EvolDir

April 1, 2011

Month in Review

Foreword

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

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

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

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Conferences

Auburn AL SEEC Mar25-27

Please Distribute Widely

LAST CALL FOR ABSTRACTS - DUE FRIDAY MARCH 11, 2011

SEEC 2011 SOUTHEASTERN ECOLOGY & EVOLUTION CONFERENCE Auburn University AUBURN, ALABAMA, USA 25-27 MARCH 2011

We invite all undergraduate, graduate, and postdoctoral researchers in ecology, evolution, environmental sciences, limnology, forestry, fisheries, marine sciences, and other related fields to submit abstracts for either oral or poster presentations at the 8th Annual Southeastern Ecology and Evolution Conference (SEEC) to be held March 25-27, 2011, at the Auburn University in Auburn, Alabama. Each year SEEC is hosted by a different southeastern university and is organized by and geared toward students. SEEC is a professional meeting intended for early-career researchers in ecology, evolution, and related fields to present their research to their colleagues in a comfortable, fun, and relaxed atmosphere. Typically 200-300 students give or attend formal presentations and find SEEC to be a valuable forum for sharing research and connecting with other young researchers in the region. This event is designed to encourage new friendships within our field and to share newly develo ped research ideas for feedback. While we expect most SEEC participants to be from the Southeast, we encourage and welcome all interested individuals to submit abstracts and/or attend.

SEEC 2011 homepage: http://gump.auburn.edu/seec2011/ Registration: http://fs22.formsite.com/SEEC2011/form1/index.html The registration fee is $35.00 up to the day of the conference. Awards for both the best oral and poster presentations will be given. There will also be tables from sponsors, including publishers, supply companies, and other organizations (see our web site for a complete list of sponsors). The abstract submission deadline is March 11, 2011, and may be completed at the following web site:

We are pleased to announce that Sunday's keynote speaker is Dr. Alan Wilson, who organized the first

Southeastern Ecology & Evolution Conference in 2004. Dr. Alan Wilson received his Ph.D. in Applied Biology from the Georgia Institute of Technology in 2006. After spending a year as a research investigator at the Cooperative Institute for Limnology and Ecosystems Research (CILER) jointly housed at the University of Michigan and NOAA's Great Lakes Environmental Research Laboratory (GLERL), Alan joined the faculty at Auburn University (AU) as a tenure-track Assistant Professor in 2007. He is jointly appointed in the Departments of Fisheries and Allied Aquacultures & Biological Sciences. Alan is a community ecologist whose research interests revolve around the ecological mechanisms mediating harmful freshwater algal blooms. He is particularly interested in understanding how within-species genetic and phenotypic variation influences community structure and ecosystem function. Alan is also initiating projects aimed at understanding how toxic algal blooms influence human and livestock health. You can learn more about Alan's research at http://wilsonlab.com/ Auburn University is located in downtown Auburn, Alabama and is convenient to numerous hotels, restaurants, and bars (to see what's happening in Auburn, check out these sites www.oanews.com, www.thecornernews.com and www.auburnalabama.org. Registration, abstract submission, travel/lodging information, and contact information may all be found at the SEEC web site: http://gump.auburn.edu/seec2011 Please help us spread the word about SEEC by forwarding this message to any students, colleagues, departments, colleges, or schools that you think might be interested in attending SEEC this year! SEEC facebook event page: http://www.facebook.com/home.php#!/-event.php?eid=167244466650559 We look forward to seeing you at Auburn University for the 8th Annual Southeastern Ecology and Evolution Conference this March!

SEEC Organizing Committee 2011seec@gmail.com

kzk0002@tigermail.auburn.edu

Beijing MicrobialSystematics May19-23

BISMiS 2011 Beijing

INAUGURAL MEETING OF BERGEY'S INTERNATIONAL SOCIETY FOR MICROBIAL SYSTEMATICS

We are pleased to announce the first meeting of BISMiS held in the Beijing Friendship Hotel, Beijing from May 19^th – 23^rd , 2011. The purpose of BISMiS is to promote the importance of teaching and research in microbial systematics and to foster communication between microbial systematists across the world. These objectives include the pressing need to promote an understanding of the vast, largely unstudied, microbial diversity which has untapped genetic and industrial potential. Indeed, a basic aim of the society is to enhance efforts to isolate microorganisms in pure culture and to describe, classify, name and identify them and, where appropriate, to use them for exploitable biotechnology. The meeting in Beijing is designed to help realise these aims.

Around 300 participants from academia, industry and research institutes are expected to attend to exchange ideas, establish or further develop research networks, promote global friendships and to explore the importance of microbial systematics, not least from the biotechnological perspective.

http://www.bismis.org/dct/page/1 *Organizing Committee*

*Chairmen:*Guoping Zhao; Li Huang and Zixin Deng

*Vice-chairmen:*H-J Busse; Paul de Vos; Xiuzhu Dong; Chengxiang Fang; M Goodfellow; Ruibo Jiang; P Kämpfer; Yuezhong Li; Bozhong Mu; KH Schleifer; JT Staley; WB Whitman; Ruifu Yang; Hua Zhang; Liping Zhang.

*Secretary-in-General:*Lixin Zhang.

*International Committee members: *Francisco (Paco) Barona-Gomez; H-J Busse; Paul de Vos; M Goodfellow; P Kämpfer; H-P Klenk; KH Schleifer; JT Staley; Ajit Varma; Arinthip Thamchaipenet; WB Whitman; Hiroshi Tomoda; Tsetseg Baljinova; Radhey Gupta.

Beile Gao <beile.gao@yale.edu>

Belfast SystematicsAssociation Jul4-8

8TH SYSTEMATICS ASSOCIATION BIENNIAL QUEEN'S UNIVERSITY BELFAST 4-8 JULY 2011

Dear Colleagues,

We are pleased to announce that registration is open for the 8th biennial conference of the Systematics Association, held for the first time in Northern Ireland!

There is an exciting programme that includes both plenaries and thematic symposia, as well as a large number of contributed sessions. Currently scheduled symposia include:

- Next Generation Systematics - Studying Evolution and Diversity in an Era of Ubiquitous Genomics - Arthropod Systematics: are Morphology, Palaeontology and Molecules Coming Together? - Algal Systematics: Where Next? - Advances in Using Museum Specimens and Ancient DNA in Systematics Research

Symposia will include a mixture of talks from invited speakers and other contributions. The Biennial also presents excellent opportunities for contributed papers on any aspect of systematics and is a great forum for students and young researchers to present their work. For further details, please see http://www.systass.org/biennial2011/ . On behalf of the conference organisers, we hope to see you there!

Juliet Brodie, President James Cotton, Programme Officer Peter Olson, Treasurer Christine Maggs, Local Organiser

Sponsors: British Phycological Society, Cambridge University Press, Genetics Society, Linnean Society, Queen's University Belfast

– The Wellcome Trust Sanger Institute is operated by Genome Research Limited, a charity registered in England with number 1021457 and a company registered in England with number 2742969, whose registered office is 215 Euston Road, London, NW1 2BE.

james.cotton@sanger.ac.uk

Berkeley HumanGenomeVariation Sep8-10

12th International Meeting On HUMAN GENOME VARIATION AND COMPLEX GENOME ANALYSIS (HGV2011)

Date: 8th-10th September 2011 Place: Claremont Hotel Club and Spa, Berkeley, CA, USA Website: http://www.hgvmeeting.org/hgv2011 Abstract deadline: 31st May 2011

* Topics to be covered include methods/strategies for utilisation of different types of DNA variation (e.g., SNPs and copy number variations-CNVs), functional genomics applications, population genetics, bioinformatics, databases, algorithm development, personal genome sequencing, The 1000 Genomes Project, and the study of human disease.

