation. Population genetics has repeatedly seized upon new technologies to dissect the evolutionary forces sorting genetic variation, now at a genome-wide scale. However, equally important is understanding the processes that generate variation: how mutations modify the activity and dynamics of cellular networks and how these molecular interactions mechanistically translate genetic variation into variation in phenotypes. In the last decade, detailed descriptions of the design and dynamics of many cellular networks have emerged from investigations in cell biology. In several cases, we have clear pictures of how cells integrate information about their external and internal environments to modify their physiology or organismal development. Current models of these networks explain some of their dynamic properties including robustness, thresholds, homeostasis, and bistability. These appear to be widespread features of mechanistic genotype-phenotype maps. In this symposium we will explore how systems-level molecular information can be used to investigate the evolution and structure of genotype-phenotype maps.

Christian Landry, PhD Professeur adjoint Nouveau chercheur des IRSC / CIHR New Investigator Département de Biologie Institut de Biologie Intégrative et des Systèmes Local 3106, Pavillon Charles-Eugène-Marchand 1030, Avenue de la Médecine Université Laval Québec (Québec) G1V 0A6 Canada

<http://www.bio.ulaval.ca/landrylab/research.htm>

Téléphone: 418-656-3954 Télécopieur: 418-656-7176

Christian Landry <christian.landry@bio.ulaval.ca>

McMasterU GeneticsSocietyCanada Jun17-20

Dear All,

The 53rd Genetics Society of Canada Annual Meeting will be held between June 17-20th, 2010 at McMaster University in Hamilton, Ontario, Canada. For details of the conference, please go to: <http://www.biology.mcmaster.ca/GSC2010/> . The conference is open to all geneticists/biologists, from budding young to established. It features several award presentations. There are eight student awards competitions open to all students. Of special note in this year's meeting to the evolutionary biology community are two symposia dealing with rapid evolution of genes and genetic systems. The preliminary program, including symposia speakers, is provided on the conference website.

Please don't hesitate to contact us (jpxu@mcmaster.ca or singh@mcmaster.ca) if you have any questions.

We look forward to your participation.

Cheers and best wishes,

JP Xu and Rama Singh Local Co-organizers

Jianping (JP) Xu Department of Biology McMaster University Hamilton, Ontario L8S 4K1, Canada Phone: 1-905-525-9140 ext. 27934 Fax: 1-905-522-6066 Email: jpxu@mcmaster.ca Html: <http://www.biology.mcmaster.ca/faculty/xu/xu.htm> <http://www.horizonpress.com/population-genetics> Jianping Xu <jpxu@mcmaster.ca>

Moscow MolecularPhylogenetics May18-21

Moscow State University and the Institute for Information Transmission Problems of the Russian Academy of Sciences organize the 2nd Moscow International Conference âMOLECULAR PHYLOGENETICS MolPhy-

2â, which will take place at the Faculty of Biology of Moscow State University during 18 â 21 May 2010.

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

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

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

Confirmed invited speakers:

Sudhir Kumar - Center for Evolutionary Functional Genomics, Arizona State University, Tempe AZ, USA Lecture title *«Statistics and truth in phylogenomics»*.

Dietmar Quandt - Nees-Institute für Biodiversität der Pflanzen, Bonn Universität, Germany Lecture title *«Mutational dynamics, phylogenetic structure and utility of fast evolving DNA»*.

Natalia Ivanova - Canadian Centre for DNA Barcoding, Biodiversity Institute of Ontario, University of Guelph, Canada Lecture title *«iBOL â the International Barcode of Life Project»*.

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

Igor B. Jouline - Joint Institute for Computational Sciences, University of Tennessee, Oak Ridge National Laboratory, TN, USA Lecture title *«Origins and diversification of a complex signal transduction system in prokaryotes»*.

Martin Embley - Institute for Cell and Molecular Biosciences, Newcastle University, UK Lecture title *«The archaeobacterial origins of eukaryotes»*.

Francois-Joseph Lapointe - Laboratoire d'Écologie Moléculaire et Évolution, Université de Montréal, Montréal, Québec, Canada Lecture

title *«Measuring and representing incongruence in phylogenetic forests»*.

Jane Rogers - The Genome Analysis Centre, Norwich Research Park, Colney Norwich, UK Lecture title *«Recent advances in plant genomics»*.

Wolfgang Wägele - Zoologisches Forschungsmuseum Alexander Koenig, Bonn, Germany Lecture title *«The instability of the animal tree of life: causes of error in molecular systematics»*.

Andrei Kozlov - Biomedical Center, St Petersburg State University, Russia Lecture title *«Expression of evolutionarily new genes in tumors and the possible role of tumors in evolution»*.

Harald Schneider - Natural History Museum, London, UK Lecture title *«Employing molecular phylogenetic hypotheses to reconstruct temporal-spatial events shaping the Tree of Life»*.

Hugues Roest Crolius - Laboratoire DYOGEN, Centre National de la Recherche Scientifique (CNRS), Paris, France Lecture title *«Paleogenomics in silico: reconstruction of ancestral genomes in vertebrates using gene phylogenies»*.

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

The working conference language is English.

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

roussine@yandex.ru

Muenster StressEvolution Jul14-16

Conference: Stress and Evolution Muenster, Germany, 14-16. July 2010 <http://evostress.com/> Dear Colleagues, An international conference on "Stress and

Evolution” will be held at the University of Muenster, Germany, 14-16. July 2010. The interdisciplinary conference, organized by Ruediger Paul and colleagues, will cover topics such as Evolution in stressful environments, Evolutionary and ecological functional genomics, Model systems for studies on stress and evolution, Stress genes and stress responses, Stress-induced variation. Please note that the number of participants is limited. For more information and for registration (no later than June 1), please visit: <http://evostress.com/> Best regards, Joachim Kurtz (on behalf of the organizing committee)

Prof. Dr. Joachim Kurtz

University of Muenster Institute for Evolution and Biodiversity, Animal Evolutionary Ecology Group Huefferstr. 1, D-48149 Muenster, Germany

Phone (office): + 49 251 83 21027 Phone (direct): + 49 251 83 24661 Fax: + 49 251 83 24668

joachim.kurtz@uni-muenster.de <http://ieb.uni-muenster.de/animalevolecol> joachim.kurtz@uni-muenster.de

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

Norman Oklahoma SSB Jun17-21 CallProposals

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, and our host is University of Oklahoma.

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

OregonStateU PhylogeneticInformatics Jun29-30 AbstractDeadline

This is a reminder that the deadline for submitting abstracts for full talks to the inaugural conference on Informatics for Phylogenetics, Evolution, and Biodiversity (iEvoBio) is Thursday, April 8, 2010, which less than 1 week away. Please see http://bit.ly/iEvoBio_CfA for the full Call for Abstracts and author instructions.

As another reminder, full talks are only 1 of 5 kinds of contributed content that iEvoBio will feature. The other 4 are: 1) Lightning talks (5 mins long), 2) Challenge entries, 3) Software bazaar demonstrations, and 4) Birds-of-a-Feather gatherings. The Call for Challenge entries is also open (see <http://ievobio.org/challenge.html>). Tentative submission deadlines are listed on the conference website (<http://ievobio.org/program.html#dates>).

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/iEvo>

Bio, and there is an announcement-only Google group at <http://groups.google.com/group/ievobio-announce>. You can use the group's RSS feed (see above URL), or join the group to receive announcements by email.

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)

hlapp@nescent.org

OregonStateU PhylogeneticInformatics Jun29-30 AbstractDeadline2

The deadline for submitting abstracts for full talks to the inaugural conference on Informatics for Phylogenetics, Evolution, and Biodiversity (iEvoBio) has been extended by one week to Thursday, April 15, 2010. We hope that this will give those interested in contributing sufficient time to do so.

Please see http://bit.ly/iEvoBio_CfA for the full Call for Abstracts and author instructions. We still expect to be able to notify accepted talks in time for the early registration deadline of iEvoBio (and Evolution).

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>, and there is a Google group you can join at <http://groups.google.com/group/ievobio-announce> to receive announcements.

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 Col-

orado at Boulder) Hilmar Lapp (NESCent) Cynthia Parr (Encyclopedia of Life) Michael Sanderson (University of Arizona)

hlapp@nescent.org

OregonStateU PhylogeneticInformatics Jun29-30 CallTalks

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

Lightning talks are short presentations of 5 minutes. They are ideal for drawing the attention of the audience to new developments, tools, and resources, or to subsequent events where more in-depth information can be obtained. Please also see our FAQ for more information (<http://ievobio.org/faq.html#lightning>). Lightning talks will be part of the more interactive afternoon program on both conference days.

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

Submissions consist of a title and an abstract at most 1 page long. The abstract should provide an overview of the talk's subject. Reviewers will judge whether a submission is within scope of the conference (see above). If applicable, the abstract must also state the license and give the URL where the source code is available so reviewers can verify that the open-source requirement(*) is met.

Review and acceptance of lightning talks will be on a rolling basis. The deadline for submission is the morning of the first day of the conference (June 29). Note that the number of lightning talk slots is finite, and given the high volume of submissions we experienced for full talks, the Lightning Talks track may fill up early. We cannot accept lightning talks until the open-source requirements are met, and so waiting with that until the deadline risks that the track is full by that time.

We ask all submitters of lightning talks to be willing to also serve as reviewers of such, as described above.

Lightning talks are only 1 of 5 kinds of contributed content that iEvoBio will feature. The other 4 are: 1) Full talks (closed), 2) Challenge entries, 3) Software bazaar demonstrations, and 4) Birds-of-a-Feather gatherings. The Call for Challenge entries remains open (see <http://ievobio.org/challenge.html>), and information on the Software Bazaar and Birds-of-a-Feather sessions is forthcoming.

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

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

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

hlapp@nescent.org

Portland Oregon Evolution Jun25-29 Mentors

Undergraduate Diversity at SSE/SSB: Call for Mentors.

Twenty-five undergraduates will be attending the 2010 Evolution meeting in Portland with support from the NSF-funded "Undergraduate Diversity at SSE/SSB" program (in partnership with NESCent). We invite

graduate students, postdocs and faculty members to serve as mentors to the undergraduates. Mentors take pairs of students and attend talks with them, introduce them to colleagues, network, and generally make the meetings a welcoming place for them. Although costs are not covered for mentors, it is an unusually rewarding experience. Contact Rich Kliman <rmkliman@cedarcrest.edu> if you are interested in serving as a mentor.

rmkliman@cedarcrest.edu

Portland Oregon Evolution June25-29 DeadlineExtended

Evolution 2010 The deadline for early meeting registration and for presentation title submission has been extended. You now have until April 26, 2010 to take action. www.evolutionssociety.org/SSE2010/ Thank you for your time!

Sincerely,

Bill Dahl Society for the Study of Evolution SSE - www.evolutionssociety.org/ Evolution 2010 - www.evolutionssociety.org/SSE2010/ The objectives of the Society for the Study of Evolution are the promotion of the study of organic evolution and the integration of the various fields of science concerned with evolution.

William Dahl <wdahl@botany.org>

Portland Oregon Evolution June25-29 DeadlineReminder

The Early Registration Deadline and Deadline for Talk and Poster Submission for Evolution 2010 in Portland, Oregon is coming up soon - 19 April 2010. The meeting will be held from June 25 - 29 at the Oregon Convention Center. More information can be found on the conference web site: <http://www.evolutionssociety.org/-SSE2010/Index.html> Latest News: - All campus dorms are sold out. Please support the meeting by reserving with one of the hotels sponsoring the conference. They are all within a few blocks of the registration site and are offering discount rates to at-

tendees. More information is available here: <http://www.evolutionarysociety.org/SSE2010/Lodging.html> – Register for the meeting: Registration and title submission is accomplished on two separate sites. You will create an account that will allow you to change your information, presentation details, and to purchase additional items by logging back in. Full details can be found here: <http://www.evolutionarysociety.org/SSE2010/Register.html>

cruzan@pdx.edu

Portland Oregon Evolution June25-29 DeadlineReminder 2

The Early Registration Deadline and Presentation Submission Deadlines are extended for one week until April 26, 2010

Evolution 2010 conference in Portland, Oregon, USA will be held from June 25 - 29, 2010 at the Oregon Convention Center.

Student Awards: The ASN and SSE travel award deadlines are extended to 26 April. The Hamilton award deadline is extended to 26 April The SSB Ernst Mayr Award deadline remains 19 April More information on awards and volunteer opportunities: <http://www.evolutionarysociety.org/SSE2010/Studentawards.html> AWARD AND VOLUNTEER APPLICATIONS ARE AVAILABLE WHEN YOU SUBMIT YOUR PRESENTATION

Registration and talk/poster submission is on TWO SEPARATE SITES. Register first and then login to submit your presentation.

Registration is now open: <http://www.evolutionarysociety.org/SSE2010/Register.html>

You can use links on this page to edit your badge, your personal information, and your talk/poster title or keywords.

Deadline for talk and poster title submission is now 26 April 2010. Deadline for early registration rates is now 26 April 2010.

Dorm rooms are sold out. The hotels listed on our web site are within a few blocks of the conference site and are supporting Evolution 2010. Please use these hotels: <http://www.evolutionarysociety.org/SSE2010/Lodging.html> cruzan@pdx.edu

Portland Oregon Evolution June25-29 DeadlineReminder 3

Early registration and title submission deadlines are Monday, 26 April (midnight Pacific Standard Time).

*****More campus dorm rooms are available for a limited time*****

Registration and title submission is a two-part process. Please register and pay if you have submitted a presentation title. Presentations submitted without a corresponding paid registration will be canceled.

To register, create an account and follow the instructions here: <http://www.evolutionarysociety.org/SSE2010/Register.html> cruzan@pdx.edu

Sete France AquaticAnimalDiversity Jun25-27

Symposium on Intra-specific Diversity in Aquatic Animals

We would like to bring your attention to this multidisciplinary symposium, which will be held over three days, from the 25th to 27th June 2010, at the Marine lab in Sète, France. Please follow this link for further information: <http://www.sebiology.org/meetings/Sete2010/Sete.html> We are accepting submissions for talks and posters, please note that the deadline for submitting abstracts is the 7th of May 2010.

best regards,

Nicolas Bierne David McKenzie Co-organisers

Nicolas Bierne <n-bierne@univ-montp2.fr>

ULaval CanSocEcolEvol May9-12

Canadian Society for Ecology and Evolution 2010 An-

nual Meeting, University of Laval, Québec 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<mailto:Louis.Bernatchez@bio.ulaval.ca>
Web: <http://www.bio.ulaval.ca/louisbernatchez/>
Louis.Bernatchez@bio.ulaval.ca

ULisbon Biodiversity Apr12

Dear All, We would like to announce a conference cycle on Biodiversity, starting next monday (April 12th) with Mike Rosenzweig at the Faculdade de Ciências da Universidade de Lisboa. The whole conference cycle and its venues are given below. This conference cycle is part of a larger programme, Bioeventos 2010 aiming at celebrating the International Year for Biodiversity, promoted by the Centro de Biologia Ambiental (CBA), and the Museu Nacional de História Natural (MNHN), from the University of Lisbon

Details on the whole Bioeventos programme can be found at <http://bioeventos2010.ul.pt> **FIRST CYCLE** (Grande Auditório da Faculdade de Ciências, Campo Grande, edifício C3)

Mike Rosenzweig April 12th BIODIVERSITY AND RECONCILIATION ECOLOGY Arizona, USA

Jonathan Marks May 10th HUMAN BIODIVERSITY, Charlotte, USA Ana Rodrigues May 17th BIODIVERSITY AND CONSERVATION PRACTICES, Montpellier, France Pierre-Henry Gouyon June 7th BIODIVERSITY, EVOLUTION AND GMOS, Paris, France

SECOND CYCLE (Fundação Calouste Gulbenkian, Av. de Berna) Ilka Hanski September 29th BIODIVERSITY AND HABITAT FRAGMENTATION, Helsingin, Finland Pier Luigi Nimis October 6th BIODIVERSITY AND BIOLOGICAL COLLECTIONS, Trieste, Italia Eric Chivian October 20th BIODIVERSITY AND HUMAN HEALTH Harvard, Boston, USA

The Bioeventos Committee Craig Moritz November 3rd BIODIVERSITY AND CONSERVATION GENETICS Sydney, Australia

snmagalhaes@fc.ul.pt

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AarhusU EelSpeciation

Ph.D. position - Speciation and selection in European and American eels (*Anguilla anguilla* and *A. rostrata*)

Applications are invited for a Ph.D. position at the Department of Biological Sciences, Aarhus University. The project concerns aspects of speciation and selection at the molecular level in Atlantic eels, using population genomics approaches.

European eel spawns in the southern Sargasso Sea, and the larvae are subsequently advected more than 5,000 kilometres towards the European and North African coasts. The American eel spawns in a largely overlapping region of the Sargasso Sea, but the distance to the North American coasts is considerably shorter. The two species are known to hybridize occasionally. The project aims to date the speciation event and assess whether speciation was sympatric or allopatric, based on mtDNA sequencing.

Furthermore, European eel appears to constitute one single panmictic population. Yet, adult eels are distributed throughout environments ranging from Subarctic in Northern Europe to subtropical in North Africa. Do these environmental differences invoke selection within generations that is evident at the molecular level, or is the European eel an example of remarkable phenotypic plasticity? This and other issues will be pursued by analyzing SNPs in unique samples of eel larvae collected in the Sargasso Sea along with continental samples of glass eels and adult eels.

The main supervisor of the Ph.D. student will be Michael M. Hansen, but the student will be involved in both national and international collaboration including Drs. Thomas Damm Als and Dorte Bekkevold (Technical University of Denmark), Dr. Tom Gilbert (Copenhagen University, Denmark), Prof. Louis Bernatchez (Université Laval, Quebec, Canada) and Dr. Gregory Maes (Katholieke Universiteit of Leuven, Belgium).

For more information, please contact Michael M. Hansen (mmh@biology.au.dk).

Applications must be submitted online to the Aarhus

Graduate School of Science (AGSOS): <http://science.au.dk/en/studies/phd-studies/for-applicants/-applying-for-admission/> Application deadline is 1 May and expected start date is 1 August 2010.

sender.logo Michael M. Hansen Head of Department
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“\”Michael Møller Hansen\” <mmh@biology.au.dk>

Auckland MothSpeciation

PhD studentship in the molecular basis of speciation in moths A PhD position is available to investigate the molecular basis of speciation in moths. The successful candidate will conduct their PhD research within the Molecular Sensing team at the Plant and Food Research laboratories in Auckland, NEW ZEALAND, while being enrolled through the School of Biological Sciences at the University of Auckland. The 25K p.a. three year stipend is funded by the Allan Wilson Centre in which you will be able to become an active member collaborating and interacting with other students and researchers in molecular ecology and evolution across New Zealand universities and research institutes. The research will involve the isolation, expression analysis and functional characterisation of odorant and pheromone receptors from tortricid moths to address questions of how evolution at the molecular level facilitates rapid evolution of olfactory systems at the species level.

For more information on any of these projects please contact A/Professor Richard Newcomb
Richard.Newcomb@plantandfood.co.nz

Relevant publications: Langhoff P, Rodrigo A, Authier A, Buckley T, Dugdale J, Newcomb RD (2009). DNA barcoding in endemic New Zealand leafroller moths. *Molecular Ecology Resources* 8: 711-724. Jordan MD, Anderson AR, Begum D, Carraher C, Kiely A, Authier A, Marshall SDG, Gatehouse L, Greenwood DR, Christie D, Kralicek AV, Trowell SC, Newcomb RD (2009). Odorant receptors from the horticultural pest, the light brown apple moth (*Epiphyas postvittana*) recognise important volatile compounds produced by plants. *Chemical Senses* 34: 383-394.

Richard Newcomb <Richard.Newcomb@plantandfood.co.nz>

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>

ETH Zurich FungalPopulationGenetics

PhD Position in Fungal Population Genetics

A 3-year fully funded PhD position is available at the Forest Pathology & Dendrology Group, Institute of Integrative Biology, ETH Zürich, to study the population genetics and mating behaviour of a fungal tree disease caused by the ascomycete *Chalara fraxinea* (*Hymenoscyphus pseudoalbidus*) to get insights in the evolutionary potential of the pathogen. This emerging

lethal disease attacks ash trees in Europe and caused severe losses in several countries. Moreover, it is envisaged to compare this pathogen with a cryptic sister species, which is assumed to be non-pathogenic. The project seeks to understand the origin of an emerging tree disease of major ecological impact. The work includes fieldwork, molecular studies and virulence assessments.

The applicant is expected to hold a superior University degree in Natural Sciences (biology, environmental sciences, microbiology, mycology, phytopathology or a related discipline, ideally with a good background in genetics, molecular biology and statistics), which allows entering a PhD program, and very good organizational, analytical and writing skills. Applicants should submit a letter that summarizes specific motivation, interests and relevant experience, a cv including undergraduate and masters/diploma transcripts, and contact information for 2-3 references (all as a single pdf) to: ottmar.holdenrieder@env.ethz.ch

Starting date: Ideally by the 1st of June 2010 or according to mutual agreement. Review of applications will continue until the position has been filled.

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

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> <
<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/> <
<http://www.doc.ic.ac.uk/%7Enatasha/> >

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 <mailto: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.

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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

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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<mailto:kjroe@iastate.edu>).

Kevin Roe Natural Resource Ecology and Management 339 Science II Iowa State University Ames, IA 50011 515 294-8332
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kjroe@iastate.edu

JagiellonianU 10 Adaptation

An international scientific consortium including: Jagiellonian University (coordinator), University of Exeter, VU Amsterdam and Wageningen University is opening applications for 10 PhD positions in evolutionary biology and ecology within International PhD Programme funded by Foundation for Polish Science.

Proposed topics of PhD projects: Transcriptomics of adaptation Accumulation of mutations and the robustness of genetic systems Interaction between natural and sexual selection in adaptation to novel, stressful environment Effect of pollution on genetic variation in natural populations Monitoring of metal availability thresholds causing changes in insect larval community structure in metal-contaminated stream systems Impact of industrial pollution (heavy metals) on stoichiometry of soil-litter food webs in forests Role of anti-competitor toxins in the origin and maintenance of diversity in structured microbial populations Relationship between the diversity of soil microbial communities and their resistance to different stressors Adaptations of plants and associated microorganisms to survival in heavy metal rich industrial wastes Metabolic performance and susceptibility to pollution in voles: an experimental evolution approach

Full description of the program, containing a detailed description of PhD projects offered can be found at:

<http://www.eko.uj.edu.pl/MPD> The studentships will be funded for 4 years, starting from 1st October 2010. The students will receive stipends from Foundation for Polish Science (3000 PLN/month during stay in Poland, and 5000 PLN/month during stay abroad).

Application deadline: 15 June 2010

Programme co-financed by European Union within the Innovative Economy Operational Programme 2007-2013

– Prof. Jacek Radwan Institute of Environmental Sciences Jagiellonian University ul. Gronostajowa 7 30-387 Krakow

tel. +48 12 664 6849 www.eko.uj.edu.pl/radwan Jacek Radwan <jacek.radwan@uj.edu.pl>

KULeuven Belgium Cichlid parasites

Dear Evoldir members,

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

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

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

The team: The Laboratory of Animal Diversity and Systematics has a strong expertise in neutral and adaptive evolution of fishes and their parasites, including field monitoring, experimental design, medium-throughput genotyping, the analysis of genetic, genomic, and phenotypic data with up-to-date statisti-

cal approaches. Topics addressed include phylogeny, barcoding, phylogeography, population genetics, local adaptation and rapid evolution (natural and fisheries induced), enhanced selection in aquaculture (aquaculture genomics), co-evolution between host and parasite, spatio-temporal dynamics of nursery grounds and the management of aquatic habitats. Our team comprises 6 PhD students, 4 postdocs, 2 technicians and a team leader. The historic KULeuven, founded in 1425, has a very stimulating research environment. The modern city of Leuven with its medieval roots offers a high quality of life.

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

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

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

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

MaxPlanckInst AvianEvolution

Evolutionary Genetics of Zebra Finch Mating Behaviour

A PhD position is available at the Max Planck Institute for Ornithology (MPIO) in Seewiesen (near Munich, Germany) starting around August 2010 to study

the quantitative and molecular genetics of individual differences in traits related to sexual selection in zebra finches, such as promiscuity, ornamentation and morphology.

We seek a highly motivated individual who shares our fascination with the diversity of personalities found in animals and who has a background or strong interest in some of the following fields: behavioural ecology, evolution, quantitative genetics and molecular genetics. Our research group within the Department of Behavioural Ecology and Evolutionary Genetics at the MPIO is focussed on the study of mating behaviour and its genetic basis. We are interested in the study of trade-offs and antagonistic sexual selection by looking at genetic correlations. Moreover, we combine QTL-mapping with candidate gene approaches to identify the underlying mechanisms. The work will involve measuring behaviour, ornamentation and morphology in our captive population of zebra finches that has been studied for 8 years, as well as in other captive populations and potentially also in the wild (Australia). Furthermore the work involves running quantitative genetic analyses (animal models), and creating and analysing molecular data. Enthusiasm, reliability and commitment will be more important than experience in those tasks listed. The PhD student will be expected to work independently as well as contributing to the research of the group. Initial appointment will be for three years with a possible extension for another year subject to research progress. Payment will be through a Max Planck PhD stipend. The Max Planck Society is an equal opportunity employer and encourages disabled persons to apply. The Society aims at increasing the number of women in fields where they are under-represented, and therefore encourages them to apply. Applications should include a concise statement of research interests and work experiences relevant to the project, curriculum vitae and contact details for 2-3 academic references. Please send your application as a single file (Word-doc or pdf) before June 1st, 2010 (but late applications may be considered) to our secretary Carmen Dobus (cdobus@orn.mpg.de). For further information please do not hesitate to contact Wolfgang Forstmeier (forstmeier@orn.mpg.de).

<http://www.orn.mpg.de/mitarbeiter/forstm.html> Max Planck Institute for Ornithology Eberhard-Gwinner-Str.

82319 Seewiesen, Germany

Dr. Wolfgang Forstmeier Max Planck Institute for Ornithology Dept. Behavioural Ecology & Evolutionary Genetics Eberhard-Gwinner-Strasse 82319 Seewiesen Germany Phone: ++49 - (0)

8157 - 932 346 FAX: ++49 - (0) 8157 - 932 400 E-mail: forstmeier@orn.mpg.de Homepage: <http://www.orn.mpg.de> <http://www.orn.mpg.de/mitarbeiter/forstm.html> forstmeier@orn.mpg.de

MaxPlanckInst Leipzig EvolutionaryGenet

PhD student ' Max Planck Institute for Evolutionary Anthropology.

We have an opening for a PhD student in the Department of Evolutionary Genetics at the Max Planck Institute for Evolutionary Anthropology in Leipzig.

The main focus of our lab is to shed light on the role that natural selection has played in the evolution of humans and other primates, and to understand the phenotypic consequences of selected genetic variants. We work towards the identification and characterization of genes evolving under natural selection, through both genome-wide analyses and detailed evolutionary and experimental approaches. The PhD student will work, broadly, on a project to study the influence of balancing selection in the human genome. The project is primarily based on data analysis of genome-wide and targeted diversity data, although a component of web lab (data production and/or functional assays) can be integrated. The student may also contribute to other ongoing projects in the lab and the department (http://www.eva.mpg.de/genetics/files/population_genomics.html).

We are seeking a creative and highly motivated individual with a prime interest in population genetics and evolutionary biology. Candidates should have a bachelor's or a master's degree in biology, evolutionary biology, population genetics, bioinformatics, computational biology, statistics, or related disciplines. Previous research experience, programming skills, and a strong background in population genetics, evolutionary biology, or statistics are a plus.

The student would be a graduate of the Leipzig School of Human Origins (<http://imprs.eva.mpg.de/start.html>), a multi-disciplinary program jointly run by the University of Leipzig and the Max Planck Institute for Evolutionary Anthropology. The Department of Evolutionary Genetics is a lively, stimulating, and highly collaborative place at the front of primate evolutionary genomics (<http://www.eva.mpg.de/genetics>).

The Institute is very international and English speaking. It is located in Leipzig, a nice and affordable city of 500,000 inhabitants that is the capital and major cultural center of German Saxony. Leipzig is at driving distance of Berlin (2 hours) and Prague (3 hours).

To apply send, in PDF format, a cover letter, your CV and transcripts, and the contact information of at least 2 potential referees to Aida Andrés at andresa@mail.nih.gov. Informal inquiries can be sent to the same address.

– Aida Andrés, PhD National Human Genome Research Institute National Institutes of Health

50 South Dr., MSC8002 Building 50, Room 5527 Bethesda, MD 20892

Phone: 301 594 9207 Fax: 301 496 0474 E-mail: andresa@mail.nih.gov

andresa@mail.nih.gov

MPI Gottingen HumanPopGenetics

PhD Student Position - Population Genomics

A 3-year PhD student position in Population Genomics is available in the newly formed lab of Dr. Oskar Hallatschek at the Max-Planck-Institute for Dynamics and Self-Organization in Göttingen. The student will join a young and interactive research group in evolutionary dynamics and biophysics, including theoreticians and experimentalists. We cultivate an international atmosphere and the everyday working language is English. The Max-Planck-Institute for Dynamics and Self-Organization is located close to the center of the medieval town of Göttingen. More information about the group is available on the web at: www.evo.ds.mpg.de

The goal of the P.h.D. project is to quantify genetic footprints of natural selection and demographic revolutions, and how they can be disentangled from one another: Kimura's neutral theory dominated the field of population genetics as long as sequence data was a rare commodity. The recent years of whole genome sequencing revealed quite surprisingly that standard neutral models rarely explain observed polymorphism data well. Many researchers take these deviations as ubiquitous signatures of acting natural selection. However, although standard neutral models seem to be a poor null model, the new interpretation in terms of natural selection is far from straight forward. Most models of natural selection make even more stringent assumptions

than neutral models, such as panmixia, demographic equilibrium and negligible epistatic interactions. These simplifications could well have dropped the baby with the bath water.

The situation clearly indicates that genetic data mining is ahead of our theoretical understanding of the how molecular evolution works ("population genetics was much more fun in lack of genetic data", Whitlock). What could replace the neutral theory as a null model of molecular evolution? The P.h.D. student will join our group effort to develop a new null model, which could well dependent on the species. Specifically, he or she will search for new sensible ways to disentangle natural selection from a typically unsteady demographic history. The project will pay attention to spatial aspects of evolution, epistatic selection and the previously unseen types and amounts of data of the coming years. Prior experience in population genetics modeling, molecular evolution or comparative genomics is helpful but not necessary.

The appointment will be on a temporary basis for a maximum of 4 years. The gross salary starts at approximately 1400,- per month depending on age and experience (TVöD 13/2, Stufe 1). The student is encouraged to apply at the Göttingen Graduate School for Neurosciences and Molecular Biosciences (GGNB, <http://www.ggnb.uni-goettingen.de/>). Applicants should have a master's degree or equivalent in biology, math, physics, or related fields. If you hold an excellent BSc (1st class honors) please contact us about possible accession. German is not required but international students will be offered opportunities to take German courses. Interested candidates should send a cover letter summarizing their research background and interest in the position, CV, and contact information of two potential referees as a single PDF file to: oskar.hallatschek.applications@gmail.com

Applications will be reviewed beginning May 1, 2010. Interviews will be held end of May. Starting date is summer 2010 or later. If you have any specific questions (e.g. details of the project), feel free to contact the group leader.

The Max-Planck-Institute for Dynamics and Self-Organization is an Equal Opportunity/Affirmative Action Employer and has an affirmative action policy for the disabled.

Oskar Hallatschek MPI for Dynamics and Self-Organization Biological Physics and Evolutionary Dynamics Bunsenstr. 10, D 37073 Goettingen phone: +49-551-5176-670 fax: +49-551-5176-669 <http://www.evo.ds.mpg.de/> oskar.hallatschek.applications@googlemail.com

Oslo AtlanticCodGenomics

Centre for Ecological and Evolutionary Synthesis (CEES, <http://www.cees.uio.no/>), Department of Biology, University of Oslo

PhD Research Fellow in Evolutionary Genomics Ref. no. 2010/4781. Closing date for applications: 15 May 2010.

The fellowship is for a period of up to 4 years, with 25 % compulsory work. Starting date no later than 1 October, 2010.

Job description:

The PhD fellow will be part of an international team working on the project: the phenotype-genotype gap using the sequenced genome of Atlantic cod: case studies of fishery-induced evolution and response to climatic change. The project will utilize information from the cod genome project (<http://www.codgenome.no/>) to address possible mechanisms for cod to adapt to a changing environment V be it either environmental or changes in the biotic components. For this purpose individuals from different cod populations will be screened for mutations and genome wide genetic variation associated with fisheries induced selection and/or climate changes.

This project will be coupled with the CEES Colloquium 2 programme, which is under development; in this colloquium we will gather a multidisciplinary group of scientists such as ecologists, population geneticists, theoretical biologists and molecular biologists, with the overall aim of improving our understanding of the relationship between the genotype and phenotype of cod.

Applicants may submit a project proposal for the qualifying work during the program. The project proposal should include research topic, main issues, as well as choice of theory and method.

Full announcement: <http://uio.easycruit.com/-vacancy/402445/64421?iso=no> Tore Wallem <tore.wallem@bio.uio.no>

Oslo InfectiousDiseaseEvolution

Centre for Ecological and Evolutionary Synthesis (CEES, <http://www.cees.uio.no/>), Department of Biology, University of Oslo

The fellowship is for a period of up to 4 years, with 25 % compulsory work. Starting date no later than 1 October, 2010.

Job description:

The PhD fellow will be part of an international team working on the project: Ecology and evolution of emerging and re-emerging infectious diseases of wildlife with relevance for human health; a synergistic study of plague and Lyme borreliosis. The focus of the PhD project will primarily be on Lyme borreliosis. In much of Europe with recent climate change and increases in deer abundance, ticks are spreading into new areas. Ticks can carry and transmit several agents of diseases (e.g., Lyme borreliosis and anaplasma). The recent spread and increased abundance of ticks is a major concern for human and animal welfare. It is therefore urgent to improve our understanding of the factors determining tick distribution and infestation load. From an ecological and wildlife perspective, ticks are also interesting as parasites in general can be an important factor for density dependent effects in animal populations. The aim of the PhD study is to (1) quantify the distribution of ticks in landscapes along the west coast of Norway relative to habitat (altitude, distance to coast, forest cover etc.), to determine (2) how distribution of ticks relates to migration and space of red deer and (3) how these patterns in turn explain variation in infestation load of ticks on red deer.

Applicants may submit a project proposal for the qualifying work during the program. The project proposal should include research topic, main issues, as well as choice of theory and method.

Full announcement: <http://uio.easycruit.com/-vacancy/401622/64322?iso=no> Tore Wallem <tore.wallem@bio.uio.no>

Paris PrimateConservation

Impacts of group living on primate population dynamics and extinction risk

Applications are invited for a 3-year PhD fellowship to study impacts of group living on primate population dynamics and extinction risk.

The present PhD proposal is part of a wider research

programme on Allee effects that is co-ordinated by Franck Courchamp (ANR PEXT 010 03 - RARE - Research on Allee and Rarity Effects). The project is integrated in Task 2 : Allee Effect and Social Systems. This task focuses specifically on how individual behavioural processes build up to population-scale phenomena. We propose an approach based on generic population dynamics models derived from 'first principles' operating at the individual level. This approach is largely based on the work previously developed by ourselves (Bessa-Gomes, 2004; Bessa-Gomes et al., 2003a, 2003b; Deygout et al., in press), and combines diverse types of models (matrix population models, branching processes, and individual based models). Other than explicitly accounting for behaviour, the general modelling framework also accounts for variation among individuals, namely in terms of their age, sex, and both social and breeding status. Although this work will generate general principles of wide application, we propose to use primates as main model systems, in collaboration with Dr Guy Cowlshaw (Institute of Zoology, London). Primates are an ideal model system to study group living consequences for population dynamics as they are among the most intensely social of all vertebrate species (which, linked to the threatened status of many species, makes them particularly vulnerable to Allee effects). Their social structure in general, and foraging strategies in particular, are well-studied (thus providing the necessary data for model parameterisation). Finally, over half of all primate species are threatened with global extinction (making this work of urgent practical value).

We expect that the PhD candidate may address the following questions: can group living in Primates lead to an Allee effect? To what extent this effect impacts species response to anthropogenic response, in particular, deforestation? To answer this questions, the PhD candidate is expected to combine two levels of approach: behavioural population models and comparative analysis.

Prospective candidates should have a keen interest in behavioural ecology, population dynamics and conservation science. They also need to really enjoy modelling, as most of the time that's what you'll be doing. Previous knowledge of R, C++ or Java are a plus.

Please send your application to Carmen.Bessa-Gomes@u-psud.fr and Franck.Courchamp@u-psud.fr . Attach a CV (with possible publications included), contact details of two references, and a letter (max 2 pages) with a description of your research interests and why you would be a suitable candidate for the project. The PhD project is scheduled to start in January 2011, but this start date is open to discussion. The position will

be open until filled.

For more information, please see the attached file or contact Dr Carmen Bessa-Gomes (Carmen.Bessa-Gomes@u-psud.fr)

Carmen Bessa Gomes

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Ploen Germany Evolutionary Biol

The newly founded International Max-Planck Research School for Evolutionary Biology at Ploen and Kiel (Germany) invites applications for PhD fellowships.

The graduate school is dedicated to highest level of research and training in all areas of contemporary Evolutionary Biology. It is a joint initiative of the Max-Planck Institute of Evolutionary Biology, the University of Kiel and the Leibniz Institute for Marine Sciences in Kiel (IFM Geomar). It offers a high class research environment, diversity of research approaches, competitive fellowships and it is located in the beautiful landscape of Northern Germany, in a lake district and at the shores of the Baltic Sea.

See imprs.evolbio.mpg.de for further information on the curriculum, research themes and the application details. The deadline for this round of applications is May 15, with an anticipated starting date of September 20, 2010.

The steering committee Diethard Tautz, Hinrich Schulenburg, Manfred Milinski and Thorsten Reusch

Prof. Dr. Diethard Tautz Max-Planck-Institut fuer Evolutionsbiologie Abteilung Evolutionsgenetik August-Thienemannstrasse 2 24306 Ploen (Germany)
Tel.: 04522 763 390 Fax: 04522 763 281

tautz@evolbio.mpg.de

Poitiers France Microbial Diversity

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 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 prokaryote-animal symbioses, *Nature Reviews Genetics* 9:218-229. [2] Bouchon D, Cordaux R, Grève P. 2008 Feminizing *Wolbachia* and the evolution of sex determination 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. Herbinière, 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>

Poitiers France Wolbachia Arthropods Interactions

PhD position: *Wolbachia*-Arthropods Interactions, LEES Poitiers (France)

Topic: In situ approaches of Arthropods-symbionts interactions: symbionts regulation

Wolbachia is the most widespread endosymbiotic bacterium in Arthropods, and therefore a perfect candidate for biological pest control strategies based on symbionts, coined SyBaP (Symbiont-Based Protection). Such applications rely on the controlled infection of hosts with natural *Wolbachia* strains. The latter must persist and remain confined within target hosts and host populations. The understanding of the mechanisms that regulate *Wolbachia* populations within their hosts is therefore an essential prerequisite.

Our main model is the *Wolbachia*/*Armadillidium vulgare* (woodlouse) symbiosis. The *Wolbachia* manipu-

late host sex-ratio by feminizing genetic males. They mainly colonize the ovaries and the nerve cord, but also the immune system (hemocytes, hematopoietic organs). Their biovolume per cell, quantifiable through Fluorescence in situ Hybridization (FISH), is very heterogeneous even within one organ. To identify genes involved in the symbiosis, several ESTs libraries have been constructed (ANR EndoSymbArt, subtracted cDNA libraries, bacterial challenges). The cDNAs have been affiliated to potential metabolic pathways (GO terms).

The successful applicant will take part in the selection of genes of interest involved in the metabolic pathways of processes influenced by the symbiosis: host immune response, development (embryogenesis, gonadogenesis), Wolbachia tolerance (host-symbiont communication, cellular stress, tropism). The place of these genes within the metabolic chains will designate them as privileged markers for the corresponding pathway. After checking their expression in target tissues by RT-qPCR, the successful applicant will quantify their expression in situ, at the cellular level. The fluctuation of Wolbachia biovolume will offer a natural series to highlight dose effects and expression thresholds. For all this the successful applicant will develop a mRNA fluorescence detection protocol compatible with the Wolbachia FISH detection.

The laboratory of "Ecology, Evolution, Symbiosis" (LEES) located at the University of Poitiers is a CNRS-University mixed research unit (UMR 6556). Our research activities revolve around the general theme of host-parasite associations and, more specifically, the interactions between isopod crustaceans and their intracellular bacteria Wolbachia. Two programs funded by the National Research Agency (Agence Nationale de la Recherche, ANR) are related with the proposed Ph. D. project. EndoSymbArt (EndoSymbiosis in Arthropods) aims to decipher the genetic, molecular and cellular bases that drive the dynamics and the evolution of bacterial symbioses in Arthropods. ADaWOL (Adaptive Success of Wolbachia in Arthropods) investigates host predisposition toward new Wolbachia strains and Wolbachia abilities to switch hosts.

A three-year research grant is attached to the Ph. D. project, within the Doctoral School "Environmental Sciences" Gay Lussac (<http://gaylussac.ed.univ-poitiers.fr>). 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 fluorescence microscopy and even Fluorescence in situ Hybridization 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: joanne.beriaux@univ-poitiers.fr

Application deadline: 12/05/2010.

Joanne Bertiaux <joanne.beriaux@univ-poitiers.fr>

RiceU PlantEvolution

My lab is broadly interested in the evolution and conservation of plants, often focusing on plant hybridization and mating patterns. My research program broadly aims to understand the evolutionary consequences of global climate change, species invasions, and species rarity. More specifically, I study (1) the mechanisms regulating genetic diversity, phenotypic evolution, and population demography in rare and invasive plants and (2) how evolutionary processes (hybridization, adaptation) and properties (mating systems, genetic diversity) affect the ecological function of plant populations (e.g., reproduction, extinction). As such, my research touches on a variety of sub-disciplines, including conservation biology, agricultural ecology, and population dynamics using a combination of field, greenhouse, and eco-informatic approaches. Students are expected to develop their own independent projects but will also have opportunities to collaborate on funded investigations of hybridization in North American agricultural and natural plant ecosystems.

Ryersons Chemistry and Biology department program boasts an exceptionally active and growing faculty. Areas of emphasis include environmental and molecular biology. Financial support is available for graduate students.

I am accepting applications from prospective MSc or PhD students to start a graduate program in September 2010. If you are interested, please email me (lgc@rice.edu) a statement of your research interests with your CV and the names and email addresses of at least 2 references.

Lesley Campbell <lgc1@rice.edu>

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

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

TexasAMU SystematicEntomology

Switzerland EvolutionaryGenomics

Systematic Entomology Research Assistantships at Texas A&M University

Two graduate Research Assistantships (Ph.D. preferred, M.S. considered) are available in the laboratory of Dr. John Oswald, Department of Entomology, Texas A&M University. The students will participate as the primary graduate student trainees in a 5-year NSF PEET project to train the next generation of insect systematists with specialized expertise in the family Myrmeleontidae (order Neuroptera) – the antlions. The students will undertake monographic research on selected antlion taxa, and conduct phylogenetic studies on antlions using both morphological and molecular data. The students will have opportunities to participate in a wide variety of systematics training activities, including (1) the development/refinement of skills in taxonomic monography; (2) participation in national (USA) and international field excursions [trips currently planned to Mexico, South Africa and Australia], museum visits and scientific meetings; (3) development/refinement of skills associated with the capture and analysis of data for morphological and molecular phylogenetics; and (4) contributing to the further development of the neuropteran biodiversity informatics portal the Lacewing Digital Library (<http://lacewing.tamu.edu/>).

Both assistantships will be filled for Fall Semester 2010 in the Department of Entomology at Texas A&M University.

Applicants for these positions should have a strong interest in insect systematics (both taxonomy and phylogenetics) and be working toward career goals that include a professional position in this field. Demonstrable experience and/or interest in several of the following areas will strengthen a candidate's qualifications: insect taxonomy, revisionary/monographic studies, insect morphology, molecular lab methods, phylogenetic analytical methods, systematics publications, biodiversity informatics (particularly web design & development), field experience, and international travel. A Masters degree in entomology or a related field is preferred, but not required. Previous experience working with one of the neuropterid insect orders (Neuroptera, Megaloptera or Raphidioptera) is not required. U.S. citizenship is not required. Proficiency in English and good communication skills are essential.

Applications should consist of: (1) a cover letter, (2) a curriculum vitae, (3) a statement of research experience that explains your background, specific interest in the project, and experience/interests in the topic areas outlined above, and (4) the names and contact information for at least three scientists who have agreed to serve as professional references. Interested persons should send their application documents as a single PDF or Word (.doc) document to: Dr. John Oswald at

j-oswald@tamu.edu.

The students selected for these assistantships will be required to successfully enroll as graduate students in the Department of Entomology at Texas A&M University, College Station, Texas, USA. For information on the department and the application process see: <http://insects.tamu.edu/futurestudents/grads.html>. For additional information about policies and entrance requirements pertaining to university admission see: <http://admissions.tamu.edu/graduate/default.aspx> < <http://www.uml.edu/grad/> >.

Dr. John D. Oswald (j-oswald@tamu.edu) Associate Professor Department of Entomology Texas A&M University College Station, TX 77843-2475 USA

Phone: 979-862-3507

j-oswald@tamu.edu

TexasTechU PlantEvolution

Position Announcement - Ph.D. Assistantship Plant and Mycorrhizal Ecology

I am soliciting an outstanding Ph.D. Graduate Research Assistant for Fall 2010 to investigate plant evolutionary or molecular ecology, field ecology, and/or mycorrhizal molecular ecology. The research program focuses on evolutionary, molecular and field ecology of natural populations of orchids and their fungal associates.

REQUIREMENTS 1. An M.S. degree in an ecology-based discipline in Plant or Biological Sciences, or a closely related field. 2. Background or strong interest in techniques and data analysis methods in molecular biology, i.e., DNA extraction, selecting suitable markers, PCR, molecular data analyses, sequencing, constructing and interpreting phylogenies, etc., for application toward plant population genetics and mycorrhizal diversity studies. 3. Keen attention to detail, organizational and coordination skills, and ability to communicate effectively. 4. Ability to complete all admission requirements for beginning the program in Fall 2010.

SALARY and BENEFITS Competitive salary. Varies with status (i.e., assistantship vs. fellowship).

APPLICATION Please see: <http://www.depts.ttu.edu/gradschool/admissions/how.php>

Please submit: 1. A one-page letter of application describing interests and qualifications. The applicant

should specifically address how their skills match the position description and requirements; 2. Curriculum Vitae, including names, complete address, phone, and e-mail for three references; 3. GRE scores; and 4. TOEFL scores (if applicable) to:

jjyotsna.sharma@ttu.edu

Dr. Jyotsna Sharma Department of Plant and Soil Science MS 42122, Texas Tech University Lubbock, Texas 79409; USA jjyotsna.sharma@ttu.edu 806.742.2637 (office); 806.742.1697 (labs)

“Sharma, Jyotsna” <jyotsna.sharma@ttu.edu>

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> < <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 <<mailto: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>

UBritishColumbia Okanagan PopulationGenomics

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

British Columbia Canada
 michael.russello@ubc.ca

UCD Dublin EvolutionaryBiology 2

This is the second announcement for the new “Masters in Evolutionary Biology” at UCDDublin, Ireland. This is a full-time, 12-month course on the nature, relevance and far-reaching implications of evolutionary theory. The course features an outstanding diversity of topics and approaches in current evolutionary research (both organism-based and theoretical), and innovative educational approaches, including field-work, critical discussion, museum and laboratory training, data analysis and modelling.

Further information can be found at the following link: (the link circulated previously was not correct)

<http://www.ucd.ie/lifesciences/-graduateschool/prospectivegraduatestudents/-taughtgraduateprogrammes/sbesnewprogrammes/-mscevolutionbiology/> First offers to be made by May 31st 2010 (for a September 2010 start). Please feel free to circulate this to potentially interested prospective students.

Masters in Evolutionary Biology UCD School of Biology & Environmental Science <http://www.ucd.ie/-bioenvsci/research/evolution.htm> evolution@ucd.ie

UCD Dublin EvolutionaryBiology 3

This is the third announcement for the new “Masters in Evolutionary Biology” at UCDDublin, Ireland. This is a full-time, 12-month course on the nature, relevance and far-reaching implications of evolutionary theory. The course features an outstanding diversity of topics and approaches in current evolutionary research (both organism-based and theoretical), and innovative educational approaches, including field-work, critical discussion, museum and laboratory training, data analysis and modelling.

Further information can be found at the following link: (the link circulated previously was not correct)

<http://www.ucd.ie/lifesciences/-graduateschool/prospectivegraduatestudents/-taughtgraduateprogrammes/sbesnewprogrammes/-mscevolutionbiology/> First offers to be made by May 31st 2010 (for a September 2010 start). Please feel free to circulate this to potentially interested prospective students.

Masters in Evolutionary Biology UCD School of Biology & Environmental Science <http://www.ucd.ie/-bioenvsci/research/evolution.htm> evolution@ucd.ie

Masters in Evolutionary Biology <evolution@ucd.ie>

UGothenburg ColourRadiationWeaverbirds

Graduate position: HEADING: UGothenburg.ColourRadiationWeaverbirds DEADLINE: 30 April 2010

PhD Student Position at Dept of Zoology, Univ. of Gothenburg, Sweden Colour signalling and adaptive radiation in African weaverbirds

PhD project You will use phylogenetic and comparative methods to explore carotenoid colour signals and adaptive diversification in African weaverbirds (Ploceidae, ca. 120 species). You will work in the ECCO group (Evolution of Colour Communication) and collaborate on model-based comparative methods within the faculty platform Centre for Theoretical Biology. Phylogenetic and comparative analyses are central aims, since much sequence and phenotypic data already have been collected. However, you will also (depending on your profile and skills) take part in either or both ecophysiological and behavioural (field and aviary) studies of carotenoid-based signals in species of particular interest. Biochemical (HPLC) and molecular systematic lab work is carried out in Gothenburg, field and aviary studies in Tanzania. Main international collaborators will be at the University of Cambridge, UK (molecular genetics), University of Pretoria, South Africa (comparative methods), and Sokoine University of Agriculture, Tanzania (fieldwork).

Qualifications Desirable theoretical skills include basic molecular systematics and phylogenetic comparative methods, combined with knowledge and dedicated interest in evolution, behavioral ecology and birds. Experiences with relevant software and programming skills (especially R) would be great bonuses. Desirable practi-

cal skills and experiences are basic molecular systematic (PCR, sequencing) and/or biochemical (HPLC) lab-work, field ornithology and bird handling. Field biology or at least travel experience in the tropics is also valuable. Excellent written and spoken English is essential, as are social competence and cooperative ability.

Starting in June 2010 (subject to negotiation), the successful candidate will be awarded a full-time study grant ('utbildningsbidrag') for two years, followed by two additional years on a full-time doctoral studentship ('doktorandtjänst'). Normally, the PhD student will be expected to devote 20% of their time to undergraduate teaching, which extends the PhD appointment to five years in total.

Web sites:

www.zoologi.gu.se/forskning/Ekologisk+zoologi/-Evolution_av_f_rgkommunikation

www.ctbio.science.gu.se/english/ The application should include 1) a letter in English (one page) specifying your motivation for applying for the position, 2) Curriculum Vitae, 3) Attested copies of education and relevant work certificates, 4) Copies of thesis / publications, if any, and 5) Name and contact details of a reference person, alternatively a written letter of recommendation.

The application should be sent to: University of Gothenburg Department of Zoology Att: Ann-Sofie Olsson, Box 463 SE-405 30 Göteborg, Sweden

The application should be received by 30 April 2010. Mark the application, ref nr: B 311 138/10 -(5)

For further information on the position and how to apply, contact the main supervisor, Prof. Staffan Andersson, tel +46 (0)31-786 3647, fax +46 (0)31-41 67 29, email: staffan.andersson@zool.gu.se +46 (0)31-41 67 29, email: staffan.andersson@zool.gu.se

UHawaii Mollusc Systematics

We have National Science Foundation funding to support a graduate student at the PhD level to work on a systematic revision of the New World Ampullariidae. For full details and application instructions please go to http://www.hawaii.edu/cowielab/GA_notice.htm . - Kenneth A. Hayes, Ph.D. University of Hawaii Center for Conservation Research and Training Gilmore 408 Honolulu, HI 96822 Tel: (808) 956-0956 Fax: (808) 956-2647 Email: khayes@hawaii.edu or hayesk@si.edu

Web: <http://invertebrates.si.edu/hayes.htm> or <http://eol.org/content/page/106> "Beginning today, treat everyone you meet as if they were going to be dead by midnight. Extend to them all the care, kindness, and understanding you can muster, and do it with no thought of any reward. Your life will never be the same again." - Og Mandino

khayes@hawaii.edu

UKiel

MicrobialDiversityinNematodes

PhD position in Kiel: microbial diversity associated with nematodes

The PhD project aims at a characterization of the microbes associated with the nematode *Caenorhabditis elegans* and related species across different locations in Germany. This nematode is one of the best studied organisms under laboratory conditions; yet we still lack understanding of the conditions under which it lives in nature, including its microbial associates. Such information is essential for full understanding of the biology of this organism, including the exact function of its generally well characterized genes. The project is part of the European ESF Eurocores initiative on Ecological and Evolutionary Functional Genomics and it involves direct collaboration with research groups in The Netherlands, Belgium, and France.

This specific PhD position (payment through the DFG according to 13 TV-L/2) will be based in the recently founded Department of Evolutionary Ecology and Genetics at the University of Kiel (Northern Germany), headed by Prof. Dr. Hinrich Schulenburg. The department itself provides an international and interactive atmosphere, while Kiel University and connected institutes (e.g., Max Planck Institute in Ploen) offer a stimulating research environment with a particular focus on evolutionary biology and also *C. elegans* genetics. The city of Kiel is a medium-sized pleasant town located at the coast of the Baltic Sea. It is the capital of the most Northern state of Germany, Schleswig-Holstein. It offers many opportunities for leisure activities, including theatres, an opera, the Schleswig-Holstein classical music festival, the heavy metal festival in Wacken, sailing, surfing, cycling, and the famous festivities of the "Kieler Woche" V one of the largest sailing events in Europe.

Requirements for the position: Master or Diploma in

Biology, high motivation, excellent background in microbiology and/or ecology and/or evolutionary biology, good knowledge of statistics, handling of complex experimental set-up, teamwork, fluency in English.

Please send applications with CV, one-page statement of research interests, and the names and addresses of two referees as a single pdf-file by email to hshulenburg@zoologie.uni-kiel.de. Deadline for applications: 15th May 2010. Start of position: July 2010 or soon afterwards. Women are especially encouraged to apply. Severely handicapped people will be preferentially considered in case of equivalent qualifications. For further details + questions, send an email to hshulenburg@zoologie.uni-kiel.de. Otherwise see: <http://www.uni-kiel.de/zoologie/evoecogen/> Hinrich Schulenburg

Zoological Institute Christian-Albrechts-Universität zu Kiel Am Botanischen Garten 1-9 24118 Kiel Germany Tel: +49-431-880-4143/4141 Fax: +49-431-880-2403 Email: hshulenburg@zoologie.uni-kiel.de Web: www.uni-kiel.de/zoologie/evoecogen/ Hinrich Schulenburg <hshulenburg@zoologie.uni-kiel.de>

ULausanne PopulationGenomics

PHD POSITION IN POPULATION GENOMICS

University of Lausanne, Department of Ecology and Evolution

We are looking for a highly motivated student to work on the population genomics of the fire ant *Solenopsis invicta*. The work will include, collection of samples in South America and the US, use of a microarray that we developed in our laboratory and computational analyses of the data.

The position is for 3 years- Gross salary follows the Swiss NSF scale and is around CHF 40,000.- per year.

Our group (<http://www.unil.ch/dee/page7717.html>) is part of the Department of Ecology and Evolution, a well-funded and vibrant research institution, with superb facilities.

http://www.unil.ch/dee/page5090_en.html Inquiries and applications can be sent to laurent.keller@unil.ch. Applications should comprise a CV, a list of publications, 1 page describing why you are interested in joining our group and contact information for three referees. Only applications with all these informations will

be considered.

Laurent Keller Department of Ecology and Evolution Biophore University of Lausanne 1015 Lausanne Switzerland

http://www.unil.ch/dee/page7717_fr.html Laurent Keller <Laurent.Keller@unil.ch>

ULausanne Theoreticalbiology

PhD position at University of Lausanne:

The research project aims at modeling the evolution of dispersal patterns (rate and distance) in heterogeneous metapopulations (accounting for heterogeneity in local adaptation, size and fragmentation).

The successful applicant should have previous experience in theoretical population dynamics and/or genetics. Familiarity with individual-based simulations is a plus.

Applications should comprise, within a single pdf. file, a motivation letter, a CV, a list of publications and contact information for two referees.

The PhD position is funded by the SNF (Swiss National Science Foundation), with salary of around CHF 40,000.- per year. Lausanne is a beautiful place to live (<http://www.lausanne.ch>) Inquiries and applications can be sent to: severine.vuilleumier@unil.ch

Application deadline is May 7th 2010

Séverine Vuilleumier Department of Ecology and Evolution Biophore University of Lausanne 1015 Lausanne Switzerland http://www.unil.ch/dee/-page5090_en.html severine.vuilleumier@unil.ch

ULisbon FishHybrids

University of Lisbon (Portugal) Faculdade de Ciências
MASTER THESIS PROPOSAL 2010

Theme: Evolutionary impact of hybridization in freshwater fishes: a cytogenomic approach Supervisors: M. Rampin & MJ Collares-Pereira Place: DBA/FCUL Cytogenetics Laboratory (Building C2, 3rd floor)

Evolutionary biology is facing important challenges which include the demonstration of the actual role and extension of hybridization and polyploidy in past and present animal diversification. Comparative genome analysis has opened new insights into these old paradigms, still almost only recognized with a primary role in plants evolution. Unlike previous karyotyping even by chromosome banding, which did not allow the detection of intergenomic differentiation, comparative genome analysis by GISH (Genomic In Situ Hybridization) has opened remarkable perspectives to disclosure genome restructuring in allopolyploids. By applying this technique to the hybridogenetic *S. alburnoides* fish complex, our main goal is to investigate genome interactions and contribute to clear up the dynamics of non-sexual genomes. We are currently looking for a motivated student, who would like to integrate such ongoing research project in molecular cytogenetics.

For further information and detailed explanations contact:

Dr. Massimiliano Rampin; e-mail: mrrampin@fc.ul.pt
Prof. Maria João Collares-Pereira: mjpereira@fc.ul.pt

Dr. Massimiliano Rampin, PhD Centro de Biologia Ambiental, Departamento de Biologia Animal Faculdade de Ciências - Universidade de Lisboa Campo Grande - 1749-016 Lisboa - Portugal Freshwater Fish Group Homepage: <http://ffishgul.fc.ul.pt> Mobile Phone: +351 965537651; +39 329 169 68 03 Tel: +351 217500000 ext 22312 Fax: +351 217500028

Massimiliano Rampin <mrrampin@fc.ul.pt>

UNewBrunswick ParasitePopulationGenetics

Ph.D. project in parasite ecology and population genetics

Project: We are seeking a self-motivated PhD candidate to work on the genetics and transmission ecology of a novel Microsporidium species and its effects on populations of its host amphipod. Briefly, the amphipod is a key species in the Bay of Fundy and occupies a central position in this intertidal food web. The unnamed Microsporidium is new to science and has been hypothesized to be involved in population regulation of the host amphipod. The project will also use genetic markers to characterize the subdivision and scale of demographic independence of amphipod populations to

better understand the local evolutionary and ecological consequences of this interaction. The position is open to all candidates but those having experience in parasite ecology, ecological and evolutionary genetics, genetic techniques, and/or modelling will be given preference. The position will start in May or September 2010.

Application: If interested, please apply as soon as possible by providing a cover letter explaining your qualifications for the position, a resumé, a copy of your transcripts (it can be an unofficial copy) and names (and contact information) for 3 referees to:

Dr. Jason Addison Dept. of Biology University of New Brunswick PO Box 4400 Fredericton, N.B. E3B 5A3, Canada jaddison@umb.ca

OR

Dr. Mark Forbes Dept. of Biology Carleton University 1125 Colonel By Drive Ottawa, Ontario K1S 5B6, Canada mforbes6@gmail.com

jaddison@umb.ca

UOslo FungalEvolutionaryGenomics

PhD position in Evolutionary Genomics of Fungi

A fully funded PhD position is available at Department of Biology, University of Oslo, Norway. The fellowship is for a period of up to 4 years, with 25 % compulsory work. Starting date no later than 1 October, 2010.

The focus in the PhD project will be on evolutionary genomics of ecological transitions in a fungal lineage. In the project we want to analyse genomic changes that have accompanied ecological transitions using genome sequencing and transcriptome analyses.

Applicants must hold a Master's degree or equivalent in biology, molecular biology or related disciplines, with a strong background in bioinformatics. The applicants should possess excellent written and oral communication abilities and experience with any or all the following topics is highly desirable: molecular biology, genome sequencing analyses, gene annotation, transcriptomics, microbiology, mycology.

Closing date for applications: 15 May, 2010

For more information see <http://-uio.easycruit.com/vacancy/401638/64322?iso=no>
havard.kauserud@bio.uio.no

UParis HumanPopGenetics

Proposal for a PhD position Supervisors: Frederic Austerlitz and Evelyne Heyer UMR 7206 Eco-anthropologie CNRS/MNHN/Universite Paris 7 Equipe “genetique des populations humaines” Museum National d’Histoire Naturelle, 61 rue Buffon, Paris, France http://www.esu-psud.fr/pages_perso/spip.php?article18 <http://www.ecoanthropologie.cnrs.fr/spip.php?article300>

Inferring the history of human populations using genetic data. Link with environmental changes.

DNA polymorphism data allow the inference of some aspects of the history of human populations. Various methods have been developed, in particular the coalescent, which allow detecting demographic processes, such as migration or population growth and inferring their chronology, using genetic polymorphism within DNA sequences, SNPs and microsatellites. Other methods based on linkage disequilibrium can bring complementary knowledge on these events, allowing in particular the inference of more recent events. These methods include likelihood method and Bayesian methods, in particular the recently developed Approximate Bayesian Computation methods. The aim of this PhD position will be to apply these methods to human populations living under contrasting life styles: hunter-gatherers, pastoral nomads, sedentary farmers. The aim will be to assess whether these populations underwent demographic events whose influence may have varied because of their different life histories, and also to determine whether the resultant fluctuations in biodiversity can be linked to known environmental factors. The available data for this study will be DNA polymorphism data available in public databases, as well as data sets already available or under development within our laboratory. These data sets concern populations of pastoral nomads and farmers from Central Asia, as well as those from hunter-gatherer (pygmies) and farmers from Central Africa, two regions that went through strong climatic changes during the past millennia. The candidate should have a strong interest in population genetics, in particular on theoretical questions, and on data analysis. Training in bioinformatics would be an advantage, but this competence could also be acquired at the beginning of the PhD. For any additional information, please contact Frederic Austerlitz (frederic.austerlitz@u-psud.fr)

or Evelyne Heyer (hey@mnhn.fr). The PhD position is funded by the French CNRS. Applications must be received before April 30th 2010. Modalities are indicated on the website (in French only, but please do not hesitate to ask us for help if it is a problem, the documents can be submitted in English):

<https://www2.cnrs.fr/DRH/doctorants-10/> specific webpage for the position:

<https://www2.cnrs.fr/DRH/doctorants-10/?pid=4&action=view&id> Potential candidates are strongly encouraged to contact us before making a formal application. The successful candidate will start the position on October 1st 2010.