* Postdoctoral fellows, junior faculty member, and under-represented groups can apply for meeting grants to help minimise their attendance costs.

ajb97b@leicester.ac.uk

BucknellU Evolution Jun13-14

Preparations continue for an international conference to be held at Bucknell University in Lewisburg, Pennsylvania, USA on Monday, June 13 and Tuesday June 14, 2011, "Evolutionary Ecology across Trophic Levels - A Symposium in Honor of Warren Abrahamson."

The website has been recently updated: http://www.bucknell.edu/abrahamsonsymposium.xml It now offers additional information on the symposium schedule, including speakers and tentative titles. A registration website is being built and should be available by April 1.

The conference will feature over 20 scientific talks to be given by alumni, collaborators, and friends of the Abrahamson Lab. Topics will address the diversity of subjects and approaches taken by Abe over his career, from the ecology and evolution of plant-insect interactions, to community and ecosystem approaches to fire ecology, restoration, and conservation of natural landscapes. Please visit the symposium website for a complete list of speakers.

A contributed poster session is also planned. Activities will include a banquet, picnic, and talent show, as well as regional natural history excursions. Events will be held in the Elaine Langone Center on the Bucknell Campus.

Anticipated costs include registration fees of $35 for students and $75 for all others. These fees will include meals and snacks but not lodging. Additional tickets to the picnic and banquet will be available at cost. Registration is not currently active, but will be available in February at the conference website.

Lodging in Bucknell dormitories will be available for $38/night single and $30/night double occupancy, with a one-time key charge of $10. There are many high-quality hotels, inns, and B&Bs in the region as well.

The Bucknell University campus provides easy access to the downtown shopping, dining, and entertainment district of Lewisburg, a town noted for its historical preservation and vibrant culture. Details can be found at: http://www.lewisburgpa.com/ This conference will celebrate Warren Abrahamson's 38 years of service to Bucknell University and the scientific community in anticipation of his upcoming retirement in the summer of 2012. During his career, Abe has supervised approximately 200 undergraduate research students, 18 Master's recipients, and 21 postdoctoral fellows, many of whom have remained active in science. In 2009 he was named a AAAS fellow. His main research interests include 1) multitrophic plant-insect interactions using the goldenrod system and 2) fire ecology and plant demography in Florida's upland communities.

Please visit the conference webpage for more information and updates: http://bucknell.edu/-x65430.xml For more information on Warren Abrhamson and his work, please visit his lab website: http://www.facstaff.bucknell.edu/abrahmsn/ Questions and comments can be addressed to steve.jordan@bucknell.edu

Steve Jordan, Associate Professor Department of Biology Bucknell University Lewisburg, PA 17837 Office: 302 Bio. Bldg. +1 570-577-1254 Lab: 331 Bio. Bldg. +1 570-577-3816 Fax: +1 570-577-3537 http://www.facstaff.bucknell.edu/sdjordan/-jordan.html steve.jordan@bucknell.edu

HarvardU InvertMorphEvolution Jun20-23

Please post:

2nd International Congress on Invertebrate Morphology - http://icim.harvard.edu/ >From June 20th to June 23rd 2011 Host: Museum of Comparative Zoology, Harvard University Cambridge, MA, USA

Plenary keynote speakers:

Claus Nielsen

Sally Leys

Marie-Ann Felix

Mark Q. Martindale

Reinhardt Kristensen

Symposium: Neurophylogeny Invertebrates as parasites Arthropod evolution controversies Sponges Meiofauna Standards in Zoomorphology 3D non invasive imaging Comparative Development

Registrations are already open (http://-icim.harvard.edu/registration-now-open). For more info, please contact icim@fas.harvard.edu

Sorry for any cross posting. Best, Sonia

Sónia Andrade Postdoctoral Fellow Giribet Lab Department of Organismic and Evolutionary Biology - MCZ Labs Harvard University 26 Oxford Street Cambridge, MA 02138 Phone: 1 617 496-5308 Fax: 1 617 496-5854 e-mail: sandrade@fas.harvard.edu

soniacsandrade@hotmail.com

Honolulu EvolutionPacificIslands May26-30

Evolution of Life on Pacific Islands and Reefs: Past, Present, and Future< http://botany.si.edu/events/-2011_pacific/ >, Honolulu, Hawaii, 26-30 May 2011 For additional information please direct the posting to the following website http://botany.si.edu/events/-2011_pacific/index.htm . Many thanks -

Nancy Khan, Conference Coordinator Smithsonian Institution, National Museum of Natural History P.O. Box 37012 Washington, DC 20013-7012 202-633-0965 (Phone) 202-786-2563 (Fax)

"Khan, Nancy" <khanna@si.edu>

Kyoto SMBE 2011 Jul26-30 UndergradTravelAwards

SOCIETY FOR MOLECULAR BIOLOGY AND EVOLUTION (SMBE) 2011 ANNUAL MEETING (July 26-30, 2011, Kyoto, Japan) UNDERGRADUATE TRAVEL AWARDS

CONFERENCE WEBSITES:

http://smbe2011.lab.nig.ac.jp/ http://smbe2011.com DEADLINE FOR RECEIPT OF APPLICATIONS: April 25, 2011

PROGRAM OUTLINE:

The Society for Molecular Biology and Evolution (SMBE) is pleased to make available 10 awards for undergraduate students to participate in a Mentoring and Diversity Program at its annual meeting.

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

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

ELIGIBILITY:

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

CONFERENCE PARTICIPATION:

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

AWARDS:

Ten awards will be given. Award recipients residing outside of Japan will receive US $2,500 to be used to help cover meeting registration, airfare, and room-and-board expenses. Students residing in Japan will receive US $1,500. Each participant will also receive an online student subscription to the journal Molecular Biology and Evolution for the year of 2012.

APPLICATION:

Please submit a single PDF file containing the following: Full Name Institutional Affiliation Major and Year in School (or Major and Graduation Date) Gender (optional) Race/Ethnicity(optional) Postal Address Country E-mail Address Telephone Number (including country code) Academic Supervisor's Name Institutional Affiliation of Academic Supervisor Postal Address of Academic Supervisor E-mail Address of Academic Supervisor CV (limited to one page) Plans for the Future (limited to 25 words) Poster Title Poster Authors Poster Abstract (no longer than 250 words)

Please name your PDF file as follows: SMBE11_yourfamilyname.pdf

The single PDF file should be e-mailed to Dr. Dan Graur (dgraur[at]uh.edu).

DEADLINE:

The deadline for receipt of nominations/applications is April 25, 2011.

dgraur@gmail.com

London PopulationGenetics Apr19-20 Registration

Dear EvolDir,

Registration for the 55th Ecological Genetics Group (EGG) meeting is now extended until March 15th for the few remaining places (max. 70 delegates). EGG is the longest running population and evolutionary genetic meeting in the United Kingdom, providing a forum for plant, insect and animal scientists alike to meet and discuss their work. The meeting is especially welcoming for all early career scientists (Post-docs and Ph. D students), being informal and modestly priced.