– Frederic Austerlitz

Charge de Recherche CNRS / CNRS researcher Laboratoire Ecologie, Systematique et Evolution UMR CNRS/Universite Paris Sud/AgroParisTech 8079 Universite Paris-Sud, Batiment 360 F-91405 Orsay cedex FRANCE tel: + 33 1 69 15 77 20 / fax: + 33 1 69 15 46 97 webpage: http://www.esu-psud.fr/pages_perso/spip.php?article26 frederic.austerlitz@u-psud.fr

UParis HumanPopGenetics 2

Proposal for a PhD position Supervisors: Frederic Austerlitz and Evelyne Heyer UMR 7206 Eco-anthropologie CNRS/MNHN/Universite Paris 7 Equipe “genetique des populations humaines” Museum National d’Histoire Naturelle, 61 rue Buffon, Paris, France http://www.esu-psud.fr/pages_perso/spip.php?article18 <http://www.ecoanthropologie.cnrs.fr/spip.php?article300>

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Charge de Recherche CNRS / CNRS researcher Laboratoire Ecologie, Systematique et Evolution UMR CNRS/Universite Paris Sud/AgroParisTech 8079 Universite Paris-Sud, Batiment 360 F-91405 Orsay cedex FRANCE tel: + 33 1 69 15 77 20 / fax: + 33 1 69 15 46 97 webpage: http://www.ese.u-psud.fr/pages_perso/-sip.php?article26 frederic.austerlitz@u-psud.fr

USheffieldOtago 2
AvianBehaviourEvolution

2 Ph-D positions, 1 Field Assistant position in Behavioural Ecology of House Sparrows - Univ. Sheffield, UK / Univ. Otago, NZ

Both PhD students will work as a team on two different topics, using our house sparrow population on Lundy Island - either on “personality and fitness consequences” or “extra-pair paternity and promiscuity networks”. There are no nationality restrictions for these PhD positions.

We are also seeking a field assistant in the same project (June - August 2010).

Requirements: We are seeking motivated and independent team players to join our house sparrow research group. The fieldwork on Lundy Island will be conducted for 4 months per year, requiring committed and collaborative individuals. Ideally, you have previous research experience, fieldwork experience, and are interested in birds and behavioural ecology. Experience in handling birds and/or a ringing licence are an advantage. For the field assistant position, they are a requirement. Funding for one PhD student is already available and for the second PhD position the amount of funding is dependent on the academic record of the applicant. The graduate positions are for 3 years, with a flexible starting date before January 2011. The supervisors are Prof. Terry Burke, Dr. Julia Schroeder (Sheffield University) and Dr. Shinichi Nakagawa (Otago University, NZ). For any further questions, contact julia.schroeder@sheffield.ac.uk.

Project 1: Personality and reproductive success in a wild passerine species In behavioural and evolutionary biology, there has been a recent explosive interest in the phenomenon known as behavioural syndromes (i.e., animal personality or consistent behavioural differences between individuals across diverse contexts). A realisation of the ubiquity of behavioural syndromes in the wild has shaken the traditional view of animal behaviour in which behavioural phenotypes are expected to be infinitely flexible so as to be adaptive in any given context. Despite much interest in animal personality research, very little is yet known about how different personalities can affect the fitness of animals. We will use a long-term monitored population of house sparrows on Lundy Island to investigate the link between fitness and personality in the wild. There are five personality traits recognised: activity, boldness, exploration, aggressiveness and sociability. We will particularly focus on the first three personality traits. Our previous studies have demonstrated that two behavioural traits, parental care and fidelity (quantified by extra-pair mating), are repeatable within individuals, meaning, for example, that some individuals express consistently high

parental care or that others are successful at gaining extra-pair paternity through their lifetime. Obviously these two traits have significant fitness consequences. A critical feature of this study is that all individuals are monitored through time and DNA profiling will be used to confirm the pedigree. Consequently, it will be possible to attach precise fitness measures to alternative behaviours. The project will therefore be among the first to investigate intricate interactions among these fitness-related behavioural traits (parental care and mate fidelity) and personality traits (e.g., activity, boldness and exploration).

Please provide us with your application online (CV, letter of motivation and two references). Only applications made through the university application system can be considered. When applying, please mention as supervisor Prof. Terry Burke: <http://www.shef.ac.uk/postgraduate/research/apply> Project 2: Understanding “promiscuity” networks in a socially monogamous species Our understanding of mating systems has dramatically changed with an introduction of molecular paternity identification methods, especially in avian species where more than 90% of species were previously thought to be monogamous. Extra-pair paternity (EPP) is ubiquitous in socially monogamous species. Despite more than 20 years of relevant research, the drivers of extra-pair paternity are still not well understood. One reason for this may be that most studies fail to consider all the parties involved in EPP: cuckolds (social males), adulteresses (social females), extra-pair males and extra-pair females (partners of extra-pair males). We propose to quantify fitness consequences of all these four parties by utilising social network analysis in conjunction with traditional regression-type approaches. Social network analysis has recently gained popularity in studying animal societies, although it has been a common tool in social sciences. This method has the potential to elucidate “promiscuity” networks in a socially monogamous species. The study will combine experimental approaches in the field with the analysis of a long-term dataset from an island population of

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USouthernDenmark EvolPlantInteractions

Header: Phd-position: Evolutionary Ecology of Plant interactions

A PhD scholarship is available in Evolutionary Ecology of plant-plant interactions, at the Institute of Biology, University of Southern Denmark. The project will focus on the importance of biotic and abiotic interactions for species co-existence and evolution of adaptation. Research will combine experimental studies under controlled conditions with field work. The successful student should have a good background in plant population/community ecology and/or population and quantitative genetics. For more information contact Bodil K Ehlers: behlers@biology.sdu.dk or see webpage <http://www.jobs.sdu.dk/> Bodil Kirstine Ehlers <behlers@biology.sdu.dk>

UTurku AvianPopulations

Open Ph.D. student post in the project on

Population growth rates of owls and kestrels in spatio-temporally varying environments for one year (12 mo).

The project is at Section of Ecology, Dept. Biol., Univ. Turku, Finland (financed by the Finnish Cultural Foundation, etc. in 2010-2011).

We have >25-yr data from fecundity (clutch size, reproductive success and age of first reproduction), natal and breeding dispersal distances, juvenile and adult survival as well as diet composition of Tengmalm's owls and Eurasian kestrels in two large study areas in western Finland. In addition, we have >20-yr data from breeding densities, reproduction rate and diet of short-eared and long-eared owls. The density estimates of main prey species of owls and kestrels have been also collected, and data from changes in habitat composition and weather conditions are also available. Therefore, these data will yield an unique possibility to comprehensively analyse effects of long-term spatio-temporal variation of the environment on numerical and functional responses of owls and kestrels. This may provide new insights for understanding ecological processes behind population dynamics.

Details on the research environment, research projects and their productivity can be found in <http://users.utu.fi/ekorpi/index.htm> The Ph.D. student will take part in the planning and execution of the project, as well as will analyse the existing long-term data, and write papers. The 1-yr post can be extended up to 4 years.

Requirements: -MSc in Biology with specialisation in ecology -theoretical interest in ecology research and experimental skills -skills to analyse data and to write mss -motivation and ambition to obtain a Ph.D. degree within 4 years.

Queries and applications (CV, list of publications, a summary of research interests and motivation for this project) to prof. Erkki Korpimäki, tel. +358-2-3335699, fax +358-2-3336550, E-mail ekorpi@utu.fi Deadline for applications is 15 May 2010. Address: Section of Ecology, Department of Biology, University of Turku, FIN-20014 Turku, Finland.

“\”Erkki Korpimäki\” <ekorpi@utu.fi>

UWyoming 2 EvolutionaryBioinfo

Ph.D. Positions in Evolutionary Bioinformatics

Positions are currently available for Ph.D. students in evolutionary bioinformatics in the Liberles Research Group at University of Wyoming. Applicants should have had coursework and/or practical experience programming in C++ and/or a scripting language (e.g. Perl) and relevant coursework in calculus, statistics, molecular biology, biochemistry, genetics, as well as an interest and coursework in evolution. The Liberles Group works in comparative genomics, and mechanistic molecular evolution, addressing (for example) how protein structure and population genetics interplay to govern protein sequence evolution. For more details on research in the Liberles Research Group, please see

<http://www.wyomingbioinformatics.org/-LiberlesGroup>.

University of Wyoming is located in Laramie, WY, 2 hours north of Denver in the rocky mountains. It is an ideal location for those with interests in skiing (both downhill and cross country), rock climbing, hiking,

To apply, please send a CV, statement of research interests, and contact information for three references, to liberles@uwyo.edu. An M.S. degree OR GRE scores

are required as well. Please indicate your experience with topics in computer science, math/stats, and biology/biochemistry as indicated above in your cover letter. Informal inquiries before application are welcome.

David Liberles <liberles@uwyo.edu>

UZurich PlantEvolution

PhD position in the molecular mechanisms of plant pollinator attraction

A position is open for a highly motivated student with a keen interest in evolutionary or ecological questions, knowledge of molecular biology and bioinformatics.

The successful candidate will be part of a team investigating the molecular basis of pollinator-mediated reproductive isolation among sexually deceptive orchids of the genus *Ophrys*. The project seeks to identify candidate genes using transcriptomics and bioinformatic approaches, and to study their molecular function by virus-induced gene silencing (VIGS) and/or experiments in *Arabidopsis*.

We offer a 3-year position as a PhD student at the University of Zurich, Switzerland, funded by the Swiss National Science Fund. The student will be part both of the Institutes of Systematic Botany and Plant Biology, located in the beautiful Botanic Gardens and within walking distance of Lake Zurich. The successful candidate will work in a young, active and interdisciplinary environment and will have access to state-of-the-art tools and techniques. The starting date is negotiable, but preferably as soon as possible.

Proficiency in English and good communication skills are essential, as is an MSc degree (or equivalent) in biology, biochemistry, or a related discipline, and the proven ability to carry out research independently. The ideal candidate would be highly motivated and well organised, with a thorough understanding of molecular biology and ample experience in molecular laboratory techniques, such as molecular cloning and RNA work (in situ hybridisation experience is a plus). Moreover, she/he would have a keen interest in evolutionary questions and experience with computer programming, bioinformatics and statistics.

Applications should consist of a CV, list of publications, a letter of motivation, and the contact details of at least two academic referees. Applications will be considered if received before 31 May 2010, or until the position is

filled. Interested persons should send applications or enquiries to Dr Philipp Schlüter, preferably by e-mail.

Dr Philipp Schlüter, Institute of Systematic Botany, Zollikerstr. 107, CH-8008 Zurich, Switzerland. E-mail: philipp.schlueter[at]systbot.uzh.ch. Telephone: +41 44 63 48328.

philipp.schlueter@systbot.uzh.ch

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/> schlotc@gmail.com

Vienna PopulationGenetics

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

WageningenU DomesticationPopula- tionGenomicsPig

PhD position at Wageningen University (Netherlands): -Genomic changes during domestication and selection of the pig'

The PhD-project -Genomic changes during domestication and selection of the pig' is part of the research project "Molecular characterization of genetic factors in the pig under selection during speciation, domestication and breeding (acronym: SelSweep). This project is a prestigious grant funded by the European Research Council (for more information see www.wi.wur.nl/-UK/newsagenda/news/p100124.htm). The ERC is the first European funding body set up to support investigator-driven frontier research. Its main aim is to stimulate scientific excellence by supporting the very best, truly creative scientists, to be adventurous and take risks in their research. The scientists are encouraged to go beyond established frontiers of knowledge and the boundaries of disciplines. Within the project the PhD student will be closely collaborating with two other PhD students and two post-docs all based at the Animal Breeding and Genomics Centre of Wageningen University (www.abg.wur.nl).

During the past decade, there has been an increasing interest in detecting genes and genomic regions that harbor regulatory elements responsible for complex disease in human and for phenotypic variation in other organisms. Ever since Darwin, domesticated species have served as models for understanding phenotypic change due to selection. The pig was domesticated around 9000 years ago from *Sus scrofa*, the wild boar, in multiple geographic distinct regions of the world. Following their domestication and subsequent episodes of selective breeding, domestic animal species have experienced strong selective pressure directed at genes controlling traits of biological, agricultural or health importance. An important and intriguing question that

you will address is, what regions and genes are affected during early domestication and breed formation. You will seek to answer this question by comparing complete genomic sequences of over 100 wild and domesticated pigs.

Animal breeders have been extremely successful in shaping natural variation by applying selection. Identification of regions that show evidence of selection within established commercial breeding lines allows a further level of resolution in the analysis of genomic regions under selection. Such footprints of selection are expected to be subtle, but provide an actual glimpse of the regions and genes affecting traits of importance for domestication and to current commercial breeding. This part of the project will be performed in close collaboration with the pig breeding industry, i.e The Institute for Pig Genetics in the Netherlands.

The animal breeding and genomics group is one of the world's leading groups in animal genomics and this project builds upon an international collaboration to sequence the porcine genome and to characterize the genetic diversity of the pig worldwide. Within the project you will closely collaborate with international experts in the field of pig genomics, genetics and evolution.

We ask

The candidate should meet the following requirements:

- A Master's degree in biology or genetics (e.g. molecular biology, population genetics, evolutionary biology).
- Strong analytical skills.
- A proven affinity with quantitative or statistical methods, either in genetics or in another field.
- Good organisational and (written and spoken) communication skills, as well as a proven ability to collaborate with others.
- Willingness to travel internationally, to attend conferences and visit other institute

Desirable: - interest in bioinformatics. - Interest in evolution and population genetics. - Interest in agriculture and domestication

We offer - A top-level research environment - Participation in the training program of the Graduate School -Wageningen Institute of - Animal Sciences' (WIAS), see www.wias.nl - Membership of a larger team of PhD-students and efficient supervision by a team of supervisors - The opportunity to spend 6 mo. at another international research institute - An excellent opportunity to develop an international scientific network

Employment basis: temporary for specified period; duration of the contract: 1.5 + 2.5 years, maximum hours per week: 38. Additional conditions of employment: To begin with, a PhD appointment for a period of 18 months. Continuation of the appointment with another

30 months will be based on performance evaluation. Gross salary per month euro 2042 in the first year rising to euro 2612 per month in the fourth year, based on a full time appointment. Start: from August/September 2010.

We are

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WageningenU PopulationGenomicsNextGenSeq

PhD position at Wageningen University (Netherlands): -Statistical analysis of whole genome re-sequencing data'

The PhD-project -Statistical analysis of whole genome re-sequencing data' is part of the research project "Molecular characterization of genetic factors in the pig under selection during speciation, domestication and breeding (acronym: SelSweep). This project is a prestigious grant funded by the European Research Council (for more information see www.wi.wur.nl/UK/-newsagenda/news/p100124.htm). The ERC is the first European funding body set up to support investigator-driven frontier research. Its main aim is to stimulate scientific excellence by supporting the very best, truly creative scientists, to be adventurous and take risks in their research. The scientists are encouraged to go beyond established frontiers of knowledge and the boundaries of disciplines. Within the project the PhD student will be closely collaborating with two other PhD students and two post-docs all based at the Animal Breeding and Genomics Centre of Wageningen University (www.abg.wur.nl).

New sequencing technologies are currently truly transforming biological and medical research. The availability of complete genome sequences of many individuals of a species or population offers, a unique view on the variation that determines why two individuals are different. However, researchers around the globe are currently

also facing the challenge of an exhausting interpretation of all this information. Within the ERC SelSweep project the genomes of more than 100 individual pigs will be completely characterized to answer questions related to speciation, domestication and selection. The analysis of such data sets and the identification of segmental duplications, SNPs and structural variants offer significant computational and analytical challenges. In a team of bioinformaticians and evolutionary genome researchers, you will focus on the implementation, development and use of tools and concepts to analyse all of that sequence data to its fullest biological extent. Particular emphasis will be on elucidating signatures of selection in the genome, on estimating past demographic parameters such as population bottlenecks, and on interpretation of patterns of divergence between wild and domesticated animals within the species *Sus scrofa*, but also between *Sus scrofa* and related pig species.

The animal breeding and genomics group is one of the world's leading groups in animal genomics and this project builds upon an international collaboration to sequence the porcine genome and to characterize the genetic diversity of the pig worldwide. Within the project you will closely collaborate with international experts in the field of pig genomics, genetics and evolution.

We ask

The candidate should meet the following requirements:
 - A Master's degree in bioinformatics or molecular biology - Strong analytical skills. - A proven affinity with quantitative or statistical methods, either in genetics or in another field. - Good organisational and (written and spoken) communication skills, as well as a proven ability to collaborate with others. - Willingness to travel internationally, to attend conferences and visit other research institutes

Desirable: - Knowledge of computer programming (e.g. Perl, Python or C++). - Knowledge of statistical genetics. - Interest in genome evolution

We offer - A top-level research environment - Participation in the training program of the Graduate School - Wageningen Institute of Animal Sciences' (WIAS), see www.wias.nl - Membership of a larger team of PhD-students and efficient supervision by a team of supervisors - The opportunity to spend 6 mo. at another international research institute - An excellent opportunity to develop an international scientific network

Employment basis: temporary for specified period; duration of the contract: 1.5 + 2.5 years, maximum hours per week: 38. Additional conditions of employment: To begin with, a PhD appointment for a period of 18 months. Continuation of the appointment with another

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Start: from August/September 2010.

We are

Wageningen UR (University and Research Centre) is an international leader in education and research. In the fields of healthy food and living environment we contribute to improving the quality of life. We are always looking for talented colleagues. Passionate people who want to put their expertise to work for tomorrow's world.

Apply now or view our other vacancies at <http://www.jobsat.wur.nl>

Additional information about the vacancy can be obtained from:

Prof. Dr. Martien Groenen

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WageningenU SpeciationGenomicsSuidae

PhD position at Wageningen University: -Genomic changes during speciation in the Suidae family'

The PhD-project -Genomic changes during speciation in the Suidae family'is part of the research project "Molecular characterization of genetic factors in the pig under selection during speciation, domestication and breeding (acronym: SelSweep). This project is a prestigious grant funded by the European Research Council (for more information see www.wi.wur.nl/UK/newsagenda/news/p100124.htm). The ERC is the first European funding body set up to support investigator-driven frontier research. Its main aim is to stimulate scientific excellence by supporting the very best, truly creative scientists, to be adventurous and take risks in their research. The scientists are encouraged to go beyond established frontiers of knowledge and the boundaries of disciplines. Within the project the PhD student will be closely collaborating with two other PhD

students and two post-docs all based at the Animal Breeding and Genomics Centre of Wageningen University (www.abg.wur.nl).

One of the most important questions in evolutionary biology pertain the mechanisms leading to speciation. The genetics behind these mechanisms is poorly understood. The fast pace of development in sequence technology now allows studying these long-standing questions from an evolutionary genomics perspective: what changes in the genome result in sexual incompatibility and how does the genome change in response to changing environment of the different species? The pig (*Sus scrofa*) is the best known member of a group of closely related species all belonging to the Suidae family consisting of at least 12 different species. In this project you will analyse whole genome sequence data for at least 4 different pig species. For each species multiple individuals will be sequenced to identify the genetic variation within each of these species. Specific research questions you will address include: 1) what is the underlying mechanisms and genomic changes that lead to speciation and 2) can differences in the genomes of these species explain the observed differences in morphological and physiological between the species?

The animal breeding and genomics group is one of the world's leading groups in animal genomics and this project builds upon an international collaboration to sequence the porcine genome and to characterize the genetic diversity of the pig worldwide. Within the project you will closely collaborate with international experts in the field of pig genomics, genetics and evolution.

We ask

The candidate should meet the following requirements: - A Master's degree in biology or genetics (e.g. molecular biology, population genetics, evolutionary biology) - Strong analytical skills. - A proven affinity with quantitative or statistical methods, either in genetics or in another field. - Good organisational and (written and spoken) communication skills, as well as a proven ability to collaborate with others. - Willingness to travel internationally, to attend conferences and visit other research institutes

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Apply now or view our other vacancies at <http://www.jobsat.wur.nl>

Additional information about the vacancy can be obtained from:

Prof. Dr. Martien Groenen Telephone number: +31 317 483747 E-mail address: martien.groenen@wur.nl

Or additional information can be obtained through one of the following links.

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Jobs

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Baja Mexico GenomicsBioinformatics

Job: CICESE. Environmental biologist with background in genomics and bioinformatics

RESEARCH PROFESSOR IN ENVIRONMENTAL BIOLOGY

The Division of Experimental and Applied Biology at CICESE, Mexico (Ensenada Center for Scientific Research and Graduate Education, www.cicese.mx), announces a full-time tenure-track position for Research Professor in Environmental Biology.

Academic profile: The applicant's education and experience must be in environmental biology, with demonstrated experience of genomics in studies of biodiversity and ecological processes, from microorganisms to flora or fauna. The applicant must be conversant in microarrays and bioinformatics, and may be able to establish links to the productive, social and public sectors for the solution of environment problems and promotion of sustainable development. Graduate teaching in the Life Sciences program and advising of thesis projects will be required. Applicants must have completed a doctoral degree and preferably have had post-doctoral experience. They must have publications in specialized, peer-reviewed, indexed publications, and be fluent in spoken and written English and Spanish.

Salary: The level of the appointment is open. Rank and salary will be determined from CICESE's statutes by prior publications and thesis advising.

Application: The application must include a letter of presentation, Curriculum Vitae, three publications and three letters of reference (sent separately). These should be sent by email to: Dr. Gisela Heckel Chair, Conservation Biology Department, CICESE email: gheckel@cicese.mx

Deadline for receiving applications is 30 April 2010.

General information on Ensenada and CICESE: Ensenada is a coastal city in northwestern Mexico, about 120 km south of the USA border, with a population of about 350,000. Its economy is diversified among industry, agriculture, education, administration, cargo port, fishing and tourism activities. The climate is mild year-round. CICESE (www.cicese.mx) is the oldest member of a system of institutes within the Mexican federal governments National Council for Science and Technology. It has 181 research professors in four divisions, plus technical staff, and 374 graduate students. Its location facilitates collaborations with various campuses of the universities of Baja California, California and Arizona.

Gisela Heckel, Ph.D. Chair, Conservation Biology Department CICESE Centro de Investigacion Cientifica y de Educacion Superior de Ensenada (Ensenada Center for Scientific Research and Graduate Education) Km 107 Carretera Tijuana-Ensenada 22860 Ensenada, Baja California Mexico

Tel. +52 646 175 05 00 X 22110 www.cicese.mx

gheckel@cicese.mx

BardCollege AssistantProfessor

The Biology Program at Bard College is seeking applicants for a full-time, two-year Visiting Assistant Professor position, beginning in the fall of 2010. The successful candidate will teach a biostatistics course one semester each year, a 100-level course each semester and an advanced seminar course one semester each year. The candidate's specific area of expertise is flexible but should complement the programs existing strengths in ecology, evolution, microbiology, molecular biology and biochemistry. The successful candidate will possess a Ph.D. and will be expected to involve undergraduates in their research. More information about the curriculum and current faculty research can be found at <http://biology.bard.edu>. Bard is a private liberal arts college with approximately 1,900 students, located 90 miles north of New York City on the Hudson River. Applicants should submit curriculum vitae, research and teaching statements, and the contact information for three references by email only to: Professor Michael Tibbetts at hr-scm10-029@bard.edu. Review of applications will begin on May 1, and will continue until the position is filled. We seek to attract and retain a highly qualified and diverse faculty. Affirmative Action/Equal Opportunity Employer.

philip johns

Assistant Professor Biology Program Bard College
Annandale-on-Hudson, NY 12504

johns@bard.edu bugs@bard.edu 845.752.2338

Philip Johns <johns@bard.edu>

BaruchCollege NY OneYear EvolutionaryBiol

ECOLOGIST / EVOLUTIONARY BIOLOGIST AT
BARUCH COLLEGE THE CITY UNIVERSITY OF
NEW YORK

We invite applications for a one-year appointment as a Substitute Instructor/Substitute Assistant Professor of

Ecology or Evolutionary Biology beginning in the Fall 2010. Applicants should have a Ph.D. (or be ABD) and a demonstrated commitment to excellence in teaching. Teaching responsibilities include lectures and laboratory sections of the introductory course, Principles of Ecology, and an upper-level lecture / laboratory course related to area of expertise. Teaching load: Substitute Instructor 15 contact hours per week per semester; Substitute Assistant Professor 12 contact hours per week per semester. Salary is commensurate with title and experience.

Applications, including curriculum vitae, statement of teaching interests, and three current letters of recommendation, which speak to teaching ability, should be sent to

Prof. John H. Wahlert, Chair Natural Sciences Department, Box A-0506 Baruch College 17 Lexington Ave., NY, NY 10010

Applications will be reviewed on receipt; the position will be open until filled. For additional information contact: john.wahlert@baruch.cuny.edu

& visit the Natural Sciences web page:
<http://www.baruch.cuny.edu/wsas/academics/-natural.science/index.htm> AN EQUAL
OPPORTUNITY/AFFIRMATIVE AC-
TION/IRCA/AMERICANS WITH DISABILITIES
ACT EMPLOYER

jason.munshisouth@gmail.com

CambridgeU FieldAssist AvianEvolution

Volunteer field assistants needed to assist multiple PhD projects on the chestnut-crowned babbler during the 2010 breeding season. Primary duties will include assisting with mist-netting and field experiments, monitoring groups for breeding activity, and data entry. The work will often require starting before dawn and days off will be irregular and dependent on the weather.

The study site is located in western New South Wales, within a research station owned and run by UNSW. The station is approximately 90 minutes' drive from the nearest settlement, and visits are generally limited to food and equipment shopping during the central part of the field season.

Successful applicants will need to be able to work in-

dependently and in a team, as well as being physically fit and having a tolerance for working in extreme environments. A positive attitude and enthusiasm for the work is essential. Previous experience working with birds would be an asset. The position would suit recent graduates from a relevant discipline that wish to develop their field experience or understanding of ecological research.

The dates of the position are approximately 15th July - 15th October with a possible extension into November depending on the quality of the breeding season. There is no salary for the position, but food and accommodation at the station will be provided. Assistants must cover their own transport costs to and from the field station.

To apply, email a letter of interest (include dates of availability), resume, and contact information for three referees to JAMES SAVAGE (jls59 AT cam.ac.uk). Applications will be reviewed as they are received; the closing date is May 31st.

james.luke.savage@googlemail.com

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 Department's 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 jkfnor@duke.edu, delivered to Julie Noor's 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 jkfnor@duke.edu

noor@duke.edu

Edinburgh LichenBiodiversity

Lichen Biodiversity Scientist £23,828 to £29,548 - Pay Band D

Applications are invited for a Lichen Biodiversity Scientist to join the Cryptogam Research Group at the Royal Botanic Garden Edinburgh.

The successful candidate will demonstrate strong potential to become a leading research scientist, with a commitment to success in publication, grant funding and student teaching/supervision. The ideal candidate will demonstrate exceptional strengths in morphological taxonomy and molecular systematics, and will be able to clearly articulate the relevance of this expertise towards issues in practical conservation.

The post holder will be expected to develop a novel research programme which builds on the legacy of taxonomic excellence at RBGE. This will make use of the well known British lichen flora - combined with modern molecular techniques to generate new insights into the pattern and process of lichen diversity. There will be opportunity to transfer research from Britain to explore aspects of global lichen diversity - particularly in reference to major focal regions for RBGE, for example Arabian Peninsula, Sino-Himalaya, SE Asia, and South America. RBGE has an existing research programme in lichen conservation biology and the post holder will be expected to champion systematics and/or molecular biology in addressing global environmental change. As well as meeting the essential criteria detailed above, applicants should also have a PhD and a current, clean driving licence.

This post attracts generous holiday entitlement and civil service pension benefits.

Applicants must be eligible to work in the UK. If the successful applicant is a resident from outwith the EU they must be able to secure their own work permit.

A full job description and person specification can be obtained from Irene Morrice on 0131 248 2814 (i.morrice@rbge.org.uk).

Applications should be made by way of CV and covering letter. Your covering letter should demonstrate excellence, including information on motivation, previous research/botanical experience and career aspirations. Applications should be sent to Irene Morrice either by e-mail or by post to the HR Department, Royal Botanic Garden Edinburgh, 20a Inverleith Row, Edinburgh, EH3 5LR. CV's must be received no later than Friday, 21 May 2010. Interviews will be held on Monday, 7 June 2010.

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

C.Ellis@rbge.ac.uk

LouisianaStateU FieldAssist BirdSongEvolution

Short-term volunteer field assistant needed to assist with song recording and behavioral experiments on white-crowned sparrows in breeding populations on the northern coast of California. Ideal assistant will have prior fieldwork and playback experience with birds.

Time period is May 9th to May 19th. All expenses, including airfare to Sacramento, will be covered.

To apply, please email a short letter stating why you are interested, a copy of your CV, including details of past field experience and any playback experience to ederry1@lsu.edu.

Elizabeth Derryberry Postdoctoral Research Associate Museum of Natural Science Louisiana State University Baton Rouge, LA 70803 Email: ederry1@lsu.edu Fax: 225 578 3075 Homepage: <http://www.museum.lsu.edu/lizhome.htm> ederry1@lsu.edu

MaxPlanckInst Leipzig BioinformaticProgrammer

Programmer/bioinformatician ' Max Planck Institute for Evolutionary Anthropology.

A research assistant position is available for a programmer/bioinformatician in the Department of Evolution-

ary Genetics at the Max Planck Institute for Evolutionary Anthropology in Leipzig. Tentative starting date is October 2010.

The main focus of our lab is to shed light on the role that natural selection has played in the evolution of humans and other primates, and to understand the phenotypic consequences of selected genetic variants. We work towards the identification and characterization of genes evolving under natural selection, through both genome-wide analyses and detailed evolutionary and experimental approaches. The programmer will have a fundamental role in the lab, with responsibilities that include the design and development of analytical tools, data management, and data analysis. S/he will work with genome-wide and targeted diversity data, and may contribute to diverse ongoing projects in the lab and the department (http://www.eva.mpg.de/genetics/files/population_genomics.html).

We are seeking a creative and highly motivated individual with a strong computational background and a prime interest in evolutionary genomics. Candidates should have good programming skills and background in bioinformatics, computer science, statistics, biology, or related disciplines. Previous research experience is a plus, as is experience with large-scale population-based genomic data, next-gen sequencing technologies, or evolutionary analysis.

The Department of Evolutionary Genetics is a lively, stimulating, and highly collaborative place at the front of primate evolutionary genomics (<http://www.eva.mpg.de/genetics>). The Institute for Evolutionary Anthropology is a multidisciplinary and very international center, and is English speaking. It is located in Leipzig, a nice city of 500,000 habitants that is the capital and major cultural center of German Saxony. Leipzig is at driving distance from Berlin (2 hours) and Prague (3 hours).

To apply send, in PDF format, a cover letter, your CV and transcripts, and the contact information of at least 2 potential referees to Aida Andrés at andresa@mail.nih.gov. Informal inquiries can be sent to the same address.

– Aida Andrés, PhD National Human Genome Research Institute National Institutes of Health

50 South Dr., MSC8002 Building 50, Room 5527 Bethesda, MD 20892

Phone: 301 594 9207 Fax: 301 496 0474 E-mail: andresa@mail.nih.gov

andresa@mail.nih.gov

MiddleburyCollege OneYearTeaching EvolBiol

ECOLOGIST/EVOLUTIONARY BIOLOGIST AT MIDDLEBURY COLLEGE.

We invite applications for a one-year appointment as an Associate in Science Instruction beginning in the Fall 2010. Applicants should have a Ph.D. (or be ABD) and a demonstrated commitment to excellence in teaching. Teaching responsibilities are the laboratory sections of the introductory course, Ecology and Evolution. Applications including a: curriculum vitae, statements of teaching interests, and two current letters of recommendation which speak to teaching ability, should be sent to the Ecology/Evolutionary Biology ASI Search Committee, Department of Biology, Middlebury College, Middlebury, VT 05753. The review of completed applications will begin on May 10, 2010. Feel free to contact Helen Young (hjyoung@middlebury.edu) for more information about the position; the department webpage is <http://www.middlebury.edu/academics/bio> Middlebury College is an Equal Opportunity Employer committed to recruiting a diverse faculty to complement the increasing diversity of our student body.

hjyoung@middlebury.edu

Munich ParasiteAdaptiveResponses

PhD position in Evolutionary Ecology (trade-offs between 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. We are using *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

NorthCarolinaStateU ResAssoc

Research Associate (AKA Ecological Tinkerer) for work on large-scale global warming experiments in North Carolina.

DESCRIPTION: We seek a person with strong technical and problem-solving skills and experience in ecology to oversee day-to-day technical work on climate chambers located at Duke Forest, near Durham, North Carolina. The chambers are part of a many collaborator, two site (Duke Forest, Harvard Forest), project to understand the effects of climate, and in particular increasing temperatures, on ant communities and the species and ecological processes that depend on them. The ideal candidate is someone who likes to tinker with

equipment and solve problems in the field, works well with others and is well organized. This position will be 70% technician/manager and 30% researcher. Scope exists for the technician to develop her or his own research projects within the context of the chamber array.

Key duties and responsibilities include: (1) Maintain climate chambers (fix broken equipment, monitor equipment, deal with problems). This work will entail knowledge and comfort with electronics, plumbing, tinkering, and, in particular, dataloggers. (2) Be in charge of day-to-day activities related to the climate chambers and research therein. (3) Assist (or if the candidate chooses, lead) ecological fieldwork. Fieldwork will include a diversity of projects, from work with leaf-litter to the collection of millipedes or even fallen bird feathers.

Salary Range: Starting at \$30,000 (plus benefits), depending on experience. This position has an initial appointment of one year, with the possibility of additional two years of additional support available, contingent on performance.

RESEARCH GROUP: The candidate would work in the lab of Rob Dunn at North Carolina State University (<http://www.antmacroecology.org/-robdund/index.html>). The lab is part of a larger lab group (the Dunn, Gross and Haddad labs) researching diverse topics from climate change to the impact of corridors on animal migration and theoretical approaches to understanding the cascading consequences of extinction. The candidate would also work with the other PIs on the project (Nathan Sanders at the University of Tennessee, Aaron Ellison at Harvard Forest and Nick Gotelli at the University of Vermont).

LOCATION: North Carolina State University, though possibilities exist for living in Durham or Chapel Hill. The position is based in the Department of Biology, a large interdisciplinary department with strong links to the research in the Genetics, Entomology and Forestry departments and also to researchers at neighboring Duke and UNC.

QUALIFICATIONS: Qualifications: MS in biology, ecology, engineering (or related disciplines) + field experience. Hire should be able to communicate well and interact with other biologists, but also students, the public, and the climate chambers, which are also known to have a mind of their own. Applicant should have demonstrated organizational abilities. The ideal candidate would be fond of tinkering with equipment in ways that better allow us to see the living world, whether that means building a new tool, dealing with plumbing or figuring out some other way to otherwise see processes and species invisible or barely visible to

the naked eye. Skills with Campbell Scientific dataloggers would also be particularly useful.

Contact: Rob_Dunn@ncsu.edu. Please send a CV along with your email.

hulcr@wisc.edu

Norway Population Genetics

Vacant research position in applied genetics:

Researcher in applied genetics

Nofima is the world leading research institute within breeding and genetics applied to aquaculture species. We are focusing increasingly on detecting and utilising genomic information with the purpose of contributing to targeted and safe genetic improvement of important species within global aquaculture production and minimise interactions with wild stocks.

Nofima is offering a research position in genetics/genomics applied to breeding in aquaculture species with focus on impact on natural populations.

The successful candidate is preferably a researcher in population genetics including molecular genetics, but with a good understanding of quantitative genetics and breeding. Important topics may be assessment of genetic impact on wild populations from escaped domesticated aquaculture species, development of genetic markers, evaluation of evolutionary forces acting on single genetic markers, individual genetic assignment, and creation of linkage maps. The work will be done in close collaboration with CIGENE; Centre for Integrative Genetics, and the Norwegian University of Life Science (UMB).

Important competence will be 1. Populations genetics theory, analytical tools, and methods 2. Bioinformatics: Handling large data sets, including genomic data 3. Fish biology 4. Molecular genetics laboratory methods Cross-discipline competence will be appreciated.

The candidate will initiate and conduct research and contribute to strategic development and positioning.

Location: The position will be located at Nofima Ås, Norway. The candidate will be a member of the Genetics&Breeding group in Nofima.

Salary: is according to qualifications and a pension deduction will be made from the salary.

Application: Is directed to our online form at <http://www.nofima.no/stilling/forsker-i-anvendt-genetikk>

[/www.nofima.no/stilling/forsker-i-anvendt-genetikk](http://www.nofima.no/stilling/forsker-i-anvendt-genetikk)

This web page is in Norwegian, but find the link “Send søknad” at the bottom of the page and you will enter an application form in English.

Contact: For further questions regarding the position or application procedure is directed to:

Dr. Kari Kolstad Phone: + 47 926 52 977 e-mail: kari.kolstad@nofima.no

Dr. Olai Einen Phone: + 47 458 66 151 e-mail: olai.einen@nofima.no

<http://www.nofima.no/> sten.karlsson@nofima.no

OceanGenomeLegacy StaffScientist

Staff Scientist I (Job Code: OGL-SS-CC)

The Ocean Genome Legacy Laboratory for Marine Genomic Research (www.oglf.org) seeks a staff scientist to participate in and manage all aspects of operation of the Ocean Genome Resource DNA and Tissue Repository. The successful candidate will have experience and general knowledge of collection management, basic techniques of molecular biology and microbiology (e.g., high throughput DNA extraction and handling, gel electrophoresis, PCR amplification, cloning, library construction, sterile technique, etc.), and excellent computer and data management skills. Knowledge of marine science, field collection, taxonomy, and systematics is also desirable. We are seeking an employee with exceptional organizational, communication, supervisory, and laboratory skills, who pays strong attention to detail and has the desire and ability to work well in a collaborative group setting. The position is available in June 2010 and offers exciting opportunities for organizational development, competitive salary and benefits, and the potential for advancement within a new academically oriented non-profit research institution.

Responsibilities of the position include:

1) Building, modifying, and maintaining the OGR collections, databases, websites, and participating in all aspects of planning, collection, acquisition, accession, preparation, preservation, identification, documentation, storage, and distribution of genome resource samples.

2) Developing research programs and scientific methodologies essential to the growth of the Ocean Genome Resource Biorepository.

3) Contributing to the broader educational, outreach, and fundraising goals of OGL.

Applicants should submit a cover letter, resume, list of publications, and contact information for at least three references by email to careers@oglf.org (referencing job code OGL-SS-ED in the subject line - required for proper processing) or by regular mail to the following address:

Daniel L. Distel Executive Director, Ocean Genome Legacy 240 County Rd., Ipswich, MA 01938 careers@oglf.org

About OGL Ocean Genome Legacy, Inc. is a publicly supported non-profit research organization dedicated to exploration, description, documentation, and preservation of the genomic diversity of the oceans. Located on the campus of New England Biolabs in Ipswich, MA. OGL is an equal opportunity employer that receives support from the National Science Foundation, the Department of Energy, and the National Institutes of Health. OGL provides a research environment that encourages creativity and career development through publication and pursuit of extramural support.

fusaro@oglf.org

SheffieldU FieldAssist AvianEvolution

We are seeking a field assistant to work on our Lundy Island house sparrow project for the time from June - August 2010.

Requirements: We are seeking a motivated and independent team player to join our house sparrow research group. The fieldwork on Lundy Island requires committed and collaborative individuals. Ideally, you have previous fieldwork experience and are interested in birds and behavioural ecology. Experience in handling birds and a ringing licence are a requirement, as is the ability to work independently.

Field work consists of nest-box monitoring, catching, handling and measuring of adults and chicks, taking blood samples, ringing and behavioural observations. Lundy is a small island in the Bristol Channel, featuring a diverse bird fauna, a marine conservation zone and magnificent wild landscape. For more information on Lundy see this website: <http://www.lundyisland.co.uk/> We offer free accommodation and food, and, depending on the level of experience, a

salary.

To apply, please email a short letter stating why you are interested, a copy of your CV, including details of past field experience and bird handling experience and a reference to julia.schroeder@sheffield.ac.uk.

julia.schroeder@gmail.com

StockholmU PlantEvolution

The Botany department at Stockholm University has a position open as University Lecturer (Lektor) in Plant Evolution

Research at the section for Plant Evolution at the Botany department deals with both evolutionary and ecological studies, and the focus is on plant population and conservation ecology, on plant-animal interactions and on landscape ecology (see www.botan.su.se for further details). The current position will be associated to the new program EkoKlim, a strategic effort towards research on the effects of climate on biodiversity and ecosystem services, together with other departments at Stockholm University

Experiences of research within the three main research topics of the EkoKlim initiative will be considered meriting:

- Climate effects. - Landscape ecology. - Plant-animal interactions

For further information see <http://www.su.se/pub/-jsp/polopoly.jsp?d=11535&a=78532> (english) <http://www.su.se/pub/jsp/polopoly.jsp?d=11535&a=78525> (swedish)

peter.hamback@botan.su.se

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

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

**UCLondon Lecturer
EvolAnthropology**

Dear all,

University College London's Anthropology department is seeking to hire a lecturer in evolutionary anthropology to join an active group of evolutionary anthropologist (<http://www.ucl.ac.uk/heeg/>).

UCL is a large and scientifically diverse place in the centre of London. The college offers great potential for collaborations, amongst others with researchers in the Centre for the Evolution of Cultural Diversity, the Centre for Genetic Anthropology, the department of Genetics, Evolution and Environment, or the Centre for Economic Learning and Social Evolution.

The official job advert is pasted below, further information is available on the UCL Human Resources job database (https://atsv7.wcn.co.uk/search_engine/-jobs.cgi?owner=5041178&ownertype=fair&jcode=1133514).

The official closing date for applications is April 30th. For informal inquiries, please contact Ruth Mace (r.mace@ucl.ac.uk).

Best regards, Max

Lectureship in Evolutionary Anthropology, UCL.

UCL Anthropology are inviting applications for a lectureship in Evolutionary Anthropology with effect from 1st September or asap thereafter. The successful applicant must hold a PhD and be able to demonstrate a strong record of research and publication. S/he will be expected to conduct research and contribute to teaching courses at undergraduate and post-graduate level with particular emphasis on the evolution of human behaviour. Applications from suitably qualified candidates specialising in human behavioural or evolutionary ecology, cultural evolution, evolutionary medicine or a related area are welcome.

Closing date APRIL 30th.

Max Reuter

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

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

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

UGuelph ResAssist PlantEvolution

Job Advertisement, Department of Integrative Biology,

University of Guelph

Research Assistant, posted March 29 2010

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

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

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

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

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

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

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

christinamariocaruso@gmail.com

UKansas Biodiversity

The Biodiversity Institute at the University of Kansas, Lawrence KS, seeks a staff research assistant in systematics and evolutionary development of Hydrozoa. Required qualifications include: bachelors degree, 1 year experience in molecular lab research, demonstrated en-

thusiasm for research in systematics, evolutionary development or invertebrate biology, ability to work independently, and with attention to lab protocols. For complete position description and application instructions visit <https://jobs.ku.edu>, position #00208310. Questions can be directed to Dr. Pauly Carwright email: pcart@ku.edu Review begins 5/15/10 EOAA employer

pcart@ku.edu

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, de-

tail 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

ULisbon ResTech PopGenetics

University of Lisbon (Portugal) CBA-FCUL (http://cba.fc.ul.pt/about/about_cba.php)

Research technician (microsatellites, population genetics)

Position Description: We seek a full-time research technician at the Center for Environmental Biology at the University of Lisbon. The position starts May, 2010 (exact start date flexible) and currently has funding for 12 months. The technician will work in the framework of landscape genetics research on several wild animal species. Tasks are fieldwork for sampling and molecular analyses of samples in the lab.

Qualifications: The successful candidate will be expected to independently perform basic molecular biology techniques such as DNA extraction, PCR, and microsatellite genotyping. A Master's degree in a relevant subject and previous experience performing molecular techniques are preferred.

Contact: for inquiries and to apply (electronic resume, cover letter, and references) email Carlos Fernandes (cafernandes@fc.ul.pt).

Closing Date: Applications will be considered as received until April 25, 2010.

Dr. Carlos Fernandes

Centre for Environmental Biology Lisbon University Building C2, 5th Floor, Room 2.5.41 1749-016 Campo Grande Lisbon, Portugal

Thomas Henry Huxley on The Origin of Species: "How extremely stupid not to have thought of that".

Carlos Fernandes <cafernandes@fc.ul.pt>

UMassachusetts Amherst LabManager EvolutionAnimalMovement

Research Fellow position available in the Patek Laboratory at the University of Massachusetts Amherst

The Patek Lab is conducting a search for a laboratory manager to assist in all aspects of laboratory experiments and day-to-day operations. Research in the Patek Lab probes the interface between physics and biology by studying the evolution of fast animal movement and communication. We examine systems such as jaw-jumping ants, sound-producing spiny lobsters and hammering mantis shrimp using tools ranging from bioacoustics and phylogenetics to high speed videography and materials testing. The Patek Lab is a member of the Biology Department and the Organismic and Evolutionary Biology graduate program at the University of Massachusetts Amherst. For more information, visit: <http://imladris.bio.umass.edu/biology/-pateklab/home> Salary and work hours: 40 hrs/wk, salary commensurate with experience Health insurance coverage provided for the Research Fellow only

Application deadline and materials Review of applications will begin on May 4, 2010 and continue until the position is filled. This position will begin at the start of the fall semester 2010 and end approximately May 31, 2011 with the possibility of extension contingent on job performance and availability of funding. To be considered for the position, applications should reference search number R38401 and be sent to Lisa Barry via email (lisab@bio.umass.edu) and include the following materials: 1) Cover letter stating why you are interested in the position and how it relates to your future career goals 2) Resume or CV 3) Three letters of reference

Examples of duties: - Assist with ongoing research projects including biomechanical measurements, materials testing, fluid dynamics, acoustic communication, and evolutionary analyses. - Assist with lab man-

agement, including working with and caring for crustaceans and other arthropods, collecting and analyzing data, entering and organizing data, maintaining and developing website materials, preparing tabular and graphical information for reports and publications, maintaining computer resources. - Provide general assistance, including photocopying, library searches, database management, running errands. - Assist with supervising laboratory experiments and training lab members. - Conduct field research in marine habitats, possibly using snorkeling or SCUBA diving.

Minimum qualifications: - BS/BA in Biology, Biological Engineering or related fields - Formal coursework in biology, calculus and physics - Experience in at least TWO of the following areas: engineering, physics, biomechanics, evolutionary/functional morphology, animal behavior, acoustics, or marine animal care - Previous undergraduate-level research experience and an interest in pursuing new research skills at a graduate level - Applicant must be dependable, organized, and motivated - Strong computing skills are needed, including basic computer programming (or a strong interest in learning how to program), word processing, spreadsheet use. - Experience in Matlab programming is preferred.

The University of Massachusetts is an Affirmative Action/Equal Opportunity Employer. Women and members of minority groups are encouraged to apply.

Erica Staaterman <estaat@bio.umass.edu>

UMassachusettsMedicalSchool Bioinformatician

BIOINFORMATICIAN Requisition 16940 Apply online at www.umassmed.edu, click "human resources" and search for req. 16940

GENERAL SUMMARY OF POSITION: Under the general direction of faculty, the Bioinformatician is responsible for the design, development, evaluation of a technical infrastructure to expedite the quantitative evaluation of data resulting from computational and laboratory studies. The position will entail the establishment and maintenance of applicable in-house bioinformatics resources and interaction with individual lab members on customized research projects, as well independent projects that are the solely computational. All functions will be under the guidance and direction of the faculty.

MAJOR RESPONSIBILITIES: * Establish general bioinformatics resources for day-to-day use by members of the laboratory. * Develop and maintain bioinformatics resources and other software solutions as needed. * Pipeline development for high-throughput analysis, such as deep sequencing. * Custom database design for the storage / retrieval of large datasets. * Provide tabular and written summaries of approaches and analyses in a form suitable for inclusion in manuscripts or grant applications, as well as media for presentation at scientific meetings. * Develop and implement custom bioinformatics programming solutions in collaboration with lab as necessary. * Coordinate and collaborate with other research computing expertise at the Medical School as necessary. * Participate in conference calls and research meetings as needed. Perform other duties as required.

MINIMUM QUALIFICATIONS: * Bachelor's degree in Computer Science or a related discipline or equivalent. * The ability to work in and support other users in a Linux environment. * Proficiency with a scripting language (e.g. Perl/Python) and/or software programming languages (e.g. C/C++/Java), in algorithm development and common bioinformatics tasks. * Working knowledge of SQL e.g. MySQL desirable. * Some web development experience in a LAMP environment using HTML, JavaScript, and CGI. * Familiarity with sequence alignment tools, practical knowledge in the use of genomic databases (UCSC, Ensembl) and familiarity with statistical analysis tools (R, Matlab). * Knowledge of Linux operating systems, shell scripting and queuing systems for parallel processing. * Experience with large scale biological data analysis would be highly desirable.

ABOUT UMMS: At the University of Massachusetts Medical School, we take seriously our mission to serve the people of Massachusetts. We do this by achieving national distinction in health sciences education, research and public service. In the area of research, UMMS has achieved world-class status. Research is conducted in the laboratory, ambulatory clinic and at the bedside, contributing significantly to medical science and to the state's economy, as well as enhancing our ability to attract outstanding faculty members for all three schools. Extramural research funding totals over \$174 million, placing UMMS in the top 40 among the nation's medical schools in funding. We are also proud to have been awarded the Nobel Prize in 2006 in Physiology or Medicine for Craig C. Mello, PhD, and his colleague Andrew Fire, PhD, of Stanford University, for their discoveries related to RNA interference.

BENEFITS AT UMMS: We offer highly competitive salaries based on experience and education. In ad-

dition, we offer an excellent benefits package including work/life balance programs consisting of meals-to-go, offsite UMass run day care centers, nursing mother rooms, lunchtime seminars, Flexible Work Options, and onsite dry cleaning drop off locations. Also, we offer state retirement, generous time off policies, 13 paid holidays, paid continuing education, health, dental and vision coverage.

As an equal opportunity and affirmative action employer, UMMS recognizes the power of a diverse community and encourages applications from individuals with varied experiences, perspectives and backgrounds.

“Archibald, Anne (HR)”
<Anne.Archibald@umassmed.edu>

UNebraskaLincoln ResTech PlantEvolutionaryGenetics

Research Technician - Plant Evolutionary Genetics,
University of Nebraska-Lincoln

The laboratory of Stacey D. Smith at the University of Nebraska-Lincoln is seeking to hire a full-time technician to assist with research projects related to the evolution and genetics of floral diversification using the Andean clade Iochrominae as a model system. Specifically, the successful candidate will undertake experiments to investigate how changes in expression and function of floral pigmentation genes have contributed flower color diversity. The person will also assist in day-to-day lab management and in the maintenance of a greenhouse collection of Iochrominae.

Ideally, applicants should have a BA in biology or a related field and be well-organized, enthusiastic, motivated and independent. Experiments will include DNA and RNA extraction, quantitative real-time PCR, cloning, and sequence alignment, so research experience in a relevant area (molecular biology, systematics, genetics and/or evolutionary biology) would be beneficial.

The position will start in September 2010, and the exact starting date is flexible. The initial appointment is for one year, but may be extended. Salary will be commensurate with experience, and will include benefits.

To apply, please email a CV, a cover letter describing your qualifications and interests, and the contact information for three references to Stacey Smith (stacey.smith@duke.edu). Review of applications will begin May 1st 2010, and will continue until the po-

sition is filled. For more information on this research program, visit <http://www.duke.edu/~sds21/-research.html> and for information about the University of Nebraska-Lincoln and the School of Biological Sciences, visit <http://www.biosci.unl.edu/sds21@duke.edu>

USouthernCalifornia ResTech DrosophilaSequencing

USC's College of Letters, Arts & Sciences, Department of Molecular and Computational Biology, is seeking a Research Lab Technician II to join the team of Dr. Sergey Nuzhdin.

The Research Lab Technician II will perform several specific duties relating to the production of Next-Generation sequencing data including molecular work with RNA and DNA to prepare libraries and the general operation of our in-house Illumina Genome Analyzer II. In addition, the position entails providing general laboratory assistance to support research activities including ordering, keeping track of grant expenditures, and supervising undergraduates. We are seeking someone interested in learning about the underlying science of evolutionary genetics who will participate in lab meetings and read primary literature relating to the projects they are involved in. Projects currently planned include identifying pathways for salinity adaptation in the model legume *Medicago truncatula* and understanding the evolution of gene expression networks in *Drosophila*.

The University of Southern California values diversity and is committed to equal opportunity in employment.

See full posting and apply online:
jobs.usc.edu/applicants/Central?quickFindU577

maren.l.friesen@gmail.com

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>

UWisconsin Madison
EvoSystemsBiology

Open Rank Faculty Position in Evolutionary Systems

Biology

The Wisconsin Institute for Discovery (WID) at the University of Wisconsin-Madison (< <http://www.discovery.wisc.edu> >www.discovery.wisc.edu) invites applications for an open rank faculty position in Evolutionary Systems Biology. We welcome candidates whose research utilizes empirical and/or theoretical approaches. Areas of research could include interactions between organisms, such as host-microbe interactions and coevolution, innate or adaptive immunity, or systems within an organism (e.g., gene regulatory networks, biochemical and metabolic pathways). This faculty member will be hired as a member of a group that aims to advance the frontiers of systems biology through a combination of experimental, computational and evolutionary approaches.

Successful candidates will occupy space in a new state-of-the-art and centrally-located WID research facility specifically designed to spark and support cross-disciplinary collaborations. WID is the public half of an exciting public-private pair of Institutes that will promote basic research and facilitate the translation of new discoveries to practice. The successful candidate will be appointed to the department of the University that most appropriately matches her/his experience and interests. S/He will be expected to develop a vigorous, independent research program; attract and maintain extramural funding for her/his research program; teach undergraduate and/or graduate courses; develop new course(s) in her/his area of expertise as appropriate; supervise graduate and postgraduate research; participate in faculty governance activities in the department, college and/or University; and actively engage with the national and international scientific community.

Applications will be accepted until an appropriate candidate is found.

We are accepting applications on-line

< <http://newfac.sysbio.discovery.wisc.edu>
><http://newfac.sysbio.discovery.wisc.edu>

Inquires about these opportunities may be submitted on-line and addressed to:

Dr. John Yin Wisconsin Institute for Discovery Theme Area: Systems Biology

–

John Yin

Systems Biology, Theme Leader Wisconsin Institute for Discovery (opening Fall 2010) University of Wisconsin-Madison 330 N. Orchard Street Madison, WI 53715 <http://discovery.wisc.edu/discovery> Professor Department of Chemical and Biological Engineering Uni-

versity of Wisconsin-Madison 1415 Engineering Drive Madison, WI 53706-1607 <http://www.engr.wisc.edu/~che/> phone: (608) 265-3779 fax: (608) 262-5434 (shared) e-mail: yin@engr.wisc.edu <http://www.engr.wisc.edu/che/faculty/yin-john.html> <http://www.engr.wisc.edu/che/faculty/yin-john.html>

UZurich AssistantProfessor StatisticalGenomics

Please post this notice and distribute widely. Applications from evolutionary biologists and bioinformaticians are very welcome. <http://www.mnf.uzh.ch/de-services/offene-stellen.html#c2876> www.sysbio.uzh.ch The Faculty of Science of the University of Zurich is seeking to fill the position of an

Assistant Professor in Statistical Genomics

We are searching for individuals with an excellent research record in statistical genomics, including - but not limited to - research on whole-genome association studies, population genomics, identification of somatic mutations in disease, and the analysis of ultra highthroughput sequencing (UHTS) data in human or other model systems. A proven research record in complex genome-scale data analysis, as well as in the development of statistical or computational methods to analyze such data, is essential. The successful candidate will have demonstrated a keen interest in advancing biological knowledge through his or her research, and be highly interactive and open to collaboration. He or she will be expected to establish an independent research group within the University Research Priority Program Systems Biology/ Functional Genomics (www.sysbio.uzh.ch), and will have access to state-of-the-art research facilities provided by the University, and by the Functional Genomics Center Zurich (www.fgc.zh.ch), a technology platform for UHTS, transcriptomics, proteomics, and metabolomics. There are excellent opportunities for interactions with other groups of the University of Zurich and the ETH Zurich, as well as with the Swiss Systems Biology Initiative (SystemsX.ch), and the Swiss Institute for Bioinformatics (SIB).

This six-year non-tenure track assistant professorship carries limited teaching responsibilities (in English or German) and includes an attractive start-up package and significant support for running operations. Applications, including detailed curriculum vitae, publica-

tions list, short statement of research and teaching interests, and the names and addresses of three academic referees should be addressed to

Prof. Michael Hengartner Dean of the Faculty of Science Winterthurerstrasse 190 8057 Zurich, Switzerland and submitted as a single PDF file to jobs@mnf.uzh.ch .

For further information, please contact Prof. J. Jiricny at jiricny@imcr.uzh.ch . The application deadline is June 15, 2010.

The University of Zurich is an equal opportunity employer. Applications from women candidates are particularly encouraged.

Kentaro K. Shimizu, Assistant Professor Institute of Plant Biology University of Zurich Zollikerstrasse 107, CH-8008 Zurich Switzerland Phone +41-44-634-8247, 8270 FAX +41-44-634-8204

University Research Priority Program of Systems Biology / Functional Genomics Evolutionary Functional Genomics <http://botserv1.uzh.ch/home/shimizu/-index.html> <http://www.sysbio.uzh.ch/index.html>
E-mail: shimizu@botinst.uzh.ch

shimizu@botinst.uzh.ch

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 e-mail 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 "Research assistant position" in the subject of the e-mail.

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/>) E-mail: d.rankin@access.uzh.ch, Tel: +41 44 63 56143

d.rankin@socialgenes.org

Vanderbilt ResearchTechII MicrobialSymbiosis

Job Description:

A full-time Research Assistant II position is available in the Bordenstein Laboratory in the Department of

Biological Sciences at Vanderbilt University. The Bordenstein Lab is interested in the mechanisms and relevance of animal-microbe interactions between viruses, bacteria, and invertebrates. This position is part of an evolutionary genomics research program and will involve interconnections among microbiology, computational biology, molecular evolution, and entomology.

Key Functions and Expected Performances:

Research projects will focus on, but are not limited to DNA isolation, cloning, genome sequencing, and sequence analysis including sequence editing, whole genome assembly and annotation, alignments, and molecular evolution analysis. Lab duties will also include laboratory upkeep such as weekly organization, ordering products, training new personnel, and basic lab maintenance.

Minimum Requirements:

This position requires a Bachelor’s degree and a minimum of 24 months related experience. Familiarity with

cloning and sequencing, molecular biology of viruses, computational skills, GenBank, Linux/Unix, or genome assembly tools are a plus and should be highlighted in your cover letter.

To apply: Visit <http://vanderbilt.jobs/> and search for Requisition Number: GC19833. Feel free to contact s.bordenstein@vanderbilt.edu for more information.

Seth Bordenstein Assistant Professor Department of Biological Sciences Vanderbilt University VU Station B, Box 35-1634 Nashville, TN 37235

email: s.bordenstein@vanderbilt.edu phone: 1.615.322.9087 fax: 1.615.343.6707 <http://-bordensteinlab.vanderbilt.edu> Shipping Address for Packages: Seth Bordenstein Vanderbilt University U7215 BSB / MRB III 465 21st Ave South Nashville, TN 37232

s.bordenstein@Vanderbilt.Edu

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ABI 377 sequencer forsale

Colleagues,

We have an ABI 377 sequencer that is just sitting unused, and a host of associated supplies (including plates). If anyone is still using an ABI 377 and is inter-

ested in these items, please email me.

Best,

Andrew Bohonak –

Andrew J. Bohonak Associate Professor and Vice Chair of Biology Director of Undergraduate Advising and Curriculum

San Diego State University Department of Biology, MC 4614 5500 Campanile Drive San Diego, CA 92182-4614 Phone: 619-594-0414 Fax: 619-594-5676 Email: bohonak@sciences.sdsu.edu Web: <http://www.bio.sdsu.edu/pub/andy/index.html> Office: 212 Life Science North

bohonak@sciences.sdsu.edu

BFast SNP users

Hello,

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

Thanks much! Marta

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

Bird DNA Samples

Dear List,

Is there anyone in the UK currently capturing birds and taking DNA samples who would mind a fellow researcher tagging along to observe how it's done? I was supposed to be meeting someone in Madeira this week to show me these techniques but, due to the current flight problems, this is no longer possible. I would greatly appreciate any help.

Thanks,

John (John.d.norrey@student.mmu.ac.uk)

john.d.norrey@stu.mmu.ac.uk

BirkbeckU LERN Event Evolutionary Theory of Socialisation

Childhood Experience and the Development of Reproductive Strategies: An Evolutionary Theory of Socialisation Revisited

By

*Prof Jay Belsky <<http://www.bbk.ac.uk/psyc/staff/-academic/jbelsky>> *

(Birkbeck <<http://www.bbk.ac.uk/>>, University of London)

* *

Abstract: Life-history theory calls attention to across- as well as within-species variation in reproductive strategies. Three decades ago Draper and Harpending (1982) reinterpreted effects of childhood father absence on adolescent sexual behaviour in reproductive strategy terms. Belsky, Steinberg and Draper (1991) subsequently expanded this framework to consider a broader array of developmental experiences, highlighting not just why but how early family experiences shape psychological, somatic and reproductive development. A critical and theoretically unique prediction was that pubertal development would be accelerated in response to a variety of family stressors. Research evaluating this prediction is reviewed and new theoretical developments are discussed.

Date: April 27th 2010, time 18.30 *Location*: Roberts Lecture Theatre (Roberts Building, Torrington place, London WC1E 7JE)*

This event is free and all are welcome!

Regards,

The LERN Committee

***<<http://maps.google.co.uk/maps?f=q&source=embed&hl=en&geocode=&q=ROBERTS+BUILDING@51.5229,-0.1321&ie=UTF8&ll=51.5229,-0.1321&z=16>>

Gillian Pepper <ht08ggp1@brunel.ac.uk>

Brian Charlesworth at 65

To mark Brian Charlesworth's 65th birthday on 29 April 2010 and honour him for his many significant contributions to population genetics and evolutionary biology, a themed issue of Philosophical Transactions of the Royal Society B has been published on 'The population genetics of mutations: good, bad and indifferent'.

It comprises papers by a number of influential individuals who have been associated with Brian over the years and was edited by Laurence Loewe and Bill Hill.

Full details are available at:

<http://rstb.royalsocietypublishing.org/content/365/-1544.toc> Articles can be downloaded if your university has a subscription. Alternatively, the print issue can be ordered from: <http://rstb.royalsocietypublishing.org/site/2010/mutations.xhtml> For a discount enter special code TB 1544 when prompted or contact debbie.vaughan@royalsociety.org

Laurence.Loewe@ed.ac.uk

Estimates with Gibbs sampling

Hi all,

I am trying to calculate h^2 with Gibbs sampling using VCE. I did with likelihood method but something fail in this method. Could you give some tips????

thanks in advance regards Rodrigo Badilla \

Rodrigo Badilla <rodrigo.badilla@gmail.com>

Evidence Evolution

Dear friends,

Some weeks ago I sent a message asking for help about good websites discussing the evidences of evolution.

Now I am using several of them in my classes and I would like to share this material with all of you:

<http://books.nap.edu/openbook.php?isbn=0309105862&page> <http://www.pbs.org/wgbh/evolution/library/04/index.html>

<http://www.talkorigins.org/faqs/comdesc/section4.html> http://www.talkorigins.org/faqs/comdesc/section2.html#morphological_vestiges

http://www.talkorigins.org/faqs/comdesc/section2.html#present_biogeography <http://www.talkorigins.org/faqs/wells/haeckel.html>

After reading several of these material I am feeling that we need more material not just describing WHAT is a homology but also discussing HOW this can be used as an evidence of biological evolution. Another point is that it is very difficult to find material like this for kids and this fact is showing us that we need more teaching material about this subject. In another discussion in the list I sent a suggestion about a slide and short movies library available for teachers and students. We need to improve this....

Thanks to all people who sent me ideas and links :)

Prof. Dr. J. C. VOLTOLINI Universidade de Taubate - Departamento de Biologia Taubate, SP. 12030-010. E-Mail: jcvoltol@uol.com.br Website do grupo de pesquisa ECOMAM: <http://jcvoltol.sites.uol.com.br/> Fotos de Projetos e Cursos: <http://jcvoltol.fotoblog.uol.com.br/> Amostra de um Curso de Campo de Ecologia: <http://trabiju.blogspot.com/> Currículo Lattes: <http://lattes.cnpq.br/8137155809735635> Fotos Artísticas: <http://voltolini.fotos.net.br/texturas> 'Siamo tutti angeli con un'ala e possiamo volare soltanto se ciabbracciamo'

VOLTOLINI <jcvoltol@uol.com.br>

Genotype reconstruction answers

Several people requested the answers to my query about software for conveniently reconstructing the genotypes at each locus of the parents of a full sibship. Here is a summary of what I learned.

MY ORIGINAL QUESTION: Hi, Has anyone written a script to choose the most likely genotypes of the two parents of a full-sibship from the genotypes of those siblings? Here I want to pre-specify the sibships and just reconstruct the most likely parental genotypes at each

locus. Thanks, Mike

RECOMMENDATIONS:

Ian Wilson's PARENTAGE program seems like the best way to go. It will also do sibship partitions with genotyping error and a number of other useful procedures.