This year's meeting takes place in London, April 19th-20st, at Queen Marys University of London (Dr. Richard Buggs) with the middle day at the Natural History Museum (Dr. Stephen Ansell). Our plenary speakers are gene flow and genomics expert Prof. Roger Butlin (University of Sheffield) and hybridisation and species adaptation expert Prof. Alex Widmer (Institute of Integrative Biology, Zurich). Comfortable and relaxing accommodation is provided at the Royal Foundation of St Katherine Conference Centre, and the central London location allows for easy access via major airports and rail stations.

Full details are provided on

http://www.ecologicalgeneticsgroup.org.uk/eco/
Stephen Ansell & Richard Buggs

Dr Stephen Ansell | Dept. Botany | Natural History Museum | Cromwell Road | London | SW7 5BD | United Kingdom.

Stephen Ansell <S.Ansell@nhm.ac.uk>

London SexualSelection Dec1-2

CONFERENCE ON SEXUAL SELECTION AND MATE CHOICE

“Why do animals mate with the ”wrong partner“?

Association for the Study of Animal Behaviour Winter Meeting, 1st & 2nd December 2011, The Zoological Society, London.

Organisers David Shuker and Nathan Bailey, University of St Andrews.

Plenary Speakers Professor Marlene Zuk (University of California Riverside) and Dr Karen Pfennig (University of North Carolina).

Our understanding of sexual selection and the evolution of animal mating systems is based on the idea of competition for mates, in terms of both the quantity and quality of those mates. It has become clear though that animals often attempt to mate with partners that appear to be of ”low quality“. Such partners range from apparently low fitness individuals of the opposite sex but of the same species, through to members of the same sex or even members of a different species, from which no fitness benefits should accrue.

In this two-day meeting we will explore the evolutionary causes and consequences of seemingly ”sub-optimal“ mate choice behaviour. There are two questions we hope will be addressed. First, are behaviours such as reproductive interference between species or same-sex matings within species biologically relevant or merely quirky pathologies that offer little insight? Second, to what extent do mate choices in one context (getting the ”right“ species or sex, or the ”sexiest“ partner) inform us about mate choice in other contexts?

We hope to stimulate both empiricists and theoreticians to think again about what we expect from mate choice, how discriminating animals should be, what we think mate ”quality“ actually is, and to consider whether unusual mate choices may help or hinder our view of mating systems and sexual selection. We are particularly keen to bring together biologists studying similar phenomena under slightly different paradigms (e.g. in terms of inter-specific interactions, evolutionary biologists studying hybridisation and reproductive character displacement, and ecologists studying reproductive interference). Although mate choice is our focus, we expect the discussion to be wide-ranging and relevant to those interested in animal decision-making, especially context-dependent choice, and individual variation in behaviour more generally.

We request offers for spoken (20 + 5 minutes) talks and poster presentations addressing the topics of the meeting. Please email an abstract to Dave Shuker at:

david.shuker@st-andrews.ac.uk

We expect to finalise the programme of talks late summer-early autumn.

We are also delighted that Professor Gene Robinson (University of Illinois) will be giving the 2011 Tinbergen Lecture during the meeting as well.

As is traditional, the ASAB Winter Meeting has no fee and does not require registration, although expressions of interest to the organisers would be welcome. Delegates make their own arrangements for travel, accommodation and main meals. Delegates are also able to access London Zoo. For further details and updates about the programme of the conference, please visit our website:

http://biology.st-andrews.ac.uk/shuker/ASAB-Winter-Meeting-2011.html Alternatively please visit the ASAB website:

http://asab.nottingham.ac.uk/meetings/index.php –

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LAB WEBSITE: http://biology.st-andrews.ac.uk/-shuker Tel: +44 1334 463 376 Fax: +44 1334 463 366

david.shuker@st-andrews.ac.uk

London SystemsBiology Apr18-19

Predictive ecology: systems approaches Loading...

* Starts: 9.00am on 18 April 2011 * Finishes: 5.00pm on 19 April 2011 * Venue: The Royal Society, London

Organised by Professor Matthew Evans, Professor Tim Benton and Professor Ken Norris

http://royalsociety.org/events/predictive-ecology/ Registration for this event is now open - http:/-

/www2.royalsociety.org/events/forms/1104.htm Prediction is needed in ecology, not least because the world is changing and there is a demand for robust predictions about the ecological impact of these changes. Prediction is best when underpinned by process-based models, but complex ecological systems are problematic to model. We will explore different modelling approaches for ecological systems and the strengths and limitations of systems approaches.

Speakers and chairs Speakers and chairs include Dr Colin Beale, Professor Tim Benton, Professor Jim Clark, Professor Matthew Evans, Professor Charles Godfray FRS, Professor Volker Grimm, Professor Peter Hudson, Professor Hanna Kokko, Professor Georgina Mace CBE FRS, Professor EJ Milner-Gulland, Professor Paul Moorcroft, Professor Ken Norris, Dr Steven Orzack, Dr Steve Penfield, Professor David Rand, Professor Mark Rounsevell, Professor Pete Smith, Professor Bill Sutherland and Dr Allan Tucker.

Registration This discussion meeting is intended for researchers in relevant fields and is free to attend, but pre-registration online is essential.

An optional lunch is offered each day for £20+VAT per day, and should be booked at registration. Payment is accepted online by Visa, MasterCard, Visa Debit, Maestro, Electron and Solo cards. – Steven Orzack

The Fresh Pond Research Institute 173 Harvey Street Cambridge, MA. 02140 617 864-4307

www.freshpond.org orzack <orzack@freshpond.org>

MichiganStateU TranscriptionEvolutionSystems Jul22-24

Michigan State University is pleased to announce the âSummer Symposium on Transcriptional Dynamics, Evolution, and Systems Biologyâ, which will be held July 22-24, 2011 in East Lansing, MI. http://www.bmb.msu.edu/GEDD/symposium11/index.html Recognizing the increasingly important connections between transcriptional research at the molecular and genomic scale, this meeting will bring together leading scientists whose focus on gene regulation includes mechanism, systems analysis, and evolution/development.Â Confirmed speakers include:

Evolution/Development:

Julien Ayroles, Harvard University

John Doebley, University of Wisconsin, Madison

Ilya Ruvinsky, Univresity of Chicago

Eran Segal, Weizmann Institute of Science

Itay Tirosh, Weizmann Institute of Science (S & E)

Gunter Wagner, Yale University

Systems Analysis:

Jeffrey Chuang, Boston College

Daniel Gilchrist, National Institute of Environmental Health Sciences

Nevan Krogan, University of California, San Francisco

John Reinitz, University of Chicago

Francois Robert, Institut de recherches cliniques de MontrÃ©al (IRCM)

Ali Shilatifard, Stowerâs Institute for Medical Research

Kevin White, University of Chicago

Transcriptional Mechanisms:

Irina Artsimovitch, The Ohio State University

Benoit Coulombe, Institut de recherches cliniques de MontrÃ©al (IRCM)

Dorothy Erie, University of North Carolina

Mikhail Kashlev, National Cancer Institute

Dmitry Vassylyev, University of Alabama, Birmingham

Robert Weinzierl, Imperial College London

Additional speakers will be selected from the poster abstracts that are submitted.Â More detailed information will be available on the conference website http://www.bmb.msu.edu/GEDD/symposium11/index.html – Ian Dworkin Assistant Professor Department of Zoology Program in Ecology, Evolutionary Biology & Behaviour Program in Genetics Michigan State University office (517) 432-6733 lab (517) 432-6730 idworkin@msu.edu https://www.msu.edu/ ˜ idworkin/ Ian Dworkin <idworkin@msu.edu>