PEDIGREE (<http://herbinger.biology.dal.ca:5080/-Pedigree/>) will do the trick but extracting your parental genotypes out of the output is very labor intensive if you have a large number of sibships.

Note that if you want to write your own script, the equations for estimating the most likely parental genotypes of a full sibship are presented in table 2 of Banks et al., 2000. Canadian Journal of Fisheries and Aquatic Sciences 57:915-927.

Several people recommended COLONY but I don't think it will actually reconstruct both parental genotypes (at least the latest version won't) - if you try it, you'll see that it identifies both parents as having the same genotype. If I'm wrong about this, please let me know.

Some other recommendations I got included the following, but of the ones we checked into it wasn't obvious that they'll do what we wanted.

FAMOZ http://www.pierroton.inra.fr/genetics/labo/-Software/Famoz/famozinstall/famozinstall_ct.html

Famsphere <http://webs.uvigo.es/acraaj/-famsphere.htm> GIMLET <http://pbil.univ-lyon1.fr/-software/Gimlet/gimlet%20frame1.html> Valiere, 2002 Mol. Ecol. Notes

KINGROUP www.kingroup.com Gerud (Jones et al. 2005) <http://www.bio.tamu.edu/USERS/ajones/-JonesLab.htm> use MLTR by Kermit Ritland to obtain the mother genotype (check on his website for the free program). The father is not as simple unless you do a paternity-type analysis (PATRI is a good one if you do not know all the potential fathers). If you know nothing about the potential fathers there is nothing that I know about right now.

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

blouinm@science.oregonstate.edu

Through funding from USAID a new Indonesian Biodiversity Research Center we be launched in June 2010, located in Denpasar, Bali. The goal of this center is to advance biodiversity research in Indonesia and to foster collaboration between US and Indonesian scientists. This center is a collaboration between UCLA, the Smithsonian, Udayana University, Diponegoro University, and the State University of Papua. The Center will house a modest molecular laboratory and digital microscopy facilities to support the research of both Indonesian and U.S. faculty and students, and will have personnel who can assist and provide guidance in negotiating Indonesian permitting policies.

As part of the Center activities, a number of short courses will be offered each summer, including Molecular Ecology, Biodiversity Inventories, and Ichthyology. These research based courses are being developed to serve both US and Indonesian students and are designed to facilitate the collection of preliminary data that would help students develop research projects in Indonesia.

To facilitate the involvement U.S. graduate students this coming summer, there is a limited amount of funding to cover travel and subsistence costs for 3-4 students. Interested students should send an email to Paul Barber (paulbarber@ucla.edu) indicating their interest in participating in this program, as well as a one page description of their research interests and how participating in this program would further their research objectives.

Sincerely, Paul Barber

Dr. Paul H. Barber Department of Ecology and Evolutionary Biology 621 Charles E. Young Dr. South University of California Los Angeles Los Angeles, CA 90095 Phone: 310-794-5349 Fax: 310-206-3987 <http://www.eeb.ucla.edu/Faculty/Barber> The Diversity Project: <http://www.eeb.ucla.edu/Faculty/-Barber/Intro.htm> Coral Triangle PIRE Project: <http://sci.odu.edu/imp/ctpire.html> PEERS: <http://www.ugeducation.ucla.edu/urc-care/progpeers.htm> Paul Barber <paulbarber@ucla.edu>

Knome sequencing program

Indonesian Biodiversity

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>

Lyon SMBE WholeGenome CallAbstracts

Dear Evoldir members,

This is a call for abstracts to be submitted to the symposium on “Whole genome sequencing in experimental evolution” at the SMBE meetings this summer in Lyon, France.

Abstracts are to be submitted through the conference website: <http://smbe2010.univ-lyon1.fr>. The abstract for the symposium (also available at <http://smbe2010.univ-lyon1.fr/en/pages/smbe2010-whole-genome-sequencing-in-experimental-evolution>) is:

Modern sequencing methods finally allow the thorough and unbiased detection of mutations in experimental evolution systems. This allows both the quantitative description of the molecular events involved but also a qualitative understanding of the bases of adaptation and a direct link to system biology in model organisms. Our symposium will discuss current progress and future prospects for experimental evolution in multiple systems, including microorganisms as well as model animal or plant genetic systems. We expect the symposium speakers to give their thoughts on what “next-generation” sequencing will reveal about the molecular basis of adaptation, and what the different challenges are in different systems.

Best,

Kevin Thornton (krthornt@uci.edu) Olivier Tenaillon

(olivier.tenaillon@inserm.fr)

Kevin Thornton Assistant Professor Ecology and Evolutionary Biology University of California, Irvine <http://www.molpopgen.org> krthornt@uci.edu

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, useC-
orrection = 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

MEEC2011 host proposals

Hi folks,

Are you interested in hosting the Midwest Ecology and Evolution Conference next year?

This year’s MEEC committee is looking for proposals from graduate student groups to host MEEC 2011. Proposals are due on Friday, April 23, 2010.

Please limit your proposal to 2 pages including the following information:

1. The name of the student organization that plans to officially host MEEC 2011 (having a student organization host MEEC is both traditional and practical, as it makes scheduling events on campus, etc., much, much easier),
2. proposed conference dates for MEEC 2011,
3. venue availability,
4. why your institution is ideal for hosting MEEC 2011
5. brief details about possible interesting field trip sites near your institution
6. a short description about your intuitions’ ecology and/or evolution program (research, academics, etc),
7. any pledged sponsorships obtained thus far,
8. any other information you feel might help us know why your institution is the best host for MEEC 2011,
9. the typed signatures of the proposed MEEC

2011 Organizing Committee Chairman and the President/Chairman of your proposed hosting student organization.

10. Please include your plans to integrate a sustainability effort with MEEC 2011.

In addition, the 2011 host will receive up to \$5,000 in carryover from MEEC 2010.

Please send your proposal via email to

2010info@midwesteec.org

Cheers,

Erik Otárola-Castillo MEEC 2010 Organizing Committee Chair

Erik Otárola-Castillo Ecology and Evolutionary Biology Graduate Program 253 Bessey Hall Iowa State University Ames, IA 50011-1050 Phone 631-796-7331 <http://www.public.iastate.edu/~eotarola/-homepage.html>

eotarola@iastate.edu

MK-type tests

Dear Evoldir members,

I have a question about MK-type tests such as MKPRF, where polymorphism data are used from only one species (species 1), and are compared to the divergence from a second (species 2): in this case is it reasonable to perform the test in both directions, i.e. setting each species to “species 1” and repeating the test? It seems possible that differences at particular loci could occur due to different patterns of polymorphism in the two lineages... but I have not seen this done in the literature.

Many thanks, Gareth

Gareth Pearson (Research Associate) MAREE-Marine Ecology and Evolution (<http://ccmar.ualg.pt/maree/>) CCMAR - Centre of Marine Sciences, and CIMAR -Laboratório Associado Faculdade de Ciências do Mar e Ambiente, Universidade do Algarve

Mailing address: F.C.M.A., Univ. Algarve, Gambelas, 8005-139 Faro, Portugal Fax: +351 289 800 069 Phone: +351 289 800 928 E-mail: gpearson@ualg.pt

gpearson@ualg.pt

NESCent Evolutionary Course Proposals

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

Jory Weintraub <jory@unc.edu>

NESCent Minority Institution Sabbaticals

NESCent Targeted Sabbaticals in Evolutionary Biology for MSI Faculty

The US National Evolutionary Synthesis Center (NESCent) is an NSF-funded evolutionary biology research center in Durham, NC representing a partnership of Duke University, North Carolina State University and The University of North Carolina at Chapel Hill.

As part of NESCent's commitment to increasing diversity in evolutionary biology we offer targeted sabbatical opportunities to evolutionary biologists from Minority-Serving Institutions (MSIs) to undertake projects that will increase minority participation in evolutionary science and/or develop evolution education activities.

NESCent provides stipends up to the equivalent of a full salary (monthly stipend equal to 1/12th of a 9-month salary at home institution). A housing allowance up to \$1,000/month can also be provided.

Deadlines for NESCent Targeted Sabbaticals are July 10th and December 1st each year. For more information and to apply, please see <http://www.nescent.org/science/targetedsabbatical.php> or contact Dr. Jory Weintraub (jory@nescent.org).

Jory Weintraub <jory@unc.edu>

NESCent Postdoc Call For Proposals

POSTDOCTORAL FELLOWSHIPS IN EVOLUTIONARY BIOLOGY AND RELATED FIELDS

We are now accepting proposals for Postdoctoral Fellowships at The National Evolutionary Synthesis Center (NESCent). We are looking to fund innovative approaches to outstanding problems in evolutionary biology. Proposals are due December 1. For more information, please see our website at <https://www.nescent.org/science/proposals.php>. CALL FOR PROPOSALS - SABBATICAL SCHOLARS AND COLLABORATIVE WORKING GROUPS

Proposals for Sabbaticals and for collaborative working groups (Working Groups and Catalysis Meetings) are now being accepted at The National Evolutionary Synthesis Center (NESCent). We are looking to fund innovative approaches to outstanding problems in evolutionary biology. In particular, proposals that have a clear interdisciplinary focus, or involve evolutionary concepts in non-traditional disciplines, are strongly encouraged, as are proposals that demonstrate international participation and a mix of senior and emerging researchers, including graduate students. Proposals for Working Groups and Catalysis Meetings are accepted twice a year, with deadlines on June 10 and December 1. Proposals for Sabbaticals may be one semester to a full year (deadlines June 10 and December 1) or they may be for short-term visits (2 weeks to 3 months; deadlines on January 1, April 1, July 1 and September 1). NESCent is also now seeking to include graduate traineeship to our portfolio by offering one-semester fellowships for graduate students to pursue research either with a NESCent sabbatical scholar or with a NESCent Working Group. For more information, please see our website at <https://www.nescent.org/science/proposals.php>. Craig R. McClain, Ph.D. Assistant Director of Science National Evolutionary Synthesis Center 2024 W. Main St. Suite A200 Box 104403 Durham, NC 27705 919-668-4590 cmclain@nescent.org

Associate Editor for Journal of Biogeography: <http://www.wiley.com/bw/journal.asp?ref=0305-0270> Deep-Sea News: <http://deepseanews.com/> National Evolutionary Synthesis Center: <http://www.nescent.org/> Research Homepage: <http://mcclain.nescent.org/>

McClain Craig <cmclain@nescent.org>

Next Generation InHouse Computing

Title of post: Next.Generation.In house.Computing

Dear EvolDir'ers

What with costs of outsourcing the standard bioinformatics needed for next gen data, quickly being able to reach dizzying heights (I was just quoted 1000 Euros for clustering and contig assembly for one cDNA library), I wonder if any advice could be given on a decent powerful set up for in-lab use?

The trade-off between computing time and accumulating outsourcing costs is important, yet would not be to upset if it took one week for contig and clustering of a cDNA library on our own machine.

Does anyone have a powerful setup of their own, which is not an expensive cluster system, able to execute the basic necessities e.g. alignments, BLASTs, SNP searches?

Thanks,

– Jack Lighten, Ph.D. Candidate, Bentzen Lab, Room 6078, Department of Biology, Dalhousie University, Halifax, NS, B3H 4J1 Canada

Office:(902) 494-1398 Email: Jackie.Lighten@Dal.Ca
Profile: www.marinebiodiversity.ca/CHONe/Members/lightenj/profile/bio Jackie Lighten
<jc807177@dal.ca>

Next Generation InHouse Computing answers

Next.Generation.InHouse.Computing

Thank you very much to everyone who provided such useful input to my original question:

³What with costs of outsourcing the standard bioinformatics needed for next gen data, quickly being able to reach dizzying heights (I was just quoted 1000 Euros for clustering and contig assembly for one cDNA library), I wonder if any advice could be given on a decent powerful set up for in-lab use?

The trade-off between computing time and accumulating outsourcing costs is important, yet would not be to upset if it took one week for contig and clustering of a cDNA library on our own machine.

Does anyone have a powerful setup of their own, which is not an expensive cluster system, able to execute the basic necessities e.g. alignments, BLASTs, SNP searches?²

There seems to be a few ways to tackle this dilemmas:

1. Outsource to a company/lab, with prices between ranging dramatically
2. Utilize a cluster/server system at your Institute or region: eg. AceNet. The speed of processing largely depends on the amount of power you are allocated. Some analyses may take a long time if the cores are at capacity.
3. Purchase your own desktop "super computer", along with software.
4. Utilize a virtual cloud system, for remote processing of data. This however seems to be hampered only by the upload time of your data, via the internet, into the system. Some people have also had problems with the output files.

We have decided to go with our own desktop solution (~\$4000 CA), along with the CLC Genomics Workbench software (~\$6000 US) for a number of reasons.

1. The software comes highly recommended and utilizes high powered desktops fully, to for example identify SNPs in assembled cDNA libraries in around 30 mins (as opposed to days, stated by outsourced companies).
2. We want to have hands on experience and expertise within the lab.
3. Our own setup will streamline data processing and customization.

There seems to be a lot of people doing in-house analyses, as such an array of software and a community for support has cropped up:

<http://seqanswers.com/forums/index.php> See below for example of a powerful machine specs all the received correspondences:

Mainboard : ASUS Z8NA-D6C ATX Dual LGA1366
 Intel 5500 DDR3 PCI-E16 - \$318 CPU # 1 : Intel Xeon E5520 Quad Core Processor LGA1366 2.26GHZ 8MB Cache 45NM - \$450 CPU # 2 : Intel Xeon E5520 Quad Core Processor LGA1366 2.26GHZ 8MB Cache 45NM - \$450 Memory : Corsair XMS3 CMX8GX3M4A1333C9 24GB DDR3 4X6GB DDR3-1333 CL 9-9-9-24 - \$1080 HDD : Western Digital WD10EADS Caviar Green 1TB SATA 32MB Cache 3.5IN Hard Drive OEM - \$95 Video Card : Sapphire ATI Radeon 5870 1GB PCIe DDR5 Graphics Card - \$460 Sound Card : on board Card Reader : Nmedia C68 3.5IN USB2.0 Flash Card Reader Silver Black with Front USB - \$24 Optical Drive : LG GH22NS50 Black 22X SATA DVD Writer OEM - \$33 Case : Supermicro eATX Server Case eATX 4X5.25 6X3.5INT No PS Front USB & Audio - \$610 O/S : Microsoft Windows 7 Professional Edition 64BIT DVD - \$164

with 24gb memory \$3684 + tax = \$4162.92 with 32gb memory \$3964 + tax = \$4479.32

Hi Jack,

There is no need to spend \$1000 doing a next-gen cDNA assembly and shame on anybody who would even charge that! For about \$1500 you can put together a Linux system to handle most of your bioinformatic needs, including assembly. Really, any workstation will do that has at least 8GB RAM and a quad core. What sorts of data are you talking about - Illumina, SOLiD, or 454? If you want to chat on the phone about assembly strategies and necessary hardware feel free to give me a call at 520-336-7592.

Best, Mike Barker

– Michael S. Barker, Ph.D. The Biodiversity Research Centre, University of British Columbia

Dear Jack,

I bot myself a system built around an Asus Z8NA-D6 i5500 RGVA motherboard with 2 Intel Xeon processors. You will have 2 Quad cores, that male 8 cores behaving as one. These Intels are hyperthreaded, which means they actually will behave like 16 processors. The whole thing will be considerably cheaper than 5k Euro. It is only one box, and will work nicely with standard Linux ditributions. This is a standard ATX set-up with up to 24 Gb of RAM. Please confront your local computer store with these details and they can tell you more.

This is good enough to do everything you wish for, but not yet whole genome de novo assembly of verebrate sized genomes. For that you would need 256 or better 512 Gb RAM. This is only possible with server configurations, prices starting at around 30k Euro - and not so easy to maintain...

More questions? Let me know.

Cheers, Robert

Robert H. S. KRAUS PhD student Resource Ecology Group Wageningen University, The Netherlands

Phone +31 317 4 83530/84700 Fax +31 317 4 84845
 Email robert.kraus@wur.nl

— / —

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>

Papers request

Dear Evoldir members:

I am looking for the papers mentioned below, to which unfortunately I do not have access:

I will greatly appreciate if someone could help me.

Many anticipated thanks.

Reply to: bcarmen@uvigo.es

A) Manning, J.T. & Ockenden, L. 1994. Fluctuating asymmetry in racehorses. *Nature* 370: 185-186.

B) Thornhill, R. & Gangestad, S.W. 1993. Human facial beauty: averageness, symmetry, and parasite resistance. *Human Nat* 4: 237-269.

Carmen Burghelea <carmen_burghelea@yahoo.es>

Phyloseminar Influenza Evolution Apr23

On April 23rd, phyloseminar.org will present Trevor Bedford speaking on "Adaptation and migration in the human influenza virus." As always, the seminar will be freely viewable by the public— see phyloseminar.org for more information.

The talk will be at 13h PDT (West Coast USA), which is 8h (on April 22nd) in Christchurch, NZ, 16h on the East coast of the USA, 21h in the UK and 22h in Germany.

Abstract: The influenza A virus infects approximately 500 million individuals each year. Owing to its RNA makeup, influenza mutates extremely rapidly allowing the virus population to escape the pull of the human immune system. A single individual may be infected year after year by antigenically novel strains. As result of this rate of mutation, the timescale of influenza evolution is a human timescale. We get the chance to observe the process of evolution in action. However, the rapid pace of evolution also causes an intrinsic link between evolutionary and ecological dynamics in the virus population. The availability of temporally spaced sequence data allows estimation of details of these dynamics unavailable in other systems. Through analysis of this data, I address open questions regarding patterns of adaptation and the effects of seasonality in the human influenza virus.

ematsen@gmail.com

Sapphire Microbiologist

Microbial Physiologist

Sapphire Energy is a venture capital-backed company developing next generation biofuels based on recent advances in metabolic engineering. The company's focus is the commercialization of high performance, low cost, and low carbon footprint biofuels that are direct replacements for conventional gasoline, diesel, and jet fuel.

We are seeking an exceptional microbial physiologist to join our Microbiology staff in San Diego, CA.

Requirements * Doctoral degree in microbiology, biology, molecular biology, experimental evolution or related field plus at least one year post-doctoral experience.

* Experience in microbial physiology is essential:

* Significant experience with methods for characterizing and understanding growth properties

* Capable of rapidly analyzing large data sets; experience with programming languages / statistical software

* Experience with microalgae a plus. * Strong leadership and organizational skills. * This position will work closely with both research and development. The ability to concisely and effectively communicate results will be extremely important. * Ability to participate in interdisciplinary teams. * Critical thinking and problem solving skills. * Demonstrated ability to independently design, execute, troubleshoot and interpret experiments. * Proficiency in written and oral presentations.

Responsibilities include, but are not limited to: * Physiological characterization of strains of algae under a variety of conditions. * Identification of growth conditions that optimize growth of algal strains of interest. * Creativity and the ability to work within and lead a team in order to achieve technical and corporate milestones. * Collaborate with section-level peers. * Provide example of professionalism and proficiency for the laboratory staff.

Sapphire offers very competitive compensation packages including bonuses and equity, as well as full benefit packages, which include health, dental, vision insurance, 401k, and paid time off. To apply, please send your CV and cover letter to hu-

man.resources@sapphireenergy.com and reference Microbial Physiologist in the subject line.

SISG Scholarship Deadline Apr15

SISG Scholarship Deadline

The deadline for applications for scholarships for the 2010 Summer Institute in Statistical Genetics at the University of Washington, June 14-July 2, is Thursday, April 15. Details are available at <http://sisg.biostat.washington.edu> Bruce Weir sisg@u.washington.edu

Bruce Weir <bsweir@u.washington.edu>

Software ComparativeGenomics MANTiS-v1.1

Dear EvolDir member,

Version 1.1 of MANTiS (which now includes an auto-update system) is available for download at:

<http://www.mantisdb.org> Check the update notes at the very end of this message.

MANTiS is a comparative genomics application system that builds a relational database integrating, in an explicit phylogenetic framework, all Ensembl genes (MANTiS covers now all recent ENSEMBL versions, up to release 57), corresponding PANTHER molecular functions and biological processes, as well as expression data from various sources. MANTiS uses ortholog/paralog prediction and a dynamical programming approach for the mapping of gene gains, duplications, and losses on the phylogenetic tree.

Through a user-friendly interface, MANTiS allows the user to identify:

- â Gene gains and losses on specific branches of the tree (but see Genome Biology, 2010 Feb, 11, 2, R16)
- â Genome content of ancestral species,
- â Statistically over- or under-represented molecular functions, biological processes and anatomical systems (expression data), see Genome Biology & Evolution 2010: 13-18 (2010)
- â Tissue specificity of gained, duplicated, and lost genes.

Finally, the entire set of information available in MAN-

TiS can be exploited further using an advanced system of queries by which gene identity, mapping, and function parameters can be combined using logical operators.

Original reference: Tzika A. C., Helaers R, Van de Peer Y. & M. C. Milinkovitch MANTiS: a phylogenetic framework for multi-species genome comparisons Bioinformatics, 24 (2):151-157 (2008)

Best wishes,

Michel.

Prof. Michel C. Milinkovitch Laboratory of Artificial & Natural Evolution Dept of Zoology & Animal Biology University of Geneva Sciences III, 30, Quai Ernest-Ansermet 1211 GenÃve 4, Switzerland

Michel.Milinkovitch@unige.ch

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www.lanevol.org —

What's new in v1.1:

General - Loading of the data at the launch of MANTiS is much faster - Expression data for EST and GNF are no more recovered from Ensembl. EST data is recovered from NCBI's Unigene (<http://www.ncbi.nlm.nih.gov/unigene>) and GNF data is recovered from BioGPS (<http://biogps.gnf.org>). - MANTiS covers now all recent ENSEMBL versions (up to release 57) WARNING: some of these versions of Ensembl contain low-coverage (2X) genomes that generate large artifacts in gene gains and losses; see: Milinkovitch M.C., Helaers R., Depiereux E., Tzika A.C., & T. Galardon 2X genomes - depth does matter Genome Biology, 2010 Feb, 11, 2, R16

Interface -MANTiS requires now JAVA 6 or better - MANTiS now uses the 'native skin' instead of the 'java' appearance.

Tools - There are new 'General statistics tools', for example, to assess patterns of changes in gene tissue specificity along lineages: see Milinkovitch M.C., Helaers R., & A.C. Tzika Historical Constraints on Vertebrate Genome Evolution Genome Biology & Evolution 2010: 13-18 (2010) - New tool named "Restrict dataset to duplicated genes". It performs a restriction by keeping only the characters coming from a duplication, excluding 'de-novo' gains. This tool is available only in the 'with duplications' dataset and uses high amount of memory, so it might be necessary to increase the amount of memory assigned to MANTiS. - New tool called 'set allowed memory' for choosing the maximum amount of RAM assigned to MANTiS. If you run MANTiS on a 32-bit OS, you are limited to 2GB. If you

run MANTiS on a 64-bit OS, you are not limited in the amount of allowable memory. - New identifier conversion tool from Entrez/Unigene to Ensembl for more species.

Dataset -New 'Phylomedb 1' dataset. A dataset with a large number of species, all with high-coverage genomes. See <http://phylomedb.org> for more details.

"Michel C. Milinkovitch"
<Michel.Milinkovitch@unige.ch>

Tel +43 (0) 512 / 507 - 6151 Fax +43 (0) 512 / 507 - 6190 Mob +43 (0) 664 / 734 35 871 wolfgang.arthofer@uibk.ac.at

GS d(-) s:(+) a+ C(++)\$ UL@ P— L+@ !E- W++\$ N+ !o !K- w(—) O- !M- V++ PS PE- Y+ PGP>+ t+ 5? X R- tv- b++ DI++ !D G e+ h— r y

http://www.uibk.ac.at/ecology/forschung/-molecular_ecology.html.de Wolfgang Arthofer
<Wolfgang.Arthofer@uibk.ac.at>

Software tinyFLP update

tinyFLP and tinyCAT are free programs for automatic scoring of AFLP data generated with Applied Biosystems instruments. (Arthofer 2010, Mol Ecol Res 10, 385-388). tinyFLP reads data tables exported from the free PeakScanner software, performs binning and returns a binary allele matrix. tinyCAT concatenates up to 16 matrices derived from different primer sets and generates files in Fasta, Nexus, Structure and GenAlEx format.

We announce a major update of both programs:

tinyFLP, now in version 1.1: * Ability to read 600bp electropherograms (500 bp in v1.0) * Ability to identify up to 600 peaks per trace (255 peaks in v1.0) * Improved sliding-windows operation * Bugfix: presence of larger peaks than 600 bp does not cause incorrect data * Milliseconds added to timestamps * Improved error messages in logfile

tinyCAT, now in version 1.0: * Output for Structure software added * Output for different programs is now directed into different files, no more need for copy-paste * Ability to deal with 600bp traces and longer matrices as produced by tinyFLP v1.1 * Milliseconds added to timestamp

The new versions (Windows executable, source code, manual) can be downloaded from <http://sourceforge.net/projects/tinyflp/> (use the 'View all files' button!)

-

Dr. Wolfgang Arthofer

University of Innsbruck Molecular Ecology Group Technikerstrasse 25 / 5. OG 6020 Innsbruck, Austria

UGroningen VisitingSciScholarships

Erasmus Mundus scholarships for visiting scientists

Four European universities:

- University of Groningen (Netherlands) - University of Montpellier II (France) - Ludwig Maximilians University of Munich (Germany) - Uppsala University (Sweden)

have joined forces to establish an international research oriented MSc programme in Evolutionary Biology (MEME), which is funded by the Erasmus Mundus Programme of the European Union. In addition to funding for student scholarships, we also have funding for inviting scholars (= visiting scientists) from non-EU/EFTA countries. We are looking for scientists at the post-doctoral level or beyond that are interested in collaborations with colleagues in one or more of our partner institutes. Each scholar is expected to contribute to the MEME program, e.g. by teaching part of a summer school.

At each of the four universities, we can offer several scholar scholarships for a stay between two weeks and three months. The scholarship amounts to 1200 euros per week. More information about the MEME program and the participating institutions can be found on www.evobio.eu. Applications including a CV and a letter of motivation should be sent before 15 May 2010 to the e-mail address below.

Franz J. Weissing Professor of Theoretical Biology Coordinator MEME Programme Centre for Ecological and Evolutionary Sciences Kerklaan 30 9751 NN Haren tel. +31 50 363 8669 (or: 2131) E-mail: f.j.weissing@rug.nl URL1: www.rug.nl/biol/theobio URL2: www.rug.nl/biol/cees p240827@rug.nl

PostDocs

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AMNH NewYork 2 HostPathogens

Postdoctoral Positions at the American Museum of Natural History (AMNH)

Two positions available June 1, 2010 to work on a grant-funded project studying the biological, systematic, and computational challenges presented by phylogenetic reconstruction of host-pathogen systems. The project will involve the development of analytical approaches and their implementation in

POY [using C and OCAML] <http://research.amnh.org/scicomp/research/projects/-invertebrate-zoology/poy?q=projects/poy.php> and Supramap <http://supramap.osu.edu/sm/supramap/-home> Applicants should have experience in system-

atics, biogeography, host-pathogen systems, and/or computational biology. Ph.D. required in biology, computer science, or related fields.

Varón A., Vinh L., Wheeler W.C. (2010). POY version 4: phylogenetic analysis using dynamic homologies. *Cladistics*. 26: 72-85.

Janies, D., T. Treseder, B. Alexandrov, F. Habib, J. Chen, R. Ferreira, Ümit atalyürek, A. Varón, W.C. Wheeler. in press. The Supramap project: Linking pathogen genomes with geography to fight emergent infectious diseases. *Cladistics*.

Janies, D., A. Hill, R. Guralnick, F. Habib, E. Waltari, W.C. Wheeler (2007) Genomic Analysis and Geographic Visualization of the Spread of Avian Influenza (H5N1). *Systematic Biology*. 56:321-9.

Interested parties should contact:

Ward Wheeler

Division of Invertebrate Zoology
 American Museum of Natural History
 wheeler@amnh.org
 crowley@amnh.org

Bard College Teaching Evolution Visiting Scientist

The Biology Program at Bard College is seeking applicants for a full-time, two-year visiting faculty position, beginning in the fall of 2010. The successful candidate will teach a biostatistics course one semester each year, a 100-level course each semester and an advanced seminar course one semester each year. The candidate's specific area of expertise is flexible but should complement the programs existing strengths in ecology, evolution, microbiology, molecular biology and biochemistry. The successful candidate will possess a Ph.D. and will be expected to involve undergraduates in their research. More information about the curriculum and current faculty research can be found at <http://biology.bard.edu>. Bard is a private liberal arts college with approximately 1,900 students, located 90 miles north of New York City on the Hudson River. Applicants should submit curriculum vitae, research and teaching statements, and the contact information for three references by email only to: Professor Michael Tibbetts at hrscm10-029@bard.edu. Review of applications will begin on May 1, and will continue until the position is filled. We seek to attract and retain a highly qualified and diverse faculty. Affirmative Action/Equal Opportunity Employer.

philip johns

Assistant Professor Biology Program Bard College
 Annandale-on-Hudson, NY 12504

johns@bard.edu bugs@bard.edu 845.752.2338

Philip Johns <johns@bard.edu>

Bigelow Lab Maine Phylogenomics

Position Description

Post-doctoral position in phylogenomics Bigelow Laboratory for Ocean Sciences, West Boothbay Harbor, Maine

A full-time post-doctoral position is available in the lab of Dr. Hwan Su Yoon at Bigelow Laboratory for Ocean Sciences in West Boothbay Harbor, Maine. This position involves participation in an NSF-funded project, "RedToL: Phylogenetic and Genomic Approaches to Reconstructing the Red Algal (Rhodophyta) Tree of Life" to study phylogenetic relationships of red algae using multi-gene dataset, and plastid genomes and transcriptome sequence data. Therefore, a post-doc with a strong background in evolutionary genomics, molecular evolution, bioinformatics, or genome analysis is requested. Primary duties include plastid DNA isolation, EST library construction, phylogenomics and bioinformatics analysis. Candidate with a Ph.D. degree in evolutionary genomics, computational biology or a relevant field is required. Experience with next generation sequence analysis (454, Illumina, or SOLiD) is desirable. Funding is available for three years.

Applicants should send their CV, a letter of intent describing candidate's motivation, qualifications, skills, and experience relevant to this position, and contact information for three references to jobs@bigelow.org. Please reference #PD10-1 in the subject line. The search committee will begin reviewing applications on May 1, 2010 and will continue until the position is filled. The position is available immediately. Bigelow Laboratory is an Equal Opportunity Employer.

Jane Gardner <jjgardner@bigelow.org>

Cornell University Computational Evolutionary Genomics

Postdoctoral position in computational evolutionary genomics at Cornell University

A POSTDOCTORAL POSITION is available in the laboratory of Dr. Adam Siepel in the Department of Biological Statistics and Computational Biology at Cornell University (Ithaca, NY). The research focus will be in the general area of computational evolutionary genomics. Specific topics of interest include microbial evolutionary genomics (focusing on pathogenic *Streptococci*), evolutionary genomics of gene regulation in primates, integrated phylogenetic and population genetic analyses, and evolutionary analyses of complete

individual human genomes. The candidate will be expected to participate in both methods development and data analysis. The ideal candidate will have a strong background in computer science, statistics, or applied mathematics, experience in genetics/genomics, and a strong record of accomplishment in research.

Qualifications

- Ph.D. in bioinformatics, computer science, statistics, genetics, molecular biology, applied mathematics, or a related field. - Research experience (with strong first-author publications) in computational genomics, phylogenetics, molecular evolution, population genetics, or a closely related field - Fluency in probabilistic modeling and computational statistics. - Proficiency in programming, ideally in C or C++ as well as in scripting languages such as perl, matlab, or R. Should be comfortable in a linux environment, with large data sets, computer clusters, and databases.

Term

The term for this position is flexible but most likely will be 2-3 years. The proposed start date is Summer 2010.

About the Siepel Lab

The Siepel Lab does interdisciplinary research in comparative and evolutionary genomics, including both the development of new theory and methods, and the analysis of large-scale genomic data sets. The group currently consists of eight postdocs, graduate students, and staff members, with backgrounds in computer science, genetics, and statistics. Recent research projects have involved novel gene discovery in mammals, the detection of lineage specific selection, and inference of ancient human demography from individual human genome sequences. The group maintains active collaborations with several computational, molecular, and evolutionary biologists at Cornell and other institutions. Its research is supported by grants from the David and Lucile Packard Foundation, the Alfred P. Sloan Foundation, Microsoft Research, the National Institutes of Health, and the National Science Foundation. For more information, see <http://compgen.bscc.cornell.edu/~acs>.