Minneapolis MarineComparative Phylogeography Jul6-11

Symposium (at 2011 Joint Meeting of Ichthyologists and Herpetologists, July 6-11, Minneapolis)

Comparative Phylogeography of the Gulf-Atlantic Coastal Plain

Freshwater bound organisms are ideal models for phylogeographic research as population dynamics and genetic structure are expected to closely follow the boundaries between freshwater habitat networks (watershed divides). With the advent and continued refinement of high-throughput genotyping technology, the field of phylogeography is increasingly able to test explicit historical hypotheses. This transition of research focus from geographical pattern to spatiotemporal process is partly responsible for the recent trend toward investigation of upland species, as their "island-like" habitats are more amenable to development and testing of biogeographic hypotheses. As a result, the majority of recent work has focused upon groups such as darters (Percidae), small salamanders (Plethodontidae), and other organisms that inhabit uplifted provinces. Phylogeographic structure of species inhabiting the Gulf-Altantic Coastal Plain remains underappreciated, having been overshadowed since the foundational work of the 1980's. However, recent efforts across numerous institutions show renewed interest in applying modern phylogeographic approaches to understanding this fauna. In addition, an immediate need exists for a renewed interest in phylogeographic structure of lowland species, as many ecosystems within the region are disproportionately affected by anthropogenic impacts (e.g. longleaf pine ecosystems, karst springfed streams, blackwater wetlands). A better understanding of historical gene flow, evolutionarily significant units, and cryptic speciation will contribute to an overall conservation strategy for species that have declined in concert with regional habitat loss.

Abstract submission: March 5, 2011. Please contact Michael Sandel (michael.sandel*at*ua.edu) or Andres Lopez (jalopez2*at*alaska.edu) for more information.

andresl.fish@gmail.com

Montpellier HumanBehaviourEvolution Jun29-Jul3

Human Behaviour & Evolution Society (HBES), 2011. June, 29th V July, 3rd 2011. Montpellier, France.

The HBES annual conference provides a forum for current research on the evolution of human nature. It is a genuinely interdisciplinary research meeting, including all of the main branches of human behaviour, from evolutionary psychology to evolutionary anthropology and cultural evolution, and including studies of animal behaviour. The conference Keynote Address will be presented by Randy Nesse, the co-founder of darwinian medicine. Our Plenary Speakers include economist Samuel Bowles, anthropologist and primatologist Sarah Hrdy; linguist Jean-Marie Hombert, biologist Tim Clutton-Brock, anthropologist Frank Marlowe, developmental psychologist Andrew Whiten. Abstract submission and registration are still open.

http://www.hbes2011.univ-montp2.fr Program committee: - Virpi Lummaa - Ruth Mace - Martin Daly - Mark Flinn

Best, Charlotte Faurie & Michel Raymond

HBES 2011 local organizers

PS. Deadline for abstract and symposium submission: May 1st 2011. Deadline for early bird registration: April 30th 2011 Deadline for low cost accommodation: April 1st 2011

Michel Raymond <michel.raymond@univ-montp2.fr>

Norman Evolution2011 Jun17-21 MSITravelAward

Evolution 2011 MSI Faculty Travel Award - Application Deadline (March 31st) Reminder Are you a biologist at a minority-serving institution? Apply now for a travel award to attend Evolution 2011 in Norman, OK.

The National Evolutionary Synthesis Center (NESCent), with support from the Society for the Study of Evolution (SSE), is pleased to announce a travel award for faculty from Minority Serving Institutions (MSIs) to attend Evolution 2011 V the annual meeting of SSE, SSB (Society of Systematic Biologists) and ASN (American Society of Naturalists) V to be held in Norman, OK from June 17-21, 2011.

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

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

To apply, please visit www.nescent.org/eog/2011facultytravelawardapplication Application Deadline: March 31st, 2011 (Awards will be announced by April 8th, 2011)

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

Jory P. Weintraub, PhD Assistant Director, Education and Outreach National Evolutionary Synthesis Center (NESCent) 2024 West Main St., Suite A200 Box 104403 Durham, NC 27705 Phone: 919.668.4578 Fax: 919.668.9198 Email: jory@nescent.org Skype: jory.weintraub Web: www.nescent.org

Jory Weintraub <jory@nescent.org>

Norman iEvoBio Jun21-22 DeadlineExtension

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 Friday, March 25, 2011. We hope that this will give those interested in contributing sufficient time to do so.

Please see http://bit.ly/iEvoBio2011_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 for the Study of Ecolution (SSE) and the Society of Systematic Biologists (SSB). Additional support has been provided by the Encyclopedia of Life (EOL).

The iEvoBio 2011 Organizing Committee: Rob Guralnick (University of Colorado at Boulder) (Co-chair) Cynthia Parr (Encyclopedia of Life) (Co-chair) Dawn Field (UK National Environmental Research Center) Mark Holder (University of Kansas) Hilmar Lapp (NESCent) Rod Page (University of Glasgow)

hlapp@nescent.org

Norman iEvoBio Jun21-22 Reminder

This is a reminder that the deadline for submitting abstracts for full talks to the 2011 conference on Informatics for Phylogenetics, Evolution, and Biodiversity (iEvoBio) is Friday, March 25, 2011, which is just two days away. Please see http://bit.ly/iEvoBio2011_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/ iEvoBio, and there is an announcement-only Google group at http://groups.google.com/group/ievobio-announce . You can use the group's RSS feed (linked from its 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 for the Study of Ecolution (SSE) and the Society of Systematic Biologists (SSB). Additional support has been provided by the Encyclopedia of Life (EOL).

The iEvoBio 2011 Organizing Committee: Rob Guralnick (University of Colorado at Boulder) (Co-chair) Cynthia Parr (Encyclopedia of Life) (Co-chair) Dawn Field (UK National Environmental Research Center) Mark Holder (University of Kansas) Hilmar Lapp (NESCent) Rod Page (University of Glasgow) hlapp@nescent.org

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Norman OK Evolution2011 Jun17-21 RegistrationOpen

REGISTRATION TO EVOLUTION 2011 IS OPEN!

The Evolution 2011 meeting will be held from the 17-21 June in Norman, Oklahoma. Registration and meeting details can be found at: www.evolution2011.ou.edu< http://www.evolution2011.ou.edu >.

Note: "Early-bird" registration deadline is 17 April. The deadline for submission of talks/posters is 1 May.

Looking forward to welcoming everyone to Norman in June!

Larry Weider, Rich Broughton, Ingo Schlupp

Tri-chairs, Evolution 2011 Organizing Committee

"Weider, Lawrence J." <ljweider@ou.edu>

NottingU ParasiteEvolution Apr12-14

LAST CALL FOR REGISTRATIONS FOR THE SPRING MEETING OF THE BRITISH SOCIETY FOR PARASITOLOGY (12th â 14th April 2011, NOTTING UNIVERSITY, UK) Calling All Parasite Ecologists and Evolutionary Biologists

Following the great success of the Ecology / Evolutionary theme at last yearâs British Society for Parasitology Spring Meeting at Cardiff University, the organising committee would like to invite you to join them again at Nottingham for this yearâs meeting which will again include a full series of sessions entirely devoted to ecological and evolutionary parasitology.