About Cornell

Cornell is home to a large, active community of researchers interested in evolutionary genomics, population genetics, and other areas of mathematical and computational biology. For more information see the website of the Cornell Center for Comparative and Population Genomics (<http://3cpg.cornell.edu>)

To Apply

Submit a CV, a short statement of research interests

and experience, and contact information for three references by e-mail to acs4@cornell.edu. Informal inquiries are welcome.

Adam Siepel 102E Weill Hall Cornell University Ithaca, NY 14853

Cornell University is an affirmative action/equal opportunity employer.

Adam Siepel <acs4@cornell.edu>

CornellU ComputationalPlantBreeding

USDA-ARS at Cornell University

Postdoctoral Position in Quantitative / Computational Genetics for Plant Breeding

Genomic selection uses novel statistical approaches to predict phenotype and breeding value from high density marker data. There is a current need for improved computational methods in the face of increasing marker densities and observation numbers. Many directions of cutting edge research are open and with the data in hand can rapidly lead to publications: - Scale-up genomic selection methods to datasets involving possibly tens of thousands of lines and markers - Extend genomic selection methods to better design training populations, reduce loss of genetic diversity, and capture epistatic effects - Develop and test methods of genomic selection that use haplotype rather than single-marker information - Propose and simulate breeding schemes that introduce genomic selection predictions to accelerate gains from breeding The posdoc will have available extensive empirical datasets to validate results and tie them to real, rather than simulated datasets. These datasets include genotypes and phenotypes from the Barley Coordinated Agricultural Project (~3,000 SNP on ~4,000 lines with extensive phenotypes); Genomic selection validation data currently collected in barley and winter wheat programs (~1500 SNP and DArT markers on ~1000 lines including parents and progeny from the two species); ongoing genomic selection for quantitative disease resistance in barley.

To analyze these data, we are assembling and adapting methods from plant, human and livestock genetics. We are a pioneering lab in many of these methods and look to train postdocs in the basics and perform research to extend the analyses. The environment at Cornell includes nationally recognized research programs in pop-

ulation genetics, genomics and plant breeding, which will provide additional resources and stimulation.

Preferred applicants should have a Ph.D. in quantitative, population, or computational genetics and strong background in statistics. US citizens or Green Card holders are also preferred (certain other nationalities may apply but initial employment will be delayed). An excellent postdoctoral salary will be offered.

A letter of interest in the position, C.V., and contact information for three references should be emailed to Jean-Luc Jannink at:

JeanLuc.Jannink@ars.usda.gov

Jean-Luc Jannink, Small Grains Quantitative Geneticist USDA-ARS, Robert W. Holley Center for Agriculture and Health Phone +1 607 255 5266 Fax +1 607 255 6683

Cornell University Dept. of Plant Breeding and Genetics 407 Bradfield Hall Ithaca, NY 14853 USA

jj332@cornell.edu

ETH Zurich PlantEvolutionaryGenomics

Post-Doctoral Position in Plant Evolutionary Genomics in the Plant Ecological Genetics group at ETH Zurich, Zurich, Switzerland, funded by a grant from the Swiss National Science Foundation (SNF) to Dr. Thomas Städler.

We seek a highly motivated post-doctoral researcher to join our small team aiming to characterize genome-wide nucleotide diversity of several wild tomato species, with particular interests in (i) inferring demographic history and speciation (neutrally evolving reference loci), and (ii) assessing evidence for natural selection (candidate genes for reproductive and other putatively adaptive traits). The analysis of previously published sequence data is also possible, as are additional side projects reflecting the successful candidate's interests.

We offer a stimulating scientific environment and first-rate computational and molecular facilities. Our group is international in composition, with all group meetings, seminars etc. being held in English. The main study organisms in other (non-tomato) research projects are species of *Silene* and *Arabidopsis* (see <http://www.peg.ethz.ch>). Zurich is a cosmopolitan

small city offering outstanding quality of life as well as a vibrant academic community (both ETH and University of Zurich). The contract will be for 12 months in the first instance, but funding is available for up to 36 months. Salary is very competitive by any standard. Starting date should be 1 July 2010 or as soon as possible thereafter.

Applicants for this position should have a Ph.D. degree (or equivalent) in molecular population genetics/genomics, plant biology, or computational biology. A background in molecular population genetics is highly desirable, and some familiarity with coalescent simulations, programming, and/or next-generation sequencing platforms (454, Illumina) are definite assets. Good quantitative, analytical, and English skills are essential, as is the ability to work independently.

Applicants should submit a single PDF file by e-mail containing the following items:

* A cover letter with a brief summary of previous research experience and professional motivation * Curriculum Vitae * Names, addresses and e-mails of 2-3 professional references.

Applications received by May 9, 2010 are assured of full consideration, but the position remains open until filled. Please send inquiries and applications to

Dr. Thomas Städler Plant Ecological Genetics Institute of Integrative Biology (IBZ) ETH Zurich Universitätstrasse 16 CH-8092 Zurich Switzerland

thomas.staedler@env.ethz.ch

Gainesville Florida AntEvolution

A postdoctoral position is available immediately in the laboratory of DeWayne Shoemaker (<http://ars.usda.gov/pandp/people/people.htm?personid=-39379>) at ARS in Gainesville, Florida. Previous and ongoing research in our laboratory mainly has focused on population and evolutionary genetic studies of introduced and native fire ants and studies of the evolutionary interactions of *Wolbachia* endosymbionts and their insect hosts. For examples of recent studies from our laboratory, see: *Systematic Biology*, 59: 162-184; *Biological Invasions*, 10:1457-1479; *Biological Journal of the Linnean Society*, 92: 541-560; *Evolution*, 59: 1733-1743; *Genetics*, 168: 2049-2058).

The major goal of the current project is to utilize existing and recently developed genomic resources for

fire ants (including full genome sequence of the single species *Solenopsis invicta*) to conduct several of a number of key evolutionary studies of these ants, such as: comparative genetic studies seeking to identify portions of the genome involved in the development of reproductive isolation in order to understand the causes of speciation in this ecologically important group of ants; identification of the factors promoting natural hybridization between the two fire ant species *S. invicta* and *S. richteri*; ecological and evolutionary functional genomics studies in an attempt to identify polymorphisms segregating at genes that affect ecological and evolutionary success in natural environments (as well as the functional consequences of such variation); linkage mapping and comparative population genomic studies within and among species; studies of genomic sequences for features of interest; or other molecular evolutionary studies of fire ants (e.g., evolution of gene families, origin and fate of gene duplications) as well as across Hymenoptera. The evolutionary genetics of invasive species is a topic of enormous current interest. Fire ants represent excellent models for these and other evolutionary genomic studies given their complex social behaviors and life histories, their stunning success as invaders and the well documented genetic and ecological changes that have taken place in invasive populations, the extensive hybridization that occurs between some species, and the ongoing need for studies aimed at delimiting species in this important group of insects.

QUALIFICATION REQUIREMENTS: Ph.D. in evolutionary or population genetics/genomics or closely related discipline appropriate to the position. The applicant must have an interest in population and evolutionary genetics and ideally would be familiarized with bioinformatics approaches relating to population and evolutionary genetics and have experience analyzing next generation sequencing data. Candidates with experience in standard molecular genetic techniques (e.g., PCR, fluorescent-based genotyping and next generation DNA sequencing, gene expression, bioinformatics) or large-scale data analyses (e.g. high-throughput genotyping, comparative genomics) are desired.

Funding is available for two years, with possible extension for an additional year, starting as early as June 2010. Review of applications will start immediately (send CV and supporting materials to: dewayne.shoemaker@ars.usda.gov).

For more specific information on this position, additional enquiries, or for instructions on submitting a formal application, please feel free to contact DeWayne Shoemaker via email at the address above or by phone at 352-374-5942.

For details and application directions, see <http://www.afm.ars.usda.gov/divisions/hrd/index.html> and click on ANN#: RA-10-036-L. US citizenship is required. To have a printed copy mailed, call (352-374-5942). U.S. citizenship is required.

INFORMATION ON APPLICATION PROCEDURES FOR POSTDOCTORAL POSITIONS IS AVAILABLE: <http://www.afm.ars.usda.gov/divisions/hrd/hrdhomepage/vacancy/pd962.html> USDA/ARS is an equal opportunity employer and provider.

Dewayne.Shoemaker@ARS.USDA.GOV

HarvardU ExperimentalEvolution

A postdoctoral position is available to work on experimental evolution in the lab of Michael Desai in the Department of Organismic and Evolutionary Biology at Harvard University.

The successful applicant will study the role of geographic structure on the evolutionary dynamics of adaptation, using budding yeast as a model system. Experimental lines will be maintained using robotic liquid handling systems and assayed with high-through flow cytometry. A motivated candidate could also embark on related projects to measure the statistical structure of fitness landscapes.

Applicants must have a Ph.D. in biology or a related field, and experience in molecular or evolutionary genetics. The postdoc will be based in the FAS Center for Systems Biology at Harvard University, an interdisciplinary center housing faculty and fellows from numerous departments (see <http://sysbio.harvard.edu/csb/> for further details). To apply, send a brief outline of research interests, a CV, and names of two or more references to Michael Desai (mdesai@oeb.harvard.edu). Review of applications will begin immediately and continue until the position is filled.

mdesai@oeb.harvard.edu

HumboldtU 7 EvolutionGameTheory

Postdoc Position Stipend (full-time position, 2100 â–p.m.)

The newly established Center (CILS) invites applications for seven 18-month Postdoc positions at Humboldt-Universität zu Berlin, starting on 1 May 2010. The successful candidates are expected to pursue one of seven designated projects in an interdisciplinary research environment during the 18 months - an extension is possible but depends on additional funding.

One of the areas of specification for the different projects is

Evolution and Behavioral Game Theory (theoretical biology, psychology, economics)

(for more details see www.cils.info)

The Center for Integrative Life-Sciences has a highly interdisciplinary research focus. Candidates should have experience in interdisciplinary work within one of the center's main research areas:

â Action and Decision-making

â Conditions of Cooperation: Perspective Taking, Empathy, Communication

â Norms, Conventions, Institutions

The application package should include:

â Letter of interest

â CV

â Proof of the candidate's doctoral degree (Xeroxes only!)

â Two letters of recommendation (in the original)

Applications received within three weeks after publication of this advertisement (16 April 2010) will be assured full consideration. Humboldt-Universität zu Berlin is an Equal Opportunity Employer. Candidates are requested to email a PDF version to anna.strasse@staff.hu-berlin.de.

Peter Hammerstein <p.hammerstein@biologie.hu-berlin.de>

Lisbon ConsGenetics Madagascar

The Population and Conservation Genetics group (<http://www.igc.gulbenkian.pt/research/unit/-88> and http://compbio.igc.gulbenkian.pt/pcg/-pcg_home.html) is looking for a post-doctoral re-

searcher to work on the impact of fragmentation on lemurs from Northern Madagascar.

The project is funded by the Portuguese Science Foundation (Fundação para a Ciência e a Tecnologia. The Project (ref. PTDC/BIA-BEC/100176/2008) will involve lab, field and simulation work under the supervision of L. Chikhi.

The post-doc (and technicians hired in the same project) will be based at the "Instituto Gulbenkian de Ciencia" (IGC, <http://www.igc.gulbenkian.pt/>), a leading Research Institute in Portugal and in Europe (selected as one of the top Post-doc Institutes in Europe). Researchers at the IGC work on a wide range of subjects from epidemiology, to genetics, evolutionary biology, bioinformatics and theoretical immunology. The IGC is located in Oeiras, a small sea-side town 20 min. by train from downtown Lisbon, along the Tagus. It is only 10-15 min. walking distance from the beaches and the quality of life is excellent. The IGC provides excellent research conditions and English is the communication language among and within groups. Several other research institutions are located nearby addressing both fundamental and applied questions in biomedical and evolutionary sciences using interdisciplinary approaches.

POST-DOC JOB in conservation genetics:

Habitat loss and fragmentation in Lemurs from Northern Madagascar

The post-doctoral candidate is expected to work in close collaboration with a field assistant and a lab technician. Since the post-doc and technicians are expected to be complementary, we are open regarding the profile that the post-doctoral should have. S/he could thus be a biologist with a strong interest for modelling, a biologist working in the laboratory or a theoretician with an equally strong interest in biological problems. Excellence and adaptability are the main selection criteria.

The Month Stipend follows the regulations of the FCT Scientific Fellowships in Portugal (euro 1495.00/month) and will initially be for 12 months but the successful candidate will be encouraged to apply for independent funding from international or Portuguese funding bodies. Note that costs are much lower in Portugal than in many European places.

Applications should be sent by e-mail in a unique pdf document named as follows "Candidate-Name_Mada_PostDoc.pdf". This document should contain the /Curriculum Vitae/ and a Letter of Motivation. Reference letters from previous supervisors should be sent *independently* by the referees to the same address using the following file name: "Candidate-

Name_Mada_PostDoc_SupervisorName_Reference.pdf": netics Web <http://webpace.qmul.ac.uk/ranichols/-research.htm>
 Email: chikhi@igc.gulbenkian.pt

Applications sent outside this format may be considered ineligible.

Application DEADLINE: 15.05.2010

Earliest STARTING DATE: 01.06.2010

chikhi@cict.fr

London Conservation Genetics

Conservation Genetics PDRA

This is a postdoctoral position for a scientist who wants to contribute to a the task of putting Conservation Genetics to practical use- i.e. to make the expertise of Conservation Geneticists available to conservation managers and policy makers. They will work as part of a European Union funded consortium, CONGRESS (Conservation of Genetic Resources for Effective Species Survival).

The PDRA's role will be to seek out and evaluate the relevant information needed by conservation managers if they are to make effective use of the advances in genetic technology, population and conservation genetics. The PDRA will identify examples of best practice, guidance and new innovations, in particular tools that European policy makers can use to incorporate genetic biodiversity into their policy framework.

The PDRA will work to School of Biological and Chemical Sciences to populate a database with information and examples that meet the standards and objectives developed by the consortium. Candidates for this position should have a PhD in a relevant field or equivalent professional experience demonstrating excellent skills that will allow them to evaluate conservation genetics research, the quality of data, methods (including those exploiting new sequencing technologies) and analytical approaches.

This is a full-time post for 18 months or a part-time post for 36 months. Salary is in the range of £33,659 per annum (full-time). The salary is inclusive of London Allowance. Benefits include 30 days annual leave and a final salary pension scheme.

For further details please contact r.a.nichols@qmul.ac.uk

Richard Nichols Professor of Evolutionary Ge-

London Modelling Systems Biology

Postdoctoral Researcher in modelling and data analysis for systems biology This is a position in the collaborative ERASYSBIO+ funded project "Living with uninvited guests - comparing plant and animal responses to endocytic invasions". The project aims to understand the way in which the Salmonella bacterium interacts with its host during invasion of the bacterium using a systems biology approach. The post is available for 36 months and is based in the Mathematical Biology group at Royal Holloway, University of London. You will develop new methods to extract information about the functionality and properties of the pathways from the systems biology data, and apply these methods to data on the Salmonella bacterium, generated within the collaborative project. You should have a PhD degree in a quantitative science (like biology, statistics, mathematics or physics), experience in modelling and statistics and an affinity towards Biology. The main aim of this post is to apply and develop methods of qualitative statistical inference to interpret systems biology data, in particular time resolved data of the infection process of the Salmonella bacterium For further information see <https://mathbio.bl.rhul.ac.uk/vacancies/vacancies>
 Vincent Jansen Professor of Mathematical Biology

School of Biological Sciences Royal Holloway, University of London Egham, Surrey TW20 0EX, U.K.

Tel : (..) 44 1784 443179 Fax : (..) 44 1784 470756 Email: vincent.jansen@rhul.ac.uk Web : <http://www.rhul.ac.uk/Biological-Sciences/-AcademicStaff/Jansen/> "Jansen, Vincent" <Vincent.Jansen@rhul.ac.uk>

MaxPlanck EvoBio Sterile Insect Resistance

Postdoctoral position: Experimentally assessing the feasibility of genetically engineered sterility in insect populations.

A two-year postdoc position is available, to start im-

mediately, to screen for the evolution of resistance to transgenic constructs which sterilize insects, in the population genetics group of the Max Planck Institute for Evolutionary Biology.

Classical sterile insect technique was developed in the 1950s to suppress pest insect populations in a response to the widespread evolution of insecticide resistance. Recently, a great deal of interest has turned towards the use of genetically engineered sterility (e.g. Cyranoski, 2008, Sterile mosquitoes near take-off. *Nature* 453:435). Funding has been obtained from the DFG (German national research foundation) to independently test for and study the possible evolution of resistance to sterilizing transgenes in laboratory populations. This will be done in the *Drosophila* model with one of two approaches currently proposed for release (we already have this system working in the lab).

I am looking for someone with a Ph.D. or equivalent degree, with a high degree of familiarity in standard molecular genetics laboratory experience (most importantly cloning, but also Southern-blotting and inverse-PCR). Experience in working with *Drosophila* is not essential and I would encourage applications from people in any molecular biological field who are willing to think creatively and learn new techniques. I think this is an exciting opportunity to contribute in a practical way to an area that is likely to attract intense scientific and public interest over the next 5 years because of regulatory moves towards implementation of this type of technology (see <http://www.epa.gov/fedrgstr/EPA-IMPACT/2009/May/Day-07/i10633.htm> and <http://www.efsa.europa.eu/en/tendersawarded/tender/cftefsagmo200901.htm>). There will also be opportunity to contribute to other projects within my laboratory which are also focused on genetically modifying pest populations for human health and conservation purposes and the detection and analysis of forms of positive selection.

I do not discourage anyone from applying based on age, sex, race, political views, or nationality. Applicants will be selected based on scientific merit. I also do not discourage applicants from applying that may have concerns over the possible applications of genetic pest management, as long as this enhances rather than inhibits research and dialogue.

The Max Planck Institute for Evolutionary Biology is located in Plön, Germany, near the Baltic coast between the northern German cities of Kiel and Lübeck. The institute has a diverse scientific environment which also includes work on questions of evolution in, for example, the mouse (recent adaptation), stickleback (including host-parasite interactions), *Cottus* (hybrid

speciation) and yeast (experimental evolution) systems with additional projects and groups focused on evolutionary theory and bioinformatics. See <http://www.evolbio.mpg.de/english/index.html> for more information. The working language of the institute is English.

Payment will be in the form of a stipend for 24 months with a pay scale that is dependent on years of postdoc experience, marital status and number of children, approximately 2100 to 2800 Euros per month. The stipend is tax free, but health insurance and retirement contributions are not covered (private insurance is required).

Interested candidates should send an email message with a statement of interest and experience, an attached CV in PDF format and the names, affiliation and email addresses of three potential references to reed@evolbio.mpg.de with "SIT resistance application" in the subject line.

Floyd A. Reed, Ph.D.

<http://www.evolbio.mpg.de/~reed/>
reed@evolbio.mpg.de

MPI Gottingen HumanPopGenetics

Postdoctoral Fellowship - Population Genomics

The newly formed group for Biophysics and Evolutionary Dynamics at the Max-Planck-Institute for Dynamics and Self-Organization in Göttingen is looking for a highly motivated postdoc to work with Oskar Hallatschek on the inference of recombination rates and (time-dependent) population sizes in the recent history of human populations.

On the basis of a novel parameter-free method to reconstruct recombination rates in Human populations, we aim at an improved Bayesian inference of past demographic events based on Human genome data sets. The project will involve a combination of theoretical and computational approaches. The successful applicant should have a PhD in Biology, Bioinformatics, theoretical Physics or Statistics, and some previous experience in population genetics, statistics and programming (e.g. in C/C++, Java, or R).

The postdoc will join a young and interactive research group focusing on nonequilibrium statistical physics and evolutionary dynamics, including theoreticians and

experimentalists. We cultivate an international atmosphere and the everyday working language is English. The MPI DS is located close to the center of the medieval town of Göttingen. More information about the group is available on the web at: <http://www.evo.ds.mpg.de> The successful applicant will receive a 2 years postdoctoral fellowship. The net salary starts at approximately 2100,- per month depending on age and experience. Interested candidates should send a cover letter summarizing their research background and interest in the position, CV, and contact information of three potential referees as a single PDF file to: oskar.hallatschek.applications@gmail.com

Applications will be reviewed beginning April 30, 2010. Interviews will be held in May. If you have any specific questions (e.g. details of the project), feel free contact the group leader.

The Max-Planck-Institute for Dynamics and Self-Organization is an Equal Opportunity/Affirmative Action Employer and has an affirmative action policy for the disabled.

oskar.hallatschek.applications@googlegmail.com

Portugal PathogenDiversity

Postdoctoral Fellowship at Instituto Gulbenkian de Ciencia:

The application to one Postdoctoral Fellowship is open under Project PTDC/BIA-BEC/103484/2008, entitled "Exploring pathogen diversity in disease epidemiology and vaccine research", financed by Fundação para a Ciência e a Tecnologia.

1. Duration: The Fellowship will have the duration of 24 months, starting by September 2010, in exclusiveness regime, as regulated by the human resources of FCT (<http://www.fct.mctes.pt/pt/apoios/formacao/ambitoprojectos>) and fellowships regulation of Instituto Gulbenkian de Ciência (<http://www.igc.gulbenkian.pt>). 2. Subject of Activities: Research on the population biology of microparasites, combining approaches from ecology and evolution. The project is primarily mathematical and computational, but an experimental component may be included depending on the profile of the selected candidate. 3. Scientific Supervision: Gabriela Gomes (Collective Dynamics). 4. Selection Criteria: PhD in Computational Biology or Genetics, and strong motivation for popu-

lation biology. 5. Month Stipend: According to the regulations of FCT Postdoctoral Fellowships in Portugal (€1495.00/month). 6. Application Documents : Curriculum Vitae, statement of research interests, and contacts for two referees. 7. Application Period : Until 30 April, 2010. Gabriela Gomes Instituto Gulbenkian de Ciência Email : ggomes@igc.gulbenkian.pt

Gabriela Gomes <ggomes@igc.gulbenkian.pt>

Rennes France QTLmapping

Post-doctoral position in QTL mapping of reproductive strategies in the pea aphid, INRA Rennes, France

A one year post-doctoral position is available in a research laboratory, UMR BiO3P (<http://www.rennes.inra.fr/bio3p>), located near Rennes (Brittany, France) and belonging to the French Institute for Agriculture Research (INRA). This post-doc position is funded by ANR (French Research Agency) and is part of a project coordinated by the host team aimed at elucidating the genetic and molecular basis of reproductive strategies in an important group of crop pests, the aphids. Aphids are among the rare organisms capable of shifting from clonal to sexual reproduction by using the same genotype (phenotypic plasticity). Furthermore, sexual (cyclically parthenogenetic) and asexual (obligately parthenogenetic) lineages frequently coexist within the same species or even the same population (genetic polymorphism). The scientific objective of the post-doc fellowship is to identify through association and quantitative genetics QTLs linked to reproductive strategies in aphids. For that, a vast panel of F2 resulting from crosses between sexual and partially asexual lineages and for which phenotypic characterization is ongoing, will be genotyped at several hundreds microsatellite markers already available in the lab. A linkage map will be constructed and QTLs will be mapped. Because this project is carried out on the pea aphid for which the complete genome has been recently published, genomic regions in the vicinity of QTLs will be analyzed and the function of neighborhood genes will be explored. The post-doctoral fellowship will be achieved in a multidisciplinary and active research group including population geneticists, genomicists, bioinformaticians, and modelers. This lab has full access to high throughput genotyping, as it hosts the genotyping platform of Biogenouest (life science core facility network).

Required skills: association or quantitative genetics,

population genomics, QTL mapping, linkage map construction, high throughput genotyping

Salary: 1850 \hat{a} -netDuration :

OneyearfromOctober2010Deadline :

June15, 2010. Please provide a cv + list of publications as well as an application to <http://eeb.rice.edu/>

Jean-Christophe SIMON, directeur de recherche INRA, tel. 0223485154, e-

mail jean - christophe.simon@rennes.inra.fr

Practical information Rennes is a medium size French city at 2h from Paris by high speed train and at 45 minutes from the sea coast and Mont Saint Michel. Our research center is located at Le Rheu, 8 km from Rennes, and is used to welcome foreigner scientists. On demand, seeking for accommodation and help with the French administrative system can be provided.

Selection of papers from the host team Halkett F., Plantegenest M., Bonhomme J. & Simon J.C. (2008) Gene flow between sexual and facultatively asexual lineages of an aphid species and the maintenance of reproductive mode variation. *Molecular Ecology* 17, 2998-3007 Le Trionnaire G, Francis F , Jaubert-Possamai S, Bonhomme J, De Pauw E, Gauthier J-P, Haubruge E, Legeai F), Prunier-Leterme N, Simon J-C, Tanguy S and Tagu D. 2009. Transcriptomic and proteomic analyses of seasonal photoperiodism in the pea aphid. *BMC Genomics* 10: 456 Nespolo R.F., Halkett F., Figueroa C.C., Plantegenest M. and Simon J.C. (2009). "Evolution of trade-offs between sexual and asexual phases and the role of reproductive plasticity in the genetic architecture of aphid life histories." *Evolution* 63(9): 2402-2412. International Aphid Genomic Consortium (2010) The complete sequence of the pea aphid genome. *Plos Biology* 8(2): e1000313. Peccoud J., Olivier A., Plantegenest M. & Simon J.C. (2009a) Ecological speciation through gradual cessation of gene flow in the pea aphid complex. *Proceedings of the National Academy of Sciences of the United States of America*, 106, 7495-7500. Peccoud J., Simon J.C., McLaughlin H.J. and Moran N.A. (2009b). "Post-Pleistocene radiation of the pea aphid complex revealed by rapidly evolving endosymbionts." *Proceedings of the National Academy of Sciences* 106(38): 16315-16320.

- Jean-Christophe SIMON UMR BiO3P INRA-Agrocampus Ouest-Universit  Rennes 1 INRA Domaine de la Motte B.P. 35327 35653 Le Rheu Cedex - France tel. +33 (0)223485154 fax + 33 (0)223485150 e-mail: jean-christophe.simon@rennes.inra.fr

jean-christophe simon <jean-christophe.simon@rennes.inra.fr>

Open Huxley Faculty Fellow Position IN EVOLUTION:

The Ecology & Evolutionary Biology Department of Rice University (<http://eeb.rice.edu/>) seeks to fill a Huxley Faculty Fellow position.

This non-tenure track faculty position is a two-year appointment and a third year extension possible, with a possible start date as early as August 2010. Our prestigious Huxley Fellow Program at Rice University, Ecology & Evolutionary Biology was established in honor of Julian Huxley, son of Thomas Huxley, and aims to recruit outstanding researchers with a PhD and, possibly, some postdoctoral experience, who merge excellence in teaching (25%) and research (75%). We invite applications from broadly trained evolutionary biologists with interests in areas including organismic evolution, molecular evolution, and evolutionary bioinformatics.

The Huxley Fellows receive faculty status, employee benefits, competitive salary, and research funds for independent or collaborative research. Collaborative interests with the existing faculty are a plus. Previous Huxley fellows who held this position moved on to tenure track faculty positions at prestigious national and international universities. Application review will begin immediately, 2010. Rice is an Equal Opportunity and Affirmative Action Employer.

Please electronically submit applications including curriculum vitae, statement of research interests, and three letters of reference to: rdh@rice.edu - Subject Huxley Search, or by regular mail to the attn. of Diane Hatton, Huxley Fellow Search, Department of Ecology and Evolutionary Biology, MS-170, Rice University, 6100 S. Main St., Houston, TX 77005, U.S.A. Review of applications will begin in May 1st, 2010 and continues until the position is filled.

Please contact Michael H. Kohn (www.ruf.rice.edu/~hmkohn/MKohn.html), Chair, Huxley Fellow Search Committee, at hmkohn@rice.edu or 713 348 3779) for any questions.

Michael H. Kohn Assistant Professor Rice University Department of Ecology & Evolutionary Biology Institute of Biosciences & Bioengineering

Mailing address: Michael H. Kohn EEB MS-170 Rice University 130 Anderson Biology P.O. Box 1892 Hous-

ton, Texas, 77251-1892 USA

For packets: Michael H. Kohn EEB MS-170 Rice University 130 Anderson Biology 6100 Main street Houston, Texas 77005 USA

Phone: 713-348-3779 (lab - Ext 6227) Fax: 713-348-5232 hmkohn@rice.edu

<http://www.ruf.rice.edu/~hmkohn/index.html> To visit our lab: we are located in 130 Anderson Biology 205. See Rice campus Map: <http://www.rice.edu/maps/-maps.html> - enter through Rice Boulevard and Entrance 20, take Visitor parking lot (on map indicated by an N, and the campus observatory is located on it) to the right (insert credit card to enter, you will not be charged when you leave if we can get you a visitor pass). Walk down Alumni Drive. Our Building (Anderson Biology) is to the left at the first intersection you encounter (corner Alumni and Laboratory drive also called Loop Road). We are in 205 on the second floor.

Michael Kohn <hmkohn@rice.edu>

RiceU MicrobialEvolution

Post Docs in Microbial Experimental Social Evolution in Social Amoebae at Rice University, then Washington University in St. Louis One or more postdoctoral positions for 2-3 years are available immediately for work on the social amoeba *Dictyostelium discoideum*, a unique and exciting model organism for social evolution. *D. discoideum* has cooperation, conflict, and complete reproductive altruism in its social stage. It also has a short generation time, sequenced genomes, a library of identified cheater knockouts, and it can be easily studied in the laboratory and the field. Projects include testing whether social conflict leads to rapid evolution and arms races, determining how cheating is controlled, kin recognition, and relating laboratory findings to social evolution in the wild. Experimental evolution projects can also be done on social function. We are a friendly and interactive team of highly motivated investigators. We are seeking an energetic postdoc with a strong background in evolutionary biology, social behavior, microbial evolution, or molecular biology with an interest in working at the interface of these disciplines. Check out our website, www.ruf.rice.edu/~evolve for more information on our research. If you are interested, please send an email to David Queller (queller@rice.edu) or Joan Strassmann (strassm@rice.edu) with a CV, statement of research

interests, and the names, phone numbers and email addresses of three references. Women and minorities are particularly encouraged to apply. We will begin reviewing applications immediately and will continue to do so until the position is filled which we hope to happen by 20 May 2010. The entire lab group will move to Washington University in St. Louis in June 2011 where we will join a very dynamic biology department in newly renovated space. David C. Queller, Joan E. Strassmann, Department of Ecology and Evolutionary Joan Strassmann <strassm@rice.edu>

SouthAfrica AquaticBiodiversity

IBOL IDRC Post Doctoral Position in South Africa

The South African Institute for Aquatic Biodiversity (SAIAB) is offering a 3 year post-doctoral position funded by the Canadian International Development Research Centre to support the growth and expansion of aquatic biodiversity DNA barcoding (www.dnabarcodes.org). The main tasks will be to support the FISH-BOL project in Africa (www.fishbol.org) and to increase the DNA barcode reference library for aquatic organisms in support of SAIABs core research initiatives.

The ideal candidate should have a PhD with a strong background in Zoology (especially Systematics) and/or with experience in molecular techniques. An interest or experience in natural history collections and field surveys will be an advantage.

The position is available immediately.

To apply, please email an expression of interest to Ernst Swartz or Monica Mwale as soon as possible or before the 14th of May 2010 (go to <http://www.saiab.ac.za/-index.php?pid=8> or fax us at +27 46 622 2403). You are welcome to contact us directly for further details (tel.: +27 46 603 5800).

SAIAB is a national facility of the National Research Foundation and is an internationally recognised centre for the study of aquatic biodiversity.