Session Topics:

Wild vertebrates as natural models in immunology Convened by Dr Joseph Jackson (Aberystwyth University) and with invited speaker Dr Andrea Graham (Princeton University, USA). Dr Grahamâs work ultimately aims to understand how natural selection has shaped strategies for both host defence and parasite transmission.

Ecological and Evolutionary Impacts of Parasites on Hosts Convened by Dr Andrew MacColl and with invited speaker Prof Armand Kuris (UCSB, USA). Prof Kuris is best known for his work revealing the role of parasites in ecosystem structure and function in marine systems, and the applied consequences of this for fisheries management and biological control.

Parasites and Behaviour Convened by Dr Jo Cable (Cardiff University) and with invited speaker Prof Janice Moore (Colarado State University, USA). Prof Mooreâs research focuses on the evolution of host behavioural manipulation by parasites.

General Ecology. A session covering a wide range of topics from the species concept through to parasite estimation methods.

Medicine Meets Ecology Convened by Prof Maria-Gloria BasaÃ±ez (Imperial College). This open session will examine how ecological and evolutionary approaches are currently, or could in the future, help to improve medical practice in dealing with parasites and related issues.

Co-infection Dynamics Convened by Dr Jo Lello (Cardiff University). This session will cover both parasite-parasite and pathogen-parasite combinations, looking at how these infections impact upon the host, the parasite dynamics and the evolution of host-parasite relationships.

Parasite Evolution Convenor TBC and with invited speaker Dr Andrew Fenton (Liverpool University). Dr Fentonâs work focuses on the use of simple population dynamic theory as a tool for understanding the epidemiology and evolution of parasites with a current focus on the evolution of macroparasite life-history strategies.

Wildlife, Biodiversity and Disease Convenor Dr Sarah Perkins (Cardiff University). This session will explore the effects of wildlife and biodiversity on the emergence and transmission of infectious diseases.

See: http://www.bsp.uk.net/events.php for further details and for registration

Dr Joanne Lello Cardiff University School of Biosciences Organism and Environment Group Biomedical Sciences Building Museum Avenue Cardiff CF10 3AX Tel: 02920 875885 E-mail: lelloj@cardiff.ac.uk

Joanne Lello <LelloJ@cardiff.ac.uk>

Ottawa EvoDevo May16-20

The Comparative Morphology & Development (CMD) section of the Canadian Society of Zoologists (CSZ) invites you to attend the following symposia at the annual CSZ meeting:

May 16-20, 2011, in Ottawa, Ontario; Canada's Capital City

SYMPOSIUM: Regeneration: Developmental & Evolutionary Perspectives (May 17, 2011)

Speakers:

Bruce Carlson (Michigan) "Regeneration - One of nature's enduring mysteries"

Catherine Tsilfidis (OHRI) "Characterizing the dedifferentiation process in newt forelimb regeneration"

Alexandra Bely (Maryland) "Evolution and development of regeneration loss in annelids"

[organized by Matthew Vickaryous, University of Guelph]

STUDENT SATELLITE SYMPOSIUM: New perspectives on adaptation to environmental variation via epigenetic mechanisms (May 17, 2011)

Lead speaker:

David Crews (UT Austin) "Life Imprints: Epigenetic modifications and the development of behavior"

Additional speakers:

Sanoji Wijenayake (Carleton) " Temperature regulation of inheritable cytosine methylation patterns in gravid female ectotherms"

Christina Castellani (Western Ontario) " Genomic exploration of monozygotic twins discordant for schizophrenia uncovers de novo mutations and reveals candidate genes"

Laia Navarro Martin (University of Ottawa) "An epigenetic mechanism involved in temperature-induced sex ratio shifts in fish populations "

[organized by Jan Edward Lim, Kristin Bianchini, and Cayleih Robertson, University of Guelph]

FOR MORE DETAILS ABOUT THESE SYMPOSIA, SEE:

http://www.biology.ualberta.ca/CMD/home.htm TO REGISTER, OR TO LEARN MORE ABOUT THE CSZ ANNUAL MEETING, SEE:

http://www.csz2011.uottawa.ca/ EARLY REGISTRATION DEADLINE: March 7, 2011

CONTRIBUTED PAPERS: Spaces are also available for contributed papers in sessions organized by the CMD section. The deadline for submitting abstracts is barely one week away, so don't delay:

ABSTRACT SUBMISSION DEADLINE: March 7, 2011

FINAL REGISTRATION DEADLINE: April 4, 2011 –

A. Richard Palmer, FRSC Systematics and Evolution Group Department of Biological Sciences University of Alberta Edmonton, Alberta T6G 2E9 CANADA phone: (780) 492-3633 message: (780) 492-3308 FAX: (780) 492-9234 http://www.biology.ualberta.ca/palmer/palmer.html Secretary-General Comparative Morphology & Development section Canadian Society of Zoologists: http://www.biology.ualberta.ca/CMD/home.htm rich.palmer@ualberta.ca

Ottawa SSE CallSymposia

Call for SSE Sponsored Symposia at Evolution 2012

The SSE Council encourages proposals for two society sponsored symposia at the 2012 meeting in Ottawa. In evaluating symposium proposals, the Council will favor those proposals whose topics concern newly emerging fields, fields ripe for syntheses, and fields different from those that have been included in recent Society symposia. *The Council particularly encourages proposals that include women, younger investigators and others traditionally underrepresented in Society symposia. *Proposals for SSE Symposia should be submitted electronically as PDF by midnight May 16, 2011 by email to bbrodie@virginia.edu. More details can be found at www.evolutionsociety.org/calls/Call_for_Symposia_2012_Ottawa.pdf . Judy Stone <jstone@colby.edu>

Paris ECM2011 Jul19-23 ChromosomeEvolution

Dear colleagues,

We invite abstract submissions for oral and poster contributions in the symposium “Chromosomes & Evolution” to be held at the European Congress of Mammalogy (ECM 2011: http://www.alphavisa.com/-ecm2011), Paris, France (July 19-23 2011).

This symposium will explore all aspects of evolutionary cytogenetics in mammals from systematics to phylogenetic approaches and comparative genomics. This session aims at integrating patterns and processes involved in chromosome change and welcomes discussions on issues such as chromosome function, epigenetics and selection. Deadline for submission: 1st April 2011.

Instructions for preparing and submitting your abstract can be found on the ECM website.

Organisers: Vitaly Volobouev & Janice Britton-Davidian Vitaly Volobouev: vitaly@mnhn.fr Janice Britton-Davidian: janice.britton-davidian@univ-montp2.fr

Janice Britton-Davidian Laboratoire Génétique & Environnement Institut des Sciences de l’Evolution - UMR5554 Université Montpellier II Pl. E. Bataillon, cc65 34095 Montpellier Cedex Tél.: 33 (0)4.67.14.39.10 Fax: 33 (0)4.67.14.36.22

janice.britton-davidian@univ-montp2.fr

Paris ECM2011 Jul19-23 UngulatePopGen

I would like to invite submissions of abstracts for oral and poster presentations for the symposium ’Conservation and population genetics/genomics of ungulates’ to be held at the European Congress of Mammalogy (ECM 2011: http://www.alphavisa.com/-ecm2011), Paris, France (July 19-23 2011).

SYMPOSIUM DESCRIPTION:

Within Europe as a whole, there are some 20 species of ungulates, the majority of which are widespread and abundant but have been subjected to anthropogenic interference for centuries. Populations are managed according to rigorous hunting schedules and kept long-term in enclosures. The reduction in the interconnectivity of ungulate populations as a result of habitat fragmentation has led to concerns about the loss of genetic variability due to isolation. Hybridisation with illegally released con-specifics, domestic forms or alien species is considered a threat to species integrity. Finally, some distinctive (sub-)species’ are very rare and require explicit management efforts for their conservation. We aim to show how molecular techniques can be used to investigate the evolutionary consequences of human interference on ungulate populations and how genetics can contribute to the development of effective, science-based management and conservation policies.

Invited speaker: Massimo Scandura (University of Sassari)

Deadline for submission: 1st April 2011.

Instructions for preparing and submitting your abstract can be found on the ECM website.

Organiser: Alain Frantz Zoologisches Institut University of Greifswald J.-S. Bach Strasse 11-12 D-17489 Greifswald Germany Tel: +49 (0) 3834 86 4068 Fax: +49 (0) 3834 86 4252

Alain Frantz <frantza@uni-greifswald.de>

Paris SexChromosomes Jun9-10

Dear Colleagues,

we are pleased to announce that registration is now open for the meeting of the SFG on 9-10 June 2011 in Paris: Genetics, Epigenetics and Evolution of Sex Chromosomes. http://www.sfgenetique.org/-meeting2011 If you need assistance, please contact the sfg: contact@sfgenetique.org

The organising committee /

Catherine Montchamp-Moreau <Catherine.Montchamp@legs.cnrs-gif.fr>

Paris Speciation Jul19-23

Dear colleagues,

We invite abstract submissions for oral and poster contributions in the symposium “Mechanisms of Speciation in Mammals” to be held at the European Congress of Mammalogy (ECM 2011: http://www.alphavisa.com/-ecm2011), Paris, France (July 19-23 2011).

This symposium will address the mechanisms of speciation in mammals, with the intention to providing an overview of theoretical background, recent advances and new challenges in this field of research. It will bring together researchers working in different disciplines and developing various approaches from genomics to behaviour, to explore the mechanisms favouring the evolution of reproductive barriers. Particular attention will be given to recent advances in understanding speciation in the context of ongoing gene flow and to studies providing new insights into the factors favouring adaptive speciation in mammals.

Deadline for submission: 1st April 2011. Instructions for preparing and submitting your abstract can be found on the ECM website.

Organisers: Guila GANEM & Carole SMADJA guila.ganem@univ-montp2.fr and carole.smadja@univ-montp2.fr

– Dr. Carole Smadja CNRS Institut des Sciences de l¹Evolution Montpellier – Web: http://www.carole-smadja.staff.shef.ac.uk/ carole.smadja@univ-montp2.fr

Roscoff France Coevolution Sep3-7

Jacques Monod Conference "Coevolutionary arms race between parasite virulence and host immune defense: Challenges from state of the art research" 3-7 September 2011 Roscoff (France)

A Jacques Monod Conference entitled "Coevolutionary arms race between parasite virulence and host immune defense: Challenges from state of the art research" will be held at the Marine Station CNRS at Roscoff (France) from 3rd to 7th September 2011.

The conference is organized by Gabriele Sorci (Dijon, France) and Manfred Milinski (Ploen, Germany).

Key-note speakers include: Shelley Adamo (Halifax, CA), Sonia Altizer (Athens, USA), Thierry Boulinier (Montpellier, France), Nathalie Charbonnel (Montpellier, France), Christine Coustaud (Sophia Antipolis, France), Rob de Boer (Utrech, The Netherlands), Dieter Ebert (Basel, Switzerland), Scott Edwards (Harvard, USA), Sylvain Gandon (Montpellier, France), Michael Hochberg (Montpellier, France), Jim Kaufman (Cambridge, UK), Kirk Klasing (Davis, USA), Jochim Kurtz (Munster, Germany), Margaret Mackinnon (Kilifi, Kenya), Polly Matzinger (Bethesda, USA), Yannis Michalakis (Montpellier, France), Yannick Moret (Dijon, France), Charles Nunn (Harvard, USA), Geoff Parker (Liverpool, UK), Wayne Potts (Salt Lake City, USA), Luis Quintana-Murci (Paris, France), Heinz Richner (Bern, Switzerland), Ana Rivero (Montpellier, France), Paul Schmid-Hempel (Zurich, Switzerland), Dominik Wodarz (Irvine, USA).

Deadline for application: May 5 2011

Registration fee (including board and lodging)

400 euros for PhD students

600 euros for other participants

Application for registration

The total number of participants is limited to 115 and all participants are expected to attend for the whole duration of the conference. Selection is made on the basis of the affinity of potential participants with the topics of the conference. Scientists and PhD Students interested in the meeting should send:

their curriculum vitae the list of their main publications for the 3 last years the abstract of their presentation

to the*Chairperson of the conference* (Gabriele.sorci@u-bourgogne.fr) before the deadline. After it, the chairman will select the participants. Except in some particular cases approved by the Chairperson, it is recommended that all selected participants present their work during the conference, either in poster form or by a brief in- session talk. The organizers choose the form in which the presentations are made. No payment will be sent with application. Information on how and when to pay will be mailed in due time to those selected.

For further information please visit the following web site (http://www.cnrs.fr/insb/cjm/2011/sorci_e.html)

Gabriele Sorci (Gabriele.sorci@u-bourgogne.fr) and Manfred Milinski (milinski@mail.evolbio.mpg.de)

gabriele.sorci@u-bourgogne.fr

Tuebingen ESEB2011 Aug20-25 RegistrationClosed

XIIIth Congress of the European Society for the Study of Evolutionary Biology

Tuebingen, Germany, 20-25 August 2011 www.eseb2011.de REGISTRATION CLOSED!

I would like to point out that the 13th Congress of the Society of Evolutionary Biology is now completely full and registration has been closed (quite a bit earlier than expected). We added a waiting list possibility to the website, which allows us to allow in more people in case others drop out. Although chances will be low to get in, entering your name would at least give us a feeling for how many more people would have registered in case we would have had a higher threshold (current n 1300). This is important information for future organizers.

SOME MEETING STATISTICS

Abstract submission ended on 28 February as planned. We have received 1023 submissions for posters and abstracts. We have 337 slots for talk (including all plenaries and invited speakers). About 500 submissions will be presented as a "regular" poster. About 200 Posters will be offered the opportunity to put up a "essence poster" = summary "mini-posters". All abstracts will be included in the abstract booklet. The refereeing process will start this week. We hope to have feedback for all around late April. The top 10 of contributing countries looks like this:

Germany 165 United Kingdom 121 Switzerland 102 USA 100 France 73 Finland 62 Sweden 65 Canada 38 Netherlands 30 Australia 27

The 29 regular symposia show a very explicit preference for these three topics:

A. Symposium 21: Evolutionary ecological genomics B. Symposium 23: Climate change and evolution C. Symposium 01: Experimental evolution across the microbe/macrobe divide

The new category of "general" symposia (for submissions outside the regular specialist symposia) received one quarter of all submissions (264). We are looking forward to seeing a very diverse collection of topics here.

All symposia will obtain a number of time slots that is correlated with the proportion of submissions they received, so acceptance rates for submitted talks will be more or less similar - roughly 20-30% - independent of the subject.