Ernst Swartz <ernst.swartz@gmail.com>

+41-(0)26-300 88 71 Fax: +41-(0)26-300 96 98
dieter.ebert@unibas.ch

Switzerland Evolutionary Genomics

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:

UArkansas Plant Evolution

A postdoctoral position in plant evolutionary ecology is available at the Department of Biological Sciences at the University of Arkansas. The USDA-funded project is evaluating mechanisms by which global change factors interact with population level phenomena to trigger outbreak population dynamics. Of special interest is the introduction and residence of transgenes in naturalized weed populations by way of crop-weed hybridization. We hypothesize that the risks of transgene establishment will increase as beneficial transgenes migrate to naturalized or weedy species, and that risks of genetic contamination will grow with escalating demand for value-added agricultural products. The successful applicant will be responsible for extended field work, greenhouse hybridization trials, and supervision of students. Applicants must have a Ph.D. in a relevant field, such as ecology or evolutionary biology. Experience in DNA sequencing and analysis, phylogenetic and phylogeographic analysis and plant hybridization expertise and expertise in statistical analysis is necessary. Previous work with domesticated plants is a plus. The initial appointment will be for one year with the possibility of extension. The deadline for applications is 1 May or until the position is filled. To apply, send a c.v., a brief (one page) statement of research goals, and the names and contact information of three references to Dr. Cynthia Sagers, Department of Biological Sciences, SCEN 601, University of Arkansas, Fayetteville, AR 72701. Electronic submission is preferred: email <csagers@uark.edu>.

csagers@uark.edu

UEastAnglia Female Sperm Selection

Please share this announcement with students and colleagues.

Postdoctoral Research Assistant: The role of immune-mediated female sperm selection in temporal dynamics

of fertilisation bias < <http://www.zoo.ox.ac.uk/jobs/> >
Grade 7: Salary £28,983 - £35,646 p.a.

A NERC funded postdoctoral position is available from June 2010 for a period of three years. The goal of the research is to establish the role of female immune-responses to semen in sperm competition and cryptic female choice in birds, using the red junglefowl, *Gallus gallus* as model system. The researcher will combine immunological assays and artificial insemination techniques to study patterns of sperm utilisation under experimental conditions.

Applicants should hold, or be about to obtain, a PhD in a relevant discipline such as immunology, physiology or ecology with a strong interest/experience in evolutionary or ecological immunology. The successful candidate will have: (1) a strong molecular background, and the ability to identify targets, design, validate and interpret real-time RTPCR assays, (2) skills in cellular biology, including isolating and handling immune and non-immune cells, culture and proliferation assays, (3) experience of antibody based techniques (ELISA, Western blotting, immunostaining), (4) ability to relate in vivo and ex vivo data sets (and to work in both areas), (5) a strong desire to explore immune function in relation to reproductive physiology and sexual selection, (6) robust skills in experimental design, quantitative analysis and data interpretation, (7) organisational skills, responsible attitude and ability to work independently and as part of a multi-disciplinary team, and (8) willingness to support and develop the skills of more junior staff and students. Field experience/animal handling will also be a benefit.

The project will be undertaken at the Department of Zoology of the University of Oxford, under the supervision of Dr. Tom Pizzari and Dr. Adrian Smith, in collaboration with Dr D.S Richardson in the School of Biological Sciences at UEA. The researcher will be based in the Department of Zoology of the University of Oxford, linking the laboratories of Dr Pizzari (Edward Grey Institute of Ornithology) and Dr. Smith (Immunology). The Department of Zoology at the University of Oxford has a long-standing reputation for world class research and teaching. The EGI is one of the fastest-growing groups of the Department, and conducts research in behaviour, ecology, evolution and conservation of birds, with a strong emphasis on understanding organisms in their natural environments. Further information about the Department and the EGI can be found at <http://www.zoo.ox.ac.uk/>.

Informal enquiries to Dr Adrian Smith (adrian.smith@zoo.ox.ac.uk <<mailto:adrian.smith@zoo.ox.ac.uk>>).

Dr T. Pizzari (tommaso.pizzari@zoo.ox.ac.uk <<mailto:tommaso.pizzari@zoo.ox.ac.uk>>)
or Dr David Richardson

(david.richardson@uea.ac.uk <<mailto:david.richardson@uea.ac.uk>>)

Further particulars, including full project details and application forms are available from <http://www.zoo.ox.ac.uk/jobs> or from the Personnel Office of the Department of Zoology, University of Oxford (Tinbergen Building, South Parks Road, Oxford OX1 3PS; phone: 01865 271190; email: recruit@zoo.ox.ac.uk <<mailto:recruit@zoo.ox.ac.uk>>).

Applications, together with a CV and contact details of three referees, should be sent to the above address quoting reference number AT10014. The closing date for applications is 7 May 2010. We hope to make an appointment by 1 June 2010.

Thank you

David S Richardson Reader in Molecular Ecology Centre for Ecology, Evolution and Conservation School of Biological Sciences University of East Anglia e-mail: david.richardson@uea.ac.uk Norwich NR4 7TJ ph: (44) 01603 591496 ENGLAND fax: (44) 01603 592250

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

UHelsinki ParasiteEvolution

PARASITE ECOLOGY AND EVOLUTION AT THE UNIVERSITY OF HELSINKI

Applications are invited for a 4-year PhD fellowship / 3-year post doc to study parasite evolution by combining ecological, evolutionary and molecular approaches.

The project is centered on the interaction between host plant *Plantago lanceolata* and its fungal pathogen *Podosphaera plantaginis* in the Åland Islands. Prior research on this interaction has shown that the pathogen persists as a metapopulation. Despite rapid turnover of local populations there is evidence of rapid ongoing evolution between these species. In your project you will ask how processes at different spatial scales â molecular, within host, within population and metapopulation â affect the diversity and evolution of pathogens. In practice, you will carry out field surveys in the Åland Islands, conduct experimental work in the laboratory and genotype pathogen isolates using SNP markers.

The tommaso.pizzari@zoo.ox.ac.uk (Dr. Tommaso Pizzari) and Liisa Laine is part of the Parasite Ecology and Evolution Research Group, Centre of Excellence

appointed by the Academy of Finland, where you'll find a wide range of expertise studying ecological and evolutionary questions within a spatial framework.

Please send your application to anna-liisa.laine@helsinki.fi by 10 May 2010. Attach a CV (with possible publications included), contact details of two references, and a letter (MAX 1 page) with a description of your researcher interests and why you would be a suitable candidate for the project. The work is scheduled to start in the summer-autumn of 2010.

For more information, please contact Dr Anna-Liisa Laine (anna-liisa.laine@helsinki.fi) and visit our websites at www.helsinki.fi/science/metapop. For information on the University of Helsinki, please visit: <http://www.helsinki.fi/university/index.html> Anna-Liisa Laine <anna-liisa.laine@helsinki.fi>

UHohenheim PlantAdaptation

The research group in Crop Biodiversity and Breeding Informatics in the Institute of Plant Breeding, Seed Science and Population Genetics focuses on the development and application of methods to study the adaptation of wild and crop plants to their environment and to utilize this knowledge for plant breeding. We have an open position for a

SENIOR POSTDOC/GROUP LEADER

We are looking for a committed scientist who works in one of the following areas:

• Environmental adaptation in model or crop plants
• Evolution and genetics of crop domestication
• Population and quantitative genetic methods for genetic mapping and plant breeding

Candidates with a Ph. D. degree in plant breeding, bioinformatics, quantitative genetics or evolutionary biology and a strong interest in current genomic or quantitative approaches are welcome to apply. Very good computing skills and an interest in applying evolutionary approaches to plant breeding are a plus. The position offers the possibility for independent research, and the acquisition of funding from national and international sources is highly encouraged.

The successful applicant will be initially appointed for three years with the possibility of extension for another three years. Salary will be according to the German

government salary scale and depends on previous experience, age and marital status. Some teaching is required, which will be conducted in English, and there is the possibility to obtain the Habilitation.

The University of Hohenheim is located on a beautiful campus in the South German city of Stuttgart and is well integrated into national and international research networks. Further information about our group can be obtained from <http://evoplant.uni-hohenheim.de> or from the contact information below.

Please send your application (Cover letter, CV, publications, statement of research interests, addresses of at least two references) until 30 April 2010 as a single PDF document to Bärbel Hessenauer (hessenauer@uni-hohenheim.de).

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

Prof. Dr. Karl Schmid F.W. Schnell Endowed Professorship of Crop Biodiversity and Breeding Informatics Institute of Plant Breeding, Seed Science and Population Genetics (350) University of Hohenheim Fruwirthstrasse 21 D-70599 Stuttgart Germany Phone: +49 711 459 23487 Fax: +49 711 459 22343 Email: karl.schmid@uni-hohenheim.de <http://www.evoplant.uni-hohenheim.de> Karl Schmid <karl@minzer-schmid.de>

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>

UKansas PlantEvoDevo

A POSTDOCTORAL POSITION is available in the laboratory of Dr. Lena Hileman at the University of Kansas, department of Ecology and Evolutionary Biology, to study the evolution of flower development. The selected candidate will be involved in a project that uses both gene expression and functional analyses to determine the fate of duplicated genes in the developmental genetic network establishing bilateral flower symmetry among close relatives of the model species snapdragon (*Antirrhinum majus*). Specific skills associated with the project include: gene isolation (PCR/cloning), mRNA expression analyses (quantitative rtPCR, in situ mRNA hybridization), functional characterization of gene products (using a transient, reverse-genetic approach, Virus Induced Gene Silencing), assessment of gene trees (phylogenetic analysis), basic plant care in greenhouses/growth chambers, and supervision of undergraduate students working on the project. Candidates will be required to have completed a PhD in Plant Biology, Evolutionary Biology, Cell/Molecular Biology or a related field. The ideal candidate will have a background in plant biology, with excellent knowledge of

plant morphology, be creative, enthusiastic and highly motivated to pursue studies on the evolution of floral development, and have excellent molecular genetic skills. Funding is available for one year with the possibility of extension. See the Hileman web page at <http://www2.ku.edu/~eeb/faculty/hileman.html>. For more information, and to find out about the application process, please contact Lena Hileman (lhileman@ku.edu).

Dr. Lena Hileman Assistant Professor University of Kansas Ecology and Evolutionary Biology 1200 Sunnyside Ave., Rm. 8003 Lawrence KS 66045 785-864-5861 785-864-5321 (fax) lhileman@ku.edu <http://www.ku.edu/~eeb/faculty/hileman.html> lhileman@ku.edu

UKonstanz MolEvolution

Postdoc: U Konstanz. Molecular Evolution, Bioinformatic, Genomics

POSTDOC POSITION - in molecular evolution, genomics or bioinformatics

At the University of Konstanz we have an opening for a postdoc position available immediately in the lab of Axel Meyer at the Department of Evolutionary Biology and Zoology at the University of Konstanz in Germany.

Through the funding of the University of Konstanz by the “excellence initiative” of the German government and the German Science Foundation we are in the process of establishing a genomics/proteomics center. It currently includes already both Roche 454 FLX and Illumina GAIx next generation sequencing platforms. Hence, we are particularly interested in a postdoc with expertise in molecular evolution, genomics and bioinformatics. This area of research at the University of Konstanz will be strengthened further by a “junior professorship” in bioinformatics that will soon be filled.

These positions are also affiliated with the new graduate school in chemical biology (for more information visit <http://www.chembiol.uni-konstanz.de/>) and the new International Max-Planck Research School in Organismal Biology (<http://cms.uni-konstanz.de/organismal-biology/>).

The postdoc projects we are interested in have to do with fish genomics and in particular comparative transcriptomics and genomics of cichlid fish. Other projects deal with the evolution of gene families and the evolution of the genome in early chordates and vertebrates.

Candidates should have a strong interest in bioinformatics, developmental and evolutionary biology and should be experienced in molecular techniques and/or computational biology.

Appointments are for two years initially with a salary according to German TV-L salary scale that includes extensive health and retirement benefits. The initial contract period would be for two years with the potential for additional years of funding. Informal inquiries should be addressed to Prof. Axel Meyer, Ph.D. (axel.meyer@uni-konstanz.de).

Further information on our research can be obtained from our web page: <http://www.evolutionbiologie.uni-konstanz.de/index.php?section> . For publications see <http://www.evolutionbiologie.uni-konstanz.de/-index.php?section> ' .

Applications should include a CV, statement of research interests and email addresses of two references. Review of applications will commence on May 1st 2010. Starting dates are flexible. Applications should be sent as one pdf file to axel.meyer@uni-konstanz.de.

This search will remain open until the positions are filled – Prof. Axel Meyer, Ph.D. Lehrstuhl für Zoologie und Evolutionsbiologie Department of Biology Building M, Room M806 University of Konstanz 78457 Konstanz Germany fon + 49 7531 88 4163 fax + 49 7531 88 3018 secretary: Ingrid.Bader@ uni-konstanz.de tel. + 49 7531 88 3069

Axel Meyer <axel.meyer@uni-konstanz.de>

ULaussane 4 AntEvolution

4 postdoctoral positions: Ant behaviour/ genomics/ bioinformatics

University of Lausanne, Department of Ecology and Evolution

We are looking for postdoctorals to work on three lines of research:

1. Ant behaviour. The idea is to study the dynamics of division of labour with a new system based on fiducial identification labels and video tracking. This system which automatically follow all the individuals in a colony will allow the first quantitative studies of behaviour.

2. Artificial evolution with robots. We want to study how the level of cooperation within colonies, the reliability

of communication systems and division of labour have been shaped by within-colony relatedness and other social factors

3. Ant genomics. We are currently sequencing the fire ant genome and are looking for bioinformaticians and molecular biologists interested in making use of this genome to address questions related to social behaviour.

These positions will be funded by an ERC-funded grant and the Swiss NSF. Other topics of research on social behaviour are also possible if they fit the research interests of our group :

<http://www.unil.ch/dee/page7717.html> The Department of Ecology and Evolution is a well-funded and vibrant research institution, with superb facilities.

<http://www.unil.ch/dee/page5090-en.html> Inquiries and applications can be sent to laurent.keller@unil.ch. Applications should comprise a CV, a list of publications, 1 page describing why you are interested in joining our group and contact information for three referees. Only applications with all these informations will be considered.

PHD POSITION IN POPULATION GENOMICS

University of Lausanne, Department of Ecology and Evolution

We are looking for for a highly motivated student to work on the population genomics of the fire ant *Solenopsis invicta*. The work will include, collection of samples in South American and the US, use of a microarray that we developed in our laboratory and computational analyses of the data.

The position is for 3 years- Gross salary follows the Swiss NSF scale and is around CHF 40,000.- per year.

Our group (<http://www.unil.ch/dee/page7717.html>) is part of the Department of Ecology and Evolution, a well-funded and vibrant research institution, with superb facilities.

<http://www.unil.ch/dee/page5090-en.html> Inquiries and applications can be sent to laurent.keller@unil.ch. Applications should comprise a CV, a list of publications, 1 page describing why you are interested in joining our group and contact information for three referees. Only applications with all these informations will be considered.

Laurent Keller Department of Ecology and Evolution Biophore University of Lausanne 1015 Lausanne Switzerland

http://www.unil.ch/dee/page7717_fr.html Laurent Keller <Laurent.Keller@unil.ch>

ULaval EvolSystBiol

Applications are invited for a postdoctoral position in evolutionary systems biology at the Laval University Institute for Integrative and Systems Biology (IBIS)(Quebec, Canada) to study how natural genetic variation in the budding yeast *Saccharomyces cerevisiae* affects evolutionarily and ecologically important traits.

The successful candidate will study the genetic architecture, evolution and robustness of signalling networks using the budding yeast and its close relatives as models. The last decade has seen exponential growth in the pace of DNA sequencing and revolutions in microscopy, computing, and molecular visualization techniques. These advances have made it possible to dissect the inner workings of cells as they respond to internal or external cues. Despite the wealth of new data produced by these technologies, it remains remarkably difficult to predict how mutations or recombination affect complex physiological and morphological traits. Understanding how genetic variation is converted into observable differences between organisms is crucial for developing personalized medical treatments, bioengineering cellular machines or fuels, and predicting the evolutionary potentials of different alleles. Several levels of organization (gene expression, protein localization, posttranslational modifications, protein-protein interactions) will be studied in order to construct genotype-phenotype maps of complex phenotypic responses. The project will be tailored according to the fellows interest.

This project is a collaboration involving Dr Scott Rifkin (University of California San Diego, USA) and Dr Madan Babu (University of Cambridge, UK) and is funded by the Human Frontier Science Program (HFSP).

Applicants must hold a PhD in biology or in a related discipline. The candidate should have strong experience in molecular biology and preferably also in microbiology. Experience with high throughput screening and genotyping, statistics and yeast genetics would be an asset.

Universit Laval is one of the first higher education institution in the Americas and is one of the leading universities in Canada. Located in Quebec City, a UNESCO world heritage city, Universit Laval offers an outstanding research and training environment for scholars.

Time of initial appointment: September 2010 (flexible).

Review of applications begins immediately and will continue until the position is filled

Initial term of one year renewable for up to three years.

Competitive salary (40,000\$/year) depending on previous experience.

Interested candidates should contact Christian Landry (clandry@post.harvard.edu) and include a cover letter describing research interests, a CV and the names of two referees.

Visit our website for more details on our research

<http://www.bio.ulaval.ca/landrylab/>

Christian Landry <Christian.Landry@bio.ulaval.ca>

UNeuchatel QstFst comparison

Postdoctoral position to work on the dioecious plant *Silene latifolia* and its pollinator-seed predator *Hadena bicurris*.

The project involves a Qst/Fst comparison for the two interacting species across a set of populations for which we are currently gathering phenotypic and genetic data. In particular we wish to compare geographic variation in traits potentially involved in this complex plant-insect interaction. Additional data sets are available allowing quantitative genetic analyses of several life history and reproductive traits of the plant, or can be completed with additional experiments.

The ideal candidate has a strong background in statistics, quantitative and population genetics and an interest in plant/insect interactions and coevolution. Ideally, the candidate should be experienced with Qst/Fst comparisons.

The University of Neuchatel (Switzerland) offers competitive conditions, up-to-date facilities, and opportunities of interaction (e.g. the Institute hosts the National Competence Center Plant Survival, <http://www2.unine.ch/nccr>) as well as good quality of life in a pleasant setting. The language in our research group is English.

Possible start date: August 1, 2010. The grant funding this position runs until January 31st 2012 (and may be potentially extended).

To apply please send as a single PDF file your CV with

publication list, and the name and phone number/email of three referees to Giorgina.bernasconi@unine.ch.

Giorgina Bernasconi Fusi Professor, Evolutionary Botany Institute of Biology University of Neuchâtel Switzerland

giorgina.bernasconi@unine.ch +41 32 718 23 40

<http://www2.unine.ch/Jahia/site/evobot/op/-edit/pid/27262> <http://www2.unine.ch/evobot/-page26093.html> References:

Labouche A. M., G. Bernasconi, Male moths increase mutualistic benefits in the *Silene latifolia* â Hadena bicruris pollination, seed predation system â Functional Ecology in press (online early)

Elzinga J A, Bernasconi G, Enhanced frugivory on invasive *Silene latifolia* in its native range due to increased oviposition â Journal of Ecology 97, 1010-1019 (2009)

Burkhardt A., L.F. Delph, G. Bernasconi, Benefits and costs to pollinating, seed eating insects: the effect of flower size and fruit abortion on larval performance â Oecologia 161, 87-98 (2009)

Jolivet C, Bernasconi G, Molecular and quantitative genetic differentiation European populations of *Silene latifolia* (Caryophyllaceae) â Annals of Botany 100, 119-127 (2007)

Jolivet C, Bernasconi G, Experimental analysis of constitutive and induced defence in a plant-seed predator system â Functional Ecology 20, 966-972 (2006)

Burkhardt A., Ridenhour BJ, L.F. Delph, G. Bernasconi, The contribution of a pollinating seed predator to selection on sexually dimorphic traits in *Silene latifolia* â in review

BERNASCONI FUSI Giorgina
<giorgina.bernasconi@unine.ch>

UNovaDeLisboa DiseaseEvolution

Dear Evoldir Members

I ask you to please advertise this position. Thanks

H.Silveira hsilveira@ihmt.unl.pt IHMT Portugal

Post-Doc grant.

One year renewable up to 32 months.

Instituto de Higiene e Medicina Tropical (IHMT), Universidade Nova de Lisboa (UNL), Portugal

Salary: 1.495,00 /month

Please quote post reference: Imunostim/MAL/1/2010

Closing date for applications: 13th April 2010

Applications are invited for a Postdoctoral Research scientist to work on a project funded by the FCT (National Scientific Foundation), Portugal to investigate the role of immune stimulatory molecules on mosquito *Anopheles gambiae* response against the malaria parasite *Plasmodium berghei* (PTDC/SAU-MII/102596/2008). The project will identify immune stimulatory molecules capable of triggering protective responses in the mosquito and characterize the molecular mechanisms of resistance to infection.

We seek a highly motivated individual with experience in molecular biology, able to use murine malaria models and an interest in innate immune system and host parasite interactions. Prior experience in bioinformatics, mainly on microarray analysis, image analysis and parasite biology would be advantageous. Applicants must have a PhD or postdoctoral experience in a relevant subject.

The successful candidate will be based at IHMT-UNL, Lisbon, the proteomics part of the project will be performed at the INSA Ricardo Jorge, Lisboa. For further information regarding the post please contact Dr. Henrique Silveira (hsilveira@ihmt.unl.pt; +351 213652657)

Applicants should send to the above address or e-mail:

- a) Letter of motivation
- b) Curriculum vitae (maximum 10 pages)
- c) Letters of recommendation
- d) Copy of degree certificate
- e) Copy of ID document

H. Silveira

e-mail: hsilveira@ihmt.unl.pt

Ref. Imunostim/MAL/1/2010

Instituto de Higiene e Medicina Tropical

Rua da Junqueira, 100

1349-008 Lisboa

Portugal

cbsilveira@netcabo.pt

UOxford Crow tool use

UNIVERSITY OF OXFORD DEPARTMENT OF ZOOLOGY

Postdoctoral Research Associate: Tool use in New Caledonian crows Grade 7, salary range: 28,983 – 35,646 GBP p.a.

A three-year postdoctoral position is available, from May 2010 onwards, to work on the ecological and social context of tool use in New Caledonian crows (*Corvus moneduloides*). The post is funded as part of a 5-year BBSRC David Phillips Fellowship to Dr Christian Rutz, and will be based at the Department of Zoology, University of Oxford, UK. The post-holder will be responsible for coordinating and conducting fieldwork in New Caledonia, South Pacific. The research project will chart the ecology and behaviour of wild, free-ranging crows, using detailed field observations, systematic surveys, and novel biollogging technologies. In addition, specific hypotheses will be examined in controlled experiments with wild and captive subjects. This is an exceptional opportunity to conduct topical field research on animal tool use and culture in a high-profile study system, and to take a leading role in a prolific and expanding research project.

The successful candidate will have a PhD in behavioural ecology, ecology, evolutionary biology or a related subject, and experience in conducting independent field research, preferably in remote study locations. Proven skills in writing and publishing papers in leading scientific journals are essential. Experience of supervision in a research context, and working as part of a multi-disciplinary team are desirable. Previous field-ornithological experience, or a background in animal-cognition research, are not essential.

Informal inquiries (with CV) should be addressed directly to Dr Christian Rutz (christian.rutz@zoo.ox.ac.uk).

Further particulars and application forms are available from <http://www.zoo.ox.ac.uk/jobs> or from the Personnel Office of the Department of Zoology, University of Oxford (Tinbergen Building, South Parks Road, Oxford OX1 3PS, UK; phone: +44(0) 1865 271190; email: recruit@zoo.ox.ac.uk). Application forms, together with a CV and contact details of three referees, electronic copies of three publications, and a cover let-

ter explaining how the candidate meets the selection criteria, as outlined in the further particulars, should be sent to the above address quoting reference number AT10013.

The closing date for applications is 7 May 2010. Interviews with short-listed candidates are expected to take place in May.

Christian Rutz <christian.rutz@zoo.ox.ac.uk>

UppsalaU DrosophilaEvolutionary-GeneticsGenomics

Postdoc opportunity for up to two years in the research group of Dr Urban Friberg at the Department of Evolutionary Biology, Uppsala University. Our research group has a broad general interest in the area of evolutionary biology/genetics and ongoing projects focus on aging, genetic conflicts and mutation rates. See <http://www.egs.uu.se/evbiol/Persons/Urban.html> for more information on previous projects. Most projects are conducted using a *Drosophila melanogaster* model system.

The successful applicant is primarily expected to work on two new projects i) genomic distribution of regulatory elements, with an emphasis on those regulating sex-biased genes and ii) the relative contributions of additive and epistatic genetic variation to variation in the transcriptome. Above and beyond these there are good opportunities to develop projects after own interests, within the field of evolutionary biology/genetics.

We are looking for a highly motivated postdoc having a PhD in biology, genetics or a related field, and a strong interest in evolutionary biology/genetics. Documented experience in one or several of the following topics is highly beneficial: statistics, quantitative genetics, programming in R, microarrays/RNAseq and *Drosophila* genetics/lab work. He/she should work well both as a member of a group as well as independently, and also be proficient in both written and spoken English.

The Program in Evolutionary Biology (<http://www.egs.uu.se/evbiol/index.html>) is situated in the Evolutionary Biology Centre Uppsala (http://www.ebc.uu.se/index_eng.php). The working atmosphere is international with English as working language. The Evolutionary Biology Centre constitutes an exciting arena for multidisciplinary research in evolutionary biology in a broad sense, with research

programs including ecology, systematics, genetics, genomics, and developmental biology. Uppsala University is the oldest university in Scandinavia and the city of Uppsala is a vibrant student town with beautiful surroundings conveniently situated 40 minutes with train from Stockholm.

To apply, send your CV, including contact information for three references, and a cover letter stating your research interest and your preferred starting date to: Urban Friberg (urban.friberg@ebc.uu.se). Review of applications will begin immediately.

urban.friberg@ebc.uu.se

URochester EvolutionaryParasitology

Post-doc in ecological parasitology at the University of Rochester

I am seeking a post-doc to join our group in the Department of Biology at the University of Rochester. The position starts as early as May 1, 2010 and extends through April 30, 2011, with possibility for a 6-month extension. The research is funded through a Grand Challenges Explorations Grant from the Gates Foundation. The aim of the initial phase of the research is to determine whether maternally transmitted symbionts interfere with the development of filarial nematodes within blackfly vectors. If the initial phase of the research is successful, there is a possibility of additional, longer-term funding.

Qualifications: The candidate should have experience with DNA isolation, PCR, and qPCR. Experience with cytological methods would also be very helpful. Pay will be commensurate with qualifications.

To apply, please send a curriculum vitae, brief description of research experience and interests, and the names of 2 references to John Jaenike, Department of Biology, University of Rochester, Rochester, NY 14627. Or, email the application to me at joja@mail.rochester.edu. Review of applications will begin immediately and continue until the position is filled.

John Jaenike <joja@mail.rochester.edu>

USheffield AvianMicroevolution

A postdoctoral position, funded by the European Research Council (ERC), is available in Dr Jon Slate's research group (<http://www.jon-slate.staff.shef.ac.uk/>) at the University of Sheffield. This is an outstanding opportunity to apply cutting edge genomics technologies (ultra-high throughput sequencing and SNP genotyping) to study microevolution in a classic long-term, individual-based study system - the great tit population at Wytham Woods Oxford (<http://www.zoo.ox.ac.uk/egi/research/studysites.htm>).

I am looking for somebody with a track record of publishing in leading journals and skills in one or more of the following areas: evolutionary quantitative genetics, QTL mapping, genomewide association studies, molecular evolution or statistical genetics. The post-doc will work as part of a team of three (with the PI and one other postdoc) investigating the genetic basis of adaptive variation in a system which has been the focus of intensive evolutionary ecology and quantitative genetics studies (e.g. Garant et al. 2005 Nature 433: 60-65; Charmantier et al 2008 Science 320: 800-803) but where genomics resources were, until recently, lacking. In this project we have used high-throughput sequencing (Roche 454) to sequence the great tit transcriptome and mine many thousands of SNPs. We will shortly be typing 10,000 SNPs in several thousand birds to build a linkage map and then perform quantitative trait /genome wide association mapping. Genotyping will be outsourced. We will then use QTL mapping approaches to address questions relevant to microevolution. For example publications from our laboratory see <http://www.jon-slate.staff.shef.ac.uk/html/publications.html>. The project involves close collaboration with Professor Ben Sheldon (Oxford University) and his research group (<http://www.zoo.ox.ac.uk/egi/index.htm>) as well as a group in the Netherlands working on a similar project.

Dr Slate's group is based within the vibrant Department of Animal & Plant Sciences at the University of Sheffield. In the latest Research Assessment Exercise (RAE 2008), Biological Sciences at Sheffield was ranked joint 3rd in the UK based on average quality score and 3rd in the UK based on the proportion of 'world-leading' (4*) and 'internationally excellent' (3*) research activity (Source: Times Higher Education) It was recently ranked 7th best Environment/Ecology

research institution in the world by Thomson Scientific. Sheffield is a fantastic place to live, situated on the edge of the Peak District National Park (<http://www.visitpeakdistrict.com/>). It is also one of the most affordable cities in the UK and has a good music, arts and culture scene.

The position is available as soon as possible and is funded for a further 3 years. The closing date is 17th May 2010. For further details and online applications see <http://www.sheffield.ac.uk/jobs/index.html>, quoting job reference number UOS001076. The salary is in the range £28,139 per annum. I welcome informal enquiries (j.slate@sheffield.ac.uk)

Dr Jon Slate Dept. Animal & Plant Sciences University of Sheffield <http://www.jon-slate.staff.shef.ac.uk/> j.slate@sheffield.ac.uk

UTurku LifeHistoryEvolution

3-4 postdoctoral/senior researcher posts in ecological interactions and ecological genetics, University of Turku, Finland

Ecological interactions and ecological genetics is one of six areas of research strength at the University of Turku. The Department of Biology hosts three ISI Highly cited scientists and a national Center of Excellence focussed on research in this area, including projects on trophic and interspecific interactions, life-history evolution, environmental ecology, and ecological and evolutionary genetics (see http://www.sci.utu.fi/biologia/en/research/research_projects/ for more details)

3-4 research positions (initially for 1 year but extension to 3 years is possible) are available to further strengthen the University's research profile in these fields. The postdoctoral/senior researchers will be expected to take part in the planning and research in existing projects and/or their own projects. Researchers selected for the posts are required to have a doctoral degree, demonstrated ability to conduct independent scientific research and to supervise MSc and PhD students. The salary is according to the salary system of Finnish universities (approx 2,900 - 4,000 per month).

Applications should include a CV including degrees obtained, prior research and supervision experience, publication list, a max. 1 page letter of motivation, a research plan (max. 5 pages) and contact information for

2 referees. The positions are available from 1st June 2010.

Turku, Finland's 5th largest city (176 000 people), is located in the South-Western part of Finland. It has a rich cultural history and is the gateway to a beautiful archipelago. The University of Turku is one of the major multidisciplinary universities in Finland and the City of Turku was ranked third in the most recent classification of medium-sized 'Smart Cities' (<http://www.smart-cities.eu>)

For more information, contact: Prof. Erkki Korpi-maki, tel. +358-2-3335699, ekorpi@utu.fi Prof. Pekka Niemela, tel. +358-2-333 5777, pekka.niemela@utu.fi Prof. Craig Primmer, tel. +358-2-333 5571, craig.primmer@utu.fi

Applications (preferably by email) to majjaliisa.airaksinen@utu.fi or Maija-Liisa Airaksinen, Department of Biology, University of Turku, FIN-20014 Turku, Finland, fax. +358-2-333 6598 Deadline for applications is 10 May 2010.

Craig Primmer

Professor of Genetics Division of Genetics and Physiology Department of Biology (Vesilinnantie 5) 20014 University of Turku FINLAND

tel. +358 2 333 5571 fax. +358 2 333 6680 craig.primmer@utu.fi <http://users.utu.fi/primmer>
Craig Primmer <craig.primmer@utu.fi>

YaleU BacteriaEvolution

A one-year postdoctoral position is available immediately under the co-supervision of Paul Turner and David Post in the Department of Ecology and Evolutionary Biology at Yale University. The project concerns empirical tests of theory on niche invasion and eco-evolutionary feedbacks, using bacteria as a model system. The project will be conducted using high-throughput, especially automated measures of evolving bacterial phenotypes and culturing of populations using liquid-handling robotics. Experience with high-throughput technology and with a bacterial system such as *E. coli* is preferred, but all strong candidates will be considered. Please direct inquiries to paul.turner@yale.edu

paul.turner@yale.edu

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Bologna HumanEvolution May17-19

Da: European Genetics Foundation [serena.paterlini@eurogene.org] Inviato: 21 April 2010 11:54 Oggetto: Course in Human Genomic and Cultural Evolution of Humans (Bologna, May 17-19, 2010)

Dear All, We are pleased to announce next ESGM course in Human Genomic and Cultural Evolution of Humans (Bologna, Italy, May 17-19,2010).