This and other information can also be found on the home page www.eseb2011.de Very best,

Nico

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

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

nico.michiels@uni-tuebingen.de

www.eseb2011.de www.evoeco.uni-tuebingen.de www.eve.uni-tuebingen.de Nico Michiels <nico.michiels@uni-tuebingen.de>

UGroningen MathModelsEcolEvol Aug17-19

The third biannual conference on Mathematical Models in Ecology and Evolution, MMEE 2011, will take place at the University of Groningen, the Netherlands, 17 - 19 August, 2011. Registration and call for abstracts are now open: please check our website:

http://www.mmee2011.evobio.eu/ The deadline for registration is May 31, 2011.

On behalf of the organising committee, Joke Bakker

ICT manager Theoretical Biology Dept, Centre for Ecological and Evolutionary Studies, University of Groningen P.O. Box 11103, 9700 CC Groningen, Netherlands Nijenborgh 7, 9747 AG Groningen, Netherlands Phone: +31 (0)50 363 8780 Fax: +31 (0)50 363 3400 Website: http://www.rug.nl/biol/theobio E-mail: Joke.Bakker@rug.nl

Joke Bakker <joke.bakker@rug.nl>

UMunich MetazoanPhylogeny Oct11-14

Dear colleagues, registration and abstract submission for the international conference âDeep Metazoan Phylogeny 2011 â new data, new challenges“, to be held from October 11-14, 2011 at the University of Munich (Germany) is now open!

The conference will bring together mathematicians, theoreticians, molecular systematists, and morphologists that aim at resolving deep branches in the animal tree of life for a better understanding of the evolution and diversification of multicellular life on Earth.

During the conference, new data, new analytical tools and new results will be discussed. Challenges and pitfalls in phylogeny reconstruction based on molecular and/or morphological data will be identified, aiming for a critical and constructive view of the state of the art of the metazoan tree of life.

The meeting will consist of sessions with several invited leaders in the field and open sessions with short presentations. In addition, there will be ample space and time to present posters.

The meeting focuses on three major themes: (1) Innovations in the analyses of molecular and morphological data (2) Molecular phylogeny: new markers and phylogenomic analyses (3) The evidence found in morphology

Full list of confirmed keynote speakers can be found at < www.palmuc.de/dmp2011 >

The conference is organised in collaboration with the Priority Program "Deep Metazoan Phylogeny“ of the German Science Foundation (DFG). This program is a joint effort of more than 20 participating workgroups bringing together molecular, morphological and bioinformatic expertise with the goal to establish a (hopefully) robust backbone metazoan phylogeny. Details on the priority project "Deep Metazoan Phylogeny“ can be found at < http://www.deep-phylogeny.org >.

More information is available on the conference website < www.palmuc.de/dmp2011 >, which will continuously be updated.

Important Dates & Deadlines: Early registration with reduced fees until 1st of May 2011 Regular registration fees then until 1st of July 2011 Latest abstract submission 1st of July 2011 Notification of oral presentations until 1st of August 2011

We look forward to welcoming you in Munich in October!

for the organizing team

Gert Wörheide

—- Prof. Dr. Gert Wörheide Molecular Geo- & Palaeobiology Department of Earth and Environmental Sciences & GeoBio-CenterLMU Ludwig-Maximilians-Universitaet Muenchen Richard-Wagner-Straße 10 80333 Muenchen Germany

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Director, Bavarian State Collections of Palaeontology and Geology Spokesman of the Executive Board, GeoBio-CenterLMU

Lab publications: www.mol-palaeo-lit.de/papers.php www.researcherid.com/rid/C-1080-2008 woerheide@lmu.de

UWashington PopGenetForensics Jul19-21

For the past 20 years, population and evolutionary genetics have been playing a role in forensic science. Some of the recent applications include the FBI investigation of the 2001 Anthrax Mailings, the determination of geographic origin of seized elephant tusks, and discussions of the way to assess the strength of matching Y-STR profiles that have not previously been seen. In July of this year, these and related topics will be discussed by population geneticists, statisticians and forensic scientists at the 8th International Conference on Forensic Inference and Statistics. The conference will be held at the University of Washington, July 19-21.

You are invited to attend to learn about this interesting field, or to present any work you have done in the field. Details are available at http://www.icfis2011.org Bruce Weir bsweir@uw.edu

Bruce Weir <bsweir@u.washington.edu>

York GeometricMorphometrics Oct10-13

The Hull York Medical School Centre for Anatomical and Human Sciences (CAHS) will host a four day workshop in York 10-13 October 2011

The course is aimed at postgraduates who already have some insight into GMM but may not have yet used these methods. During the four days of the course the basics of geometric morphometrics will be covered and key multivariate morphometric methods reviewed. Frequent examples will be presented using available GMM software and students will gain experience in using different software tools during the course of each afternoon's practical sessions using datasets we will provide.

Faculty Paul O'Higgins CAHS, Hull York Medical School

Andrea Cardini Dipartimento di Biologia, Università di Modena e Reggio Emilia and CAHS, Hull York Medical School

FOR MORE INFORMATION AND TO BOOK ON THE COURSE PLEASE VISIT http://sites.google.com/site/hymsfme/gmm-course-2011
Paul O'Higgins <Paul.Ohiggins@hyms.ac.uk>

GradStudentPositions

Berlin AquaticInsectEvolution

PhD Student Position – Aquatic Insect Evolution and Biodiversity

Berlin, Germany

The Leibniz-Institute of Freshwater Ecology and Inland Fisheries (IGB) in Berlin invites applications for a PhD student position studying the evolution and biodiversity of European mayflies (Insecta, Ephemeroptera).

The successful candidate will participate in a 3-year project funded by the Leibniz society on freshwater biodiversity in Europe. The project includes field sampling in several locations in Europe, laboratory analysis of collected organisms (morphological identification, DNA sequencing), and the organization of existing DNA sequence data for phylogenetic and comparative phylogeography analysis. There is sufficient scope within the project to develop your own interests in population genetics, phylogeography, evolution and genomics. The start date is negotiable but should be no later than July 2011.

Applicants must have a degree in biology, ecology, genetics, or evolution; experience with DNA sequencing (laboratory methods or data analysis) or field sampling of aquatic insects; good command of written and spoken English. For additional information, please contact Dr Michael T. Monaghan (monaghan@igb-berlin.de).

Applicants should submit a CV, a cover letter highlighting your experience and research interests, and the contact details of two or more referees to monaghan@igb-berlin.de by 15 April 2011.

For more information please see the following links:

Berlin – www.berlin.de/international/index.en.php IGB – www.igb-berlin.de PhD position – www.igb-berlin.de/doktorarbeiten-details/items/70.html Me – www.igb-berlin.de/mitarbeitende-igb.html?show'5
monaghan@igb-berlin.de

Denmark DNAanalysis FishCollections

PhD Scholarship in Genetic Analysis of Archived Tissue Collections from Fish

A PhD Scholarship on genetic analysis of archived tissue collections is available at the National Institute of Aquatic Resources (DTU Aqua) with starting date August 2011. The scholarship is financed by DTU Aqua. Deadline for applications is March 30th.

The project will be carried out in the Section for Population Ecology and Genetics in Silkeborg.

DTU Aqua is an institute at the Technical University of Denmark. The purpose of DTU Aqua is to provide research, advice and education at the highest international level within the sustainable exploitation of living marine and freshwater resources, the biology of aquatic organisms and the development of ecosystems as well as their integration in ecosystem-based management. The institute has an international research staff comprising approx. 90 academic employees.

Project description Archived historical material from fish in the form of scales and otoliths is found in many research institutions across the Nordic countries. Such population samples constitute a unique source of DNA for conducting retrospective analysis of genetic changes over time. They allow identification of historical changes in the distribution, migration and abundance of fish populations, as well as temporal evolutionary changes within populations in response to environmental change. This project aims at performing genetic/genomic analysis on historical collections of cod and potentially other fish species from several Nordic populations in order to estimate the temporal stability of population structure as well as adaptive microevolution in relation to climatic variation. The insights on relationships between population structure, evolution and climate should be used in conjunction with forecasting models of environmental change in order to predict future distribution and abundance of fish populations. The project is part of a Nordic Centre of Excellence and will include collaboration with and visits to research institutions in Norway and Greenland.

Qualifications We are looking for a candidate who has:

Master of Science (M.Sc.) degree, or equivalent, in Population- or Evolutionary Genetics Previous experience with molecular genetic analysis Proficiency in written and spoken English Keen interest in research and a wish to work in the field of population genetics and evolution of aquatic organisms

Approval and Enrolment Scholarships for a PhD degree are subject to academic approval, and the successful candidate will be enrolled in one of the general degree programmes at DTU. For information about the general requirements for enrolment and the general planning of the scholarship studies, please see the DTU PhD Guide.

Salary and appointment terms The salary and appointment terms are consistent with the current rules for PhD degree students at DTU. The period of employment is 3 years.

Further information For further information about the project, please contact Professor Einar Eg Nielsen, een@aqua.dtu.dk, (+45) 40210231.

See the full position announcement at with further information on the online application procedure: http://www.aqua.dtu.dk/Om_DTU_Aqua/-Stillinger.aspx?guid=fa652131-600a-44ca-a5c9-3f0aee1f686c Einar Eg Nielsen <een@aqua.dtu.dk>

EAWAG Switzerland AnimalMigration

The Department of Aquatic Ecology (Eawag, Switzerland) and the Department of Ecohydrology (EPFL Lausanne, Switzerland) seek a PhD student in Ecology and Ecohydrology.

Project title: Experimental and theoretical evaluations of travelling waves of organisms spreading in differently structured aquatic systems.

The PhD student will participate in a collaborative research project with Dr. Florian Altermatt (Aquatic Ecology, Eawag) and Prof. Dr. Andrea Rinaldo (Ecohydrology, EPFL) to experimentally study travelling waves of aquatic organisms in landscapes of different structures. Understanding the spread of organisms in natural landscapes is a central issue of ecology and is currently receiving a large theoretical interest. We will use microcosm-system with protozoans, in which the propagation front can be accurately measured in the laboratory. These estimates are then used to parametrize a broad class of models. Ultimately, we want to get a more comprehensive understanding of the spread of organisms, such as disease vectors or invasive species, in bifurcating waterways and rivers. For this project, financed by Eawag, we are looking for a highly motivated candidate with interests in ecology, ecohydrology and river network dynamics. The project combines laboratory microcosm-experiments with protozoans and mathematical modeling.

We offer a stimulating research environment in lively and social institutes in DuÌbendorf (near ZuÌrich) and in Lausanne. At both localities, the departments host other research groups in ecology and ecohydrology. The position will be for a period of three years, and should start as soon as possible (June 2011 or soon thereafter). The PhD student will be enrolled at EPFL, but the lab- and working-environment is shared between the two localities (i.e., a large part of the PhD will be done in DuÌbendorf, the other part in Lausanne). The ideal candidate has good experimental skills and/or a strong background in quantitative modeling. Excellent communicational and writing skills in English, good work ethics, and creative thinking are desired. A Diploma or Masters degree (or equivalent) in biology, physics or related subject is necessary for admission. The working language in the groups is English.

Applications should include a letter of interest with a description of pertinent experience, curriculum vitae, a list of publications (if any), the names (with e-mail addresses) of three potential referees, and copies of certificates of academic qualifications.

Applications must be submitted with the online-application tool, using the following link: http://-internet1.refline.ch/673277/0028/++publications++/-1/index.html Please submit your application by 10 April 2011.

For further information, consult www.eawag.ch http://-www.eawag.ch/about/personen/homepages/altermfl/-index_EN http://www.epfl.ch/ http://echo.epfl.ch/-page-12889.html or contact Florian Altermatt (Tel. +41 58 765 55 92) florian.altermatt@eawag.ch

Eawag, the Swiss Federal Institute of Aquatic Science and Technology, is a Swiss-based internationally active research institute within the ETH Domain (ETH Zurich and EPFL). It is committed to the ecologically, economically and socially responsible management of water. EPFL is the Ecole Polytechnique FeÌdeÌrale de Lausanne. Its mission are education, research and technology transfer at the highest international level.

florian.altermatt@eawag.ch

JagiellonianUniv 8 EcolEvolutionaryBiology

8 PhD POSITIONS IN ECOLOGY AND EVOLUTIONARY BIOLOGY AT THE INSTITUTE OF ENVIRONMENTAL SCIENCES, JAGIELLONIAN UNIVERSITY, KRAKOW, POLAND

The leading Polish institute in: Behavioral ecology, Evolutionary genetics and life histories, Physiological and bioenergetics, Ecotoxicology and industrial pollutants, Ecosystem ecology, environmental education and management

is opening applications for

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

Topics offered by for the candidates: 1. Divergence population genetics of newts (Supervisor: Wieslaw Babik)

2. Molecular basis of adaptation in the bank vole (Wieslaw Babik & Jacek Radwan)

3. Sexual selection and the maintenance of enzyme polymorphisms in the bulb mite (Jacek Radwan)

4. Genetic differences between cuckoos parasiting broods of two sympatric species of warblers from the Acrocephalus genus (Mariusz Cichon & Andrzej Dyrcz)

5. Functions of plumage colour ornaments in blue tit females (Mariusz Cichon)

6. Laboratory model of adaptive radiation: correlated responses to a multidirectional artificial selection in the bank vole (Pawel Koteja)

7. Endophytes and biofuel production (Katarzyna Turnau)

8. Toxicokinetics of metals in arthropods (Ryszard Laskowski)

9. Stoichiometry of predator â prey trophic link in selected arachnids (Anna Rozen)

10. The role of fungivory in maintaining the stoichiometric balance of the detritus/detritivore trophic link (January Weiner)

11. Effect of natural and anthropogenic factors on microbial community structure and activity during litter decomposition (Maria Niklinska & Ryszard Laskowski)

12. Effective application of human dimension and public participatory approaches to natural resource management in Poland (Malgorzata Grodzinska-Jurczak)

13. Nature conservation management/policy on the jurisdictional, institutional and ecological scales (MaÅgorzata Grodzinska-Jurczak)

Candidates are suggested to contact potential supervisors prior to the application

Application deadline: 10 June 2011

Detailed information, containing the description of research projects proposed for PhD students, profile of the applicant and the application instructions are available at: www.eko.uj.edu.pl/ecology "ecology@uj.edu.pl" <ecology@uj.edu.pl>

MaxPlanckInst 2 PlantInsect

The department of Molecular Ecology at the Max Planck Institute for Chemical Ecology invites applications for two PhD fellowships for the Project:

"Mobile signals in plant defense against insects"

Upon insect attack, plants activate a highly effective immune system. Interestingly, this does not only happen locally above ground, but involves the belowground tissues as well: Roots provide toxic secondary metabolites for the leaves and serve as dynamic storage organs for future regrowth. But how exactly do the leaves "tell" the roots about the ongoing attack?

Using an interdisciplinary approach that combines molecular biology, phytochemistry, plant physiology and plant-insect ecology, you will attempt to identify