The course will be held at the EuroMediterranean University Centre of Ronzano, (Bologna) and it will provide detailed information on the tools useful for the study of human genomic evolution High-throughput, large scale genotyping, using both microarrays and massive sequencing to survey both SNPs 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. Workshops will show how bioinformatic tools can be used to analyse 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 biological and cultural evolution. It will also

provide a rapid exposure to the “state of the art” for investigators contemplating studies, or the utilization of tools, in this and other fields, like linguistics.

Directors: D. Luiselli (Bologna, Italy), D. Pettener (Bologna, Italy), M. Rocchi (Bari, Italy), R. Stanyon (Florence, Italy).

Faculty: G. Barbujani (Ferrara, Italy), F. Calafell (Barcelona, Spain), L.L. Cavalli Sforza (Stanford, UK), 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). Registration fee: 500 (+ vat 20%) including accommodation in double room, tuition, lunches, coffee breaks and shuttle bus. Please note that the European Society of Human Genetics (www.eshg.org < <http://www.eshg.org> >) makes available fellowships for young participants. For further info visit EGF website (www.eurogene.org < <http://www.eurogene.org> >) or write to serena.paterlini@eurogene.org <mailto:serena.paterlini@eurogene.org>

Thank you in advance, Serena Paterlini

Serena Paterlini Training and EU Projects European Genetics Foundation Via di Gaibola, 16 40138 Bologna tel:0039051-2088414 fax:0039-0515870611

serena.paterlini@eurogene.org

Denmark SystemsBiology Sep5-8

PhD course 5th -8th September 2010

Introduction to systems biology in evolutionary and conservation biology

Organizers: Pernille Sarup, Torsten Kristensen, Vanessa Kellermann, Department of Biological Sciences, Aarhus University, Ny Munkegade 1540, 8000 Aarhus C, Denmark.

Venue: Sandbjerg Estate, Sandbjerg 102, 6400 Sønderborg

<http://www.sandbjerg.dk/eng/welcome.aspx> Supported by: Nordforsk Network and Aarhus Stress Network

Exploring the use of omics technology in natural populations

5th - 8th September 2010

Workshop contacts: Pernille Sarup (pernille.sarup@biology.au.dk), Vanessa Kellermann (vanessa.kellermann@biology.au.dk)

The use of omics technology (genomics, transcriptomics, proteomics, metabolomics) in evolutionary and ecological biology is increasing. This workshop will aim to explore the different levels of omics technology in an ecological and evolutionary context with a focus on methods and analysis of different omics technology as well as exploring how these different technologies can be integrated to form a systems view of evolutionary biology.

In this Ph.D course and workshop we bring together researchers with a primary focus on the use and integration of omics techniques in evolutionary and conservation biology. We have organised attendance from leading scientists in the field that will give lectures on relevant topics. The students will receive a compendium with original research articles representing the latest research within the topic. During the course time will be set aside for group discussions on central themes based on the articles, and also there will be time to discuss your own projects. Students will be expected to actively participate in the workshop with a presentation of either a talk or poster on your design or results in order to obtain 5 ECTS.

Additional information will be available on the NordForsk website: <http://www.helsinki.fi/biosci/egru/-norden/workshops.html> Deadlines:

Sign up by sending an email to the workshop contacts before 1st of June. Send in your abstract before 15th of August.

Payment:

For members of the NordForsk network participation is for free. Also you can apply for travel grants. Participants from outside Scandinavia please contact for course costs.

List of confirmed speakers

Prof Douglas Crawford, The University of Miami, USA.

Assistant Prof Dr Margie Oleksiak, The University of Miami, USA

Prof Christian Schlötterer, The Veterinärmedizinische Universität Wien, Austria

Anders Malmendal, The Interdisciplinary Nanoscience Center at Aarhus University, DK.

Jesper Bechsgaard, Department of Biological Sciences, Aarhus University, DK.

Jesper Sørensen, National Environmental Research Institute, Aarhus University, DK.

Torsten Nygård, Faculty of agricultural sciences, Aarhus University, DK.

Peter Sørensen, Faculty of agricultural sciences, Aarhus University, DK.

Prof Ole Nørregaard Jensen, Department of Biochemistry and Molecular Biology, University of southern Denmark, DK.

– Department of Biology Aarhus University

pernille.sarup@biology.au.dk

Edinburgh EvoSysBio2010 Oct15

We invite abstract submissions for oral and poster presentations at the workshop “Evolutionary systems biology”, to be held for half a day on 15 October 2010 after the International Conference on Systems Biology (ICSB) in Edinburgh, UK (10-15 October 2010):

<http://evolutionarysystemsbiology.org/meeting/2010-ICSB/index.html> Registration is free but places are limited and there are two abstract registration

deadlines:

1) The official ICSB abstract deadline is on ** Mon 3rd May 2010 **. Most places will be allocated to participants of ICSB on a first come first served basis. To register here, go through the normal ICSB registration process at <http://www.icsb2010.org.uk/> 2) The workshop abstract deadline is on ** 21 May 2010 **. A few places will be reserved for researchers wishing to come only to the EvoSysBio workshop but not to ICSB. To register, directly email Laurence Loewe as soon as possible.

The workshop is aimed at researchers with an interest in bridging the genotype-phenotype gap with mechanistic models. These models may quantify aspects of any level of the adaptive landscape with a view towards connecting empirical evidence from different levels. This can be done using theoretic, computational, genomic, experimental, systems biology or other approaches and might target anything from very specific molecular systems to whole organisms.

Confirmed speakers: Juliette de Meaux, Institute for Evolution and Biodiversity, Westfälische Wilhelms-Universität, Münster, Germany John Yin Systems Biology Theme Leader, Wisconsin Institute for Discovery, Department of Chemical and Biological Engineering, University of Wisconsin-Madison, USA

Updates on this workshop will be posted on its website: <http://evolutionarysystemsbiology.org/meeting/2010-ICSB/index.html> We are looking forward to seeing you in Edinburgh.

The organizers Laurence Loewe, Centre for Systems Biology at Edinburgh University of Edinburgh, UK Email: Laurence.Loewe@evolutionary-research.net Martin Lercher Chair for Bioinformatics Heinrich Heine University, Düsseldorf, Germany <http://www.cs.uni-duesseldorf.de/AG/BI/Englisch> Chris Knight Faculty of Life Sciences, University Manchester, UK <http://www.mcisb.org/people/knight/> About evolutionary systems biology

Evolutionary genetics has a long history of successful quantitative modelling, especially in areas where functional details can be abstracted by selection coefficients. Molecular biology has a long history of uncovering functional details and has recently started to engage in quantitative modelling at a larger scale, giving rise to current systems biology. We propose to bring these two fields together to help elucidate some fundamental problems in evolutionary biology. Such a synthesis has the potential to provide a mechanistic basis for in silico predictions of many important parameters of evolution, including distributions of mutational effects, robustness

and epistasis. Central to this approach is the definition of fitness correlates that can be computed using mechanistic models of individuals. One possible aim for modelling in evolutionary systems biology could be to define computable fitness correlates that can be calibrated experimentally by measuring mutant properties.

This ambitious goal can inspire experimental and theoretical work at many levels of the adaptive landscape. These levels include: 1. Changes in genotypes impact predicted molecular structures (like protein structures). 2. Changes in molecular structures impact predicted molecular functions (like enzyme reaction rates). 3. Changes in molecular functions impact predicted properties of reaction networks (see systems biology). 4. Changes in reaction network properties impact predicted fitness correlates (need to be defined for each model). How fitness correlates are mapped to fitness is defined at even higher levels (see life-history evolution). All levels ultimately need to be brought together to facilitate computational predictions of realistic mutational effects, robustness, epistasis and adaptive evolution.

Here we aim to bring together researchers with an interest in the adaptive landscape at any level and researchers who want to contribute towards a synthesis of evolutionary genetics with mechanistic models of life. We believe that the new excitement in systems biology is an excellent opportunity for progress in many fundamental evolutionary questions, if the new models that are being constructed can be extended to include fitness correlates that turn them into powerful tools for investigating

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Fiskebackskil Sweden EvoDevo Jul12-23

EMBO course “Marine animal models in evolution and development”

12 - 23 July 2010 in Fiskebackskil, Sweden

<http://cwp.embo.org/pc10-34/> Please advertise the course to potential students.

This course focuses on the establishment of molecular

techniques and genomic resources in established and emerging marine animal models for the study of developmental biology and evolution (evo- devo), marine neurobiology and behavioral and comparative genomics.

Students can register before April 30th using this link: <http://cwp.embo.org/pc10-34/application.html>
Best wishes,

Andreas Hejnol

Andreas Hejnol, Group Leader Sars International Centre for Marine Molecular Biology Thormøhlensgate 55 NO-5008 Bergen NORWAY

Phone: +47 55 58 43 28 Fax: +47 55 58 43 05 email: andreas.hejnol@sars.uib.no

<http://www.sars.no/research/HejnolGrp.php>

New Open Access Journal "EvoDevo": <http://evodevojournal.com/> andreas.hejnol@sars.uib.no

Germany Evolution Diversity Arthropod Symbiosis Jun30-Jul3 2

In the frame of the COST Action FA0701 « Arthropod Symbioses: from fundamental studies to pest and disease management » We are pleased to announce the workshop entitled: Evolution and Diversity of Symbioses of Arthropods The workshop will be held from the 30th of June to the 3rd of July 2010 in Bad Bevensen, Germany.

Symbioses with bacteria and other microorganisms have contributed greatly to the ecological and evolutionary success of arthropods, either by providing essential nutrients or digestive functions, or more unusual functions such as bioluminescence or contributing to healthcare of their hosts. Other endosymbionts engage in more parasitic interactions with their hosts by distorting their hosts sex ration to ensure their own transmission. This stunning diversity of symbioses already became evident early in the 20th century, e.g. by the wide range of associations included in Paul Buchners seminal book "Endosymbiose der Tiere mit Pflanzlichen Mikroorganismen" published in 1953.

Since then numerous symbiotic associations have been characterized in great detail, with microbial partners being identified, genomes of endosymbionts being sequenced and functions of the symbionts uncovered. The use of culture independent techniques has led to a

great leap forward in uncovering the diversity present in arthropod hosts as well as their specificity. Recent work on a broad range of arthropod symbioses will be presented, with a wide range of microorganisms involved that are located in a variety of organs such as antennal glands, gut, malphigian tubules or reproductive tissue.

Whereas biologists recently became aware of the importance of mechanisms of hostsymbiont interactions and the involvement of the immune system as an interface between the two, we are only beginning to understand how the crosstalk between different endosymbionts can alter the outcome of symbiotic associations when hosts harbour endosymbiont consortia and how diverse some of these consortia can be. In addition more and more players in symbiotic interactions are uncovered as well as new functions. Are such endosymbiont consortia stable in composition? Does competition among different endosymbionts for host resources harm the host as certain functions are provided in a lesser manner? How easily can such endosymbiont consortia including gut microflora be invaded by other microorganisms?

In this workshop, we welcome talks on different kinds of symbiotic interactions from mutualistic to parasitic and comprising either single endosymbionts or endosymbiont consortia. The very beginning of endosymbiosis will be discussed. How are free living organisms incorporated into other organisms to become endosymbionts?

Tentative list of invited speakers: James Lake (UCLA, USA) William Martin (University Düsseldorf, Germany) Andreas Brune (Max-Planck Institute Marburg, Germany) Molly Hunter (University of Arizona, USA) Edouard Jurkevitch (University Jerusalem, Israel) Martin Kaltenpoth (Max-Planck Institute Jena, Germany) Eva Novakova (University South Bohemia, Czech Republic) Ameer Cherif (University Tunis, Tunisia) Daniele Daffonchio (University Milano, Italy) Fabrice Vavre (University Lyon, France) Alison Dunn (University Leeds, UK) Massimo Marzorati (University Gent, Belgium) Jan Engelstädter (ETH Zürich, Switzerland) Cara Gibson (National Ecological Observatory Network (NEON), Boulder, USA) Einat Zchori-Fein (Newe Ya'ar Research Center, Israel) Peter Neumann (Swiss Bee Research Centre Agroscope, Switzerland) Alexandre Aebi (Forschungsanstalt Agroscope, Switzerland) Richard Cordaux (University Poitiers, France) Julien Varaldi (University Lyon, France) Matthias Horn (University Wien, Austria) Rok Kostanjsek (University Ljubljana, Slovenia)

Outline of the program June 30: arrival day, welcome reception. July 1st: Oral communications, Evening poster session. July 2nd: Oral communica-

tions, Evening poster session. July 3rd: departure Day Communications and Poster session Communications will be on invitation. However, a poster session will be organized and there will be time for discussions. Participants willing to present a poster should send a title and an abstract to Heike Feldhaar (feldhaar@biologie.uni-osnabrueck.de) before May 10th, 2010. In case that there is still time for oral contributions we will contact registered participants.

Location and access The workshop will be held in the Gustav-Stresemann Institute in Bad Bevensen, Germany. Bad Bevensen can be reached easily by train either from Hamburg or Hannover. Both towns have an international Airport (alternatively from Frankfurt Airport via Hannover by train). Bad Bevensen is a small town in Northern Germany, close to the Lüneburg Heath, which is renowned for hiking. The conference venue is situated in vicinity of the abbey Medingen that was built in the 13th century.

Registration and accomodation The Conference Registration and Accomodation Form should be completed



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Hinxtion HumanGenomeAnalysis Jul21-27

Wellcome Trust Advanced Course Human Genome Analysis: Genetic Analysis of Multifactorial Diseases 21-27 July 2010 Wellcome Trust Genome Campus, Hinxtion, Cambridge

NEW EXTENDED Deadline for applications: 23 April 2010

Course summary An intensive, residential, computer-based course aimed at scientists actively involved in genetic analysis of multifactorial traits.

Programme This advanced course covers statistical methods currently used to map disease susceptibility genes, with an emphasis on (but not limited to) methods that can analyse family data or a combination of families and individuals. Discussions of the latest statistical methodology are complemented by practical hands-on computer exercises using state-of-the-art soft-

ware. The statistical basics behind each method will be carefully explained so that participants with a non-statistical background can understand.

With a focus on family data, we will discuss fundamental issues needed to increase success in gene mapping studies including: optimal study design, power to detect linkage and association, determining the most appropriate statistical methods and software, interpretation of statistical results and trouble shooting. We will also cover the basic principles of statistical inference, hypothesis testing, population and quantitative genetics and Mendelian inheritance. Our interactive and intensive educational program will enable one to better carry out sophisticated statistical analyses of genetic data, and will also improve one's interpretation and understanding of the results. All the software used is freely available, so that skills learned can be easily applied after the course.

Teaching will take the form of lectures by invited speakers, informal tutorials, hands-on computer sessions, and analysis of disease family data sets. There will also be an opportunity to discuss participants' own data sets.

Course organisers Daniel Weeks (University of Pittsburgh, USA) Mark Lathrop (Centre National de Genotypage, Evry, France) **Course instructors** Heather Cordell (Institute of Human Genetics, University of Newcastle upon Tyne, UK) Janet Sinsheimer (University of California, Los Angeles, USA) Eric Sobel (University of California, Los Angeles, USA) Joe Terwilliger (Columbia University, New York, USA) Chad Garner (University of California, Irvine, USA) Simon Heath (Centre National de Genotypage, Evry, France)

Guest speakers Dr. Simon E. Fisher (Wellcome Trust Centre for Human Genetics, Oxford, UK) Dr Jonathan Marchini (Department of Statistics, University of Oxford, UK) Professor Chris Holmes (Department of Statistics, University of Oxford, UK) Professor David J Balding (Institute of Genetics, University College London, UK) Professor Matthew Stephens (University of Chicago, USA)

Cost The course tuition fees are subsidised by the Wellcome Trust for scientists based in non-commercial institutions anywhere in the world. This is a residential course, without exception, and there is a registration fee of £800 towards board and lodging for non-commercial applicants. The fee for commercial applicants is £3000.

Bursaries Limited bursaries are available for academics (50 per cent of fee) and are subject to open competition. Please see our bursaries page for application information and terms and conditions.

Applications Applicants will be required to complete

an application form containing a 300-word outline of the relevance of the course to their research. Please note that documentation supporting their application will be required from the applicant's supervisor/head of department.

See <http://www.wellcome.ac.uk/Education-resources/-Courses-and-conferences/Advanced-Courses/Courses/-WTX026851.htm> for the application

For inquiries:

F +44 (0) 1223 495130 E advanced-courses@hinxton.wellcome.ac.uk

Janet@mednet.ucla.edu

ImperialCollege London Pops under pressure Jun9-11

Dear colleagues,

Here is a second announcement of the Populations under Pressure symposium which will run again between June 9th-11th at Imperial College London, Silwood Park, UK.

The symposium is aimed at convening PhD students and early stage post-docs for interdisciplinary discussions within the broad field of applied population biology and conservation. This year's themes are Range Limits and Global Change and Uncertainty in Models.

Participants will gather in a friendly setting where they will have the opportunity to present their own work and participate in workshops with an international group of researchers from different backgrounds. The workshops will be complemented by plenary presentations from leading researchers in applied population biology and a number of transferrable skills sessions, alongside evening social events.

We ask you to please forward this invitation to students and colleagues in your lab and department as well as other interested parties.

Full details of the invited speakers, the workshop topics, contact email addresses and application procedures can be found on our website: <http://www.iccs.org.uk/-PuP10.htm>. Deadline for applications is 30th April 2010.

With thanks,

Lynsey & the rest of the PuP 2010 organising committee

Lynsey McInnes PhD Student Imperial College London Silwood Park Campus

<http://www.bio.ic.ac.uk/research/apurvis/lynsey.htm>

http://www.justgiving.com/offset_silwood_carbon

lynsey.mcinnnes01@imperial.ac.uk

IST Austria 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 Schlotterer (Vetmeduni Vienna) Daniel Kronauer (Harvard U) Daven Presgraves (U Rochester)

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

Application deadline: May 15th.

Michael Alfaro <michaelalfaro@ucla.edu>

Portugal TreeAnalysis

Dear Brian

There is a new course available in Portugal that concerns tree analysis and manipulation. I think that it should be interesting to let the community know

ETE10 - Analysis and manipulation of phylogenomic data using ETE

<http://gtpb.igc.gulbenkian.pt/bicourses/ETE10/>
Cheers Pedro

Pedro Fernandes Centro Português de Bioinformática
Instituto Gulbenkian de Ciência Apartado 14 2781
OEIRAS PORTUGAL

Pedro Fernandes <pfern@igc.gulbenkian.pt>

SantaBarbara R Jun17-21

Announcement: Comparative Methods and Macroevolution In R Summer Short Course

We are pleased to announce an intensive short course on using R to perform comparative methods to be held in Santa Barbara on June 17-21. This course is funded by the National Science Foundation, and a number of stipends to cover or defray travel, room, and board are available to qualified students and post-docs. Topics covered will include an introduction to the R programming language, tree manipulation, independent contrasts and phylogenetic generalized least squares, ancestral state reconstruction, models of character evolution, diversification analyses, and community phylogenetic analysis. If you are interested please send your CV along with a short (maximum 1 page) description of your research interests, background, and reasons for taking the course. We especially encourage applications from graduate students with data sets to analyze. Please contact the co-organizers, Michael Alfaro (michaelalfaro@ucla.edu) and Luke Harmon lukeh@uidaho.edu with any questions.

Seattle WomenEvolving Oct24-27 Applications

Dear Colleagues,

We are writing to remind you that applications for WEBS 2010 are due April 15. WEBS (Women Evolving Biological Sciences) is an annual three-day symposium aimed at addressing the retention of female scientists and issues related to the transition of women from early career stages to tenure track positions and leadership roles in academic and research settings. The inaugural WEBS symposia were huge successes. Early career participants as well as our senior scientist panelists reported feeling inspired and equipped with new connections and tools that they expect will help them in their career in the years to come. We are now accepting applications online (<http://www.webs.washington.edu> < <http://www.webs.washington.edu/> >) for participation in the 2010 symposium.

WEBS will target early career women in the Biological Sciences with an emphasis on ecology and evolutionary biology. In particular, it will focus on women who have earned their doctoral degrees within the past two to eight years and who do not have tenure in order to address the critical transition period from graduate studies and post-doctoral positions to permanent research and teaching positions. The symposia will provide a forum for professional development, including awareness and improvement of academic leadership skills; opportunities to establish mentoring relationships; and resources for developing professional networks. The 2010 symposium will be held at the Pack Forest Conference center near Seattle, WA from October 24-27, 2010.

Please visit our website (<http://www.webs.washington.edu> < <http://www.webs.washington.edu/> >) for details and application materials. Feel free to contact us with any questions you might have (webs@u.washington.edu).

Sincerely, Samantha Forde, Ph.D. Claire Horner-Devine, Ph.D. Joyce Yen, Ph.D. University of California Santa Cruz University of Washington University of Washington

forde@biology.ucsc.edu

Switzerland Speciation SummerSchool Aug30-Sep3

Announcement: Summer school “Methods of Empirical Speciation Research”

We are happy to announce an international PhD summer school on “Methods of Empirical Speciation Research” that takes place from August 30 to September 3 2010 at the EAWAG Center of Ecology, Evolution & Biogeochemistry in Switzerland.

The school is part of the European Science Foundation Networking Programme Frontiers in Speciation Research (FroSpects) and is open for PhD students and exceptionally well qualified MSc students from all ESF member countries. We have limited travel support and free accommodation for 25 students, and consider applications from now to June 30th. The EAWAG Center of Ecology, Evolution & Biogeochemistry is located in Kastanienbaum, 10 kilometers from Lucerne town on the shores of beautiful Alpine fjord Lake Lucerne.

Speciation research is currently one of the most productive fields of science in evolutionary biology (Sobel et al. 2009 Evolution). Its recent great success is driven significantly by advances in empirical speciation research. A wave of advance came about in the 1990s when molecular population genetics data became readily available and researchers began to integrate these with evolutionary ecology. We are now experiencing a second wave of advance, ushered in by the genomics era. However, studying speciation is a deeply interdisciplinary endeavour. Successful speciation research requires good understanding of several different fields in ecology and evolution. This makes speciation research sometimes more difficult to access for young scientists than more strictly disciplinary research questions in ecology and evolution. The school will introduce advanced graduate students to the way successful speciation researchers integrate concepts and methods from various disciplines to test hypotheses about mechanisms, modes and drivers of speciation.

Our summer school combines modular lecture series, workshops and field excursions to speciation research sites in the Alps. Topics taught include major mechanisms of speciation, hybrid zones, hybrid speciation, adaptive radiation, Fst outlier analysis, speciation genes, natural and sexual selection and their interac-

tion, studying mate choice, role of floral traits in speciation, inferring causality in speciation research. The course emphasizes the integration of theoretical speciation research with empirical methods from different disciplines. The target audience is PhD students and exceptionally well qualified MSc students with background in evolutionary biology.

Distinguished Professors on the course are Roger Butlin (U Sheffield), Scott Hodges (UC Santa Barbara), Catherine Peichel (Fred Hutchinson Cancer Research Centre), Glenn-Peter Saetre (CEES Oslo), and Sander van Doorn (U Bern). The team of Swiss speciation researchers that coordinate the school and contribute to teaching include Elena Conti (U Zürich), Martine Maan (U Bern, Eawag), Walter Salzburger (U Basel), Ole Seehausen (U Bern, Eawag), Arjun Sivasundar (U Bern), Piet Spaak (Eawag) and Alex Widmer (ETHZ).

Prospective participants should send a letter of application and a CV to Nadja Pepe at nadja.pepe@eawag.ch. Applications will be accepted until June 30th. Later applications can be considered if places are available.

For questions, please contact Professor Ole Seehausen (ole.seehausen@eawag.ch).

For more information on the ESF Networking Programme FroSpects, see <http://www.iiasa.ac.at/-Research/EEP/FroSpects/> For more information on the Eawag Center of Ecology, Evolution & Biogeochemistry see http://www.eawag.ch/-organisation/abteilungen/fishec/index_EN
Ole.Seehausen@eawag.ch

Trento Italy ForestGenomics Aug23-26 DeadlineReminder

The registration deadline to the Workshop ‘ Landscape Genomics of Forest Trees and Applications to Climate Change’ is coming up soon - 01 May 2010. Dates of the Workshop have been slightly postponed: the Workshop will be held from August 24 - 27 at the Centro di Ecologia Alpina, Viote del Monte Bondone (TN) Italy. More information can be found on the Workshop web site: <http://-conferences.cealp.eu/conferenceDisplay.py?confId=4>
Cristiano Vernesi Centro di Ecologia Alpina Centro Ricerca e Innovazione - Fondazione Edmund Mach postal address: Viote del Monte Bondone - 38040 Trento - Italy tel +390461939523 - fax +390461948190

- skype name: cvernesi

Please, consider your environmental responsibility before printing this email

Cristiano Vernesi <vernesi@cealp.it>

UCopenhagen HumanPopGenetics Aug16-20

PhD Course in Human Population Genetic Analyses (5 ECTS) Date: August 16 -20, 2010, Dept. of Biology, University of Copenhagen, Copenhagen, Denmark.

Instructors: Andrew G. Clark, John Wakeley, Paul Joyce, Rasmus Nielsen, Ida Moltke, Anders Albrechtsen and Line Skotte.

This course provides a one-week comprehensive introduction to a number of topics and common research tools used in analyses of human population genetic data. Topics include: genetic drift, coalescence theory, natural selection, population structure, human disease and evolution, linkage disequilibrium, association mapping, genomic control, detecting epistatic interactions, haplotype structure, IBD mapping, admixture mapping, genotyping data, re-sequencing data, HapMap data, 1000 genomes project, online resources.

The fee for the course is 1800 DKK (approx. US \$550). The course is free for PhD students at the following Danish universities: KU, AU, AUC, KVL/LIFE, SDU and DTU. The fee does not include food and accommodation. For sign up and questions, please email: cph-summercourse@gmail.com

rasmus_nielsen@berkeley.edu

UCopenhagen SocialEvolution Jul5-9

Residential Ph.D. course:

Evolutionary Genetic Approaches to Study Social Evolution

University of Copenhagen, Denmark, 5-9 July, 2010

FIRST ANNOUNCEMENT

AIMS: To introduce population genetic and quantitative genetic theory and empirical approaches to study social evolution.

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 15-20 students.

TOPICS:

The course will consist of lectures, readings, and discussion on the following subjects:

Population genetics: ' Overview of theory; Subdivided populations; Maternal effects and indirect genetic effects arising from social interactions

Quantitative genetics: ' Overview of theory; Interacting phenotypes and indirect genetic effects; Empirical approaches to studying the genetic architecture of social traits

Kin selection and levels of selection: ' Overview of theory and relation between these two approaches to study social evolution; Empirical measurement of selection; Incorporation of quantitative genetic parameters

Patterns of sequence variation: ' Theory and empirical results comparing sequence variation at loci with direct and indirect genetic effects within and between populations

Evolution of interspecific interactions using a community genetics perspective

Participants will also briefly describe their own research and some of the course topics will depend on interest

TEACHERS: Tim Linksvayer, U. Copenhagen, Denmark Mike Wade, Indiana University, USA

COST: Final cost to be determined, but max DKK 6000 per participant

ECTS credits: 4-5, depending on final program

APPLICATION AND CONTACT:

To apply please send a CV 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.

A second and final announcement will be forthcoming. Please contact Tim Linksvayer (talinksvayer@bio.ku.dk) with any questions.

tlinksvayer@gmail.com

UGroningen EvolBiol

Erasmus Mundus Joint Master in Evolutionary Biology (MEME)

MEME is a new two-year research oriented master programme for talented and motivated students who are interested in understanding evolution in all its facets. The MEME programme will address the driving forces of evolution at all levels of organismal organisation (from cells and individuals to populations and ecosystems), and it will allow students to study all kinds of organisms (microorganisms, plants, animals) in all kinds of habitats (marine as well as terrestrial) with a diversity of approaches (field, lab, theory). The focus of the programme is not only on how evolution shaped life on our planet in the past, but also on how understanding the principles underlying evolution can provide new insights and help to cope with present-day challenges in a variety of fields, including ecology, epidemiology, physiology, immunology, genetics/genomics, bioinformatics, economics and the social sciences.

Only few universities in the world would be able to offer a programme of such broad scope without compromising scientific quality. For this reason, four European universities: - University of Groningen (Netherlands) - University of Montpellier II (France) - Ludwig Maximilians University of Munich (Germany) - Uppsala University (Sweden) have joined forces with Harvard University (USA). Together, this consortium is able to put together an attractive multidisciplinary programme that meets highest standards. All students have to study at at least two partner universities, and they will receive either a joint MSc degree from the whole consortium or double degrees from two partner universities.

Being financed by the European Community, MEME has to satisfy the high quality standards imposed the prestigious Erasmus Mundus Programme. Full scholarships are available for MEME students and will be awarded in a selective procedure.

Starting date: September 2010

Application deadline: April 15, 2010 (European stu-

dents, the deadline for non-European students has already passed)

More information and how to apply: www.evobio.eu

Questions about the application procedure: Piet van den Berg (pieter.van.den.berg@rug.nl) Questions about the contents of the programme: Franjo Weissing (f.j.weissing@rug.nl)

Franz J. Weissing Professor of Theoretical Biology Director Groningen Graduate School of Science Faculty of Mathematics and Natural Sciences Nijenborgh 9 9747 AG Groningen tel. +31 50 363 8669 (or: 2131) E-mail: f.j.weissing@rug.nl URL1: www.rug.nl/gradschoolscience URL2: www.rug.nl/biol/theobio

UGroningen EvolBiol scholarships

Still scholarships available for European students!

There are still a number of scholarships available for European students for following the Erasmus Mundus Master Programme in Evolutionary Biology (MEME). The MEME programme is new two-year research-oriented Master programme in evolutionary biology for talented and motivated students. It is jointly organized by the University of Groningen (Netherlands), the University of Montpellier II (France), Ludwig Maximilians University of Munich (Germany) and Uppsala University (Sweden).

Scholarships for the MEME programme include complete payment of tuition fees, insurance, language courses and travel costs, as well as a monthly allowance of 500 euros per month.

Application deadline: April 15, 2010

More information: www.evobio.eu Franz J. Weissing Professor of Theoretical Biology Director Groningen Graduate School of Science Faculty of Mathematics and Natural Sciences Nijenborgh 9 9747 AG Groningen tel. +31 50 363 8669 (or: 2131) E-mail: f.j.weissing@rug.nl URL1: www.rug.nl/gradschoolscience URL2: www.rug.nl/biol/theobio p240827@rug.nl

Instructions

Instructions: To be added to the EvolDir mailing list please send an email message to Golding@McMaster.CA. At this time provide a binary six letter code that determines which messages will be mailed to you. These are listed in the same order as presented here — Conferences; Graduate Student Positions; Jobs; Other; Post-doctoral positions; WorkshopsCourses. For example to receive the listings that concern conferences and post-doctoral positions this would be 100010. Messages are categorized on the basis of their subject headings. If this subject heading is not successfully parsed, the message will be sent to me at Golding@McMaster.CA. In addition, if it originates from ‘blackballed’ addresses it will be sent to me at Golding@McMaster.CA. These messages will only be read and dealt with when I have time. The code 000000 has all channels turned off and hence gets only a once monthly notification of the availability of a monthly review pdf file.

To be removed from the EvolDir mailing list please send an email message to Golding@McMaster.CA. Note that ‘on vacation’, etc, style messages are automatically filtered and should not be transmitted to the list (I hope), but should you wish to avoid the e-mail’s your code can be temporarily changed to 000000.

To send messages to the EvolDir direct them to the email evoldir@evol.biology.McMaster.CA. Do not include encoded attachments and do not send it as Word files, as HTML files, as L^AT_EX files, Excel files, etc. . . . plain old ASCII will work great and can be read by everyone. Add a subject header that contains the correct category “Conference:, Graduate position:, Job:, Other:, Postdoc:, Workshop:” and then the message stands a better chance of being correctly parsed. Note that the colon is mandatory.

The message will be stored until the middle of the night (local time). At a predetermined time, the collected messages will be captured and then processed by programs and filters. If the message is caught by one of the filters (e.g. a subject header is not correctly formatted) the message will be sent to me at Golding@McMaster.CA and processed later. In either case, please do not expect an instant response.

Afterword

This program is an attempt to automatically process a broad variety of e-mail messages. Most preformatting is collapsed to save space. At the current time, many features may be incorrectly handled and some email messages may be positively mauled. Although this is being produced by L^AT_EX do not try to embed L^AT_EX or T_EX in your message (or other formats) since my program will strip these from the message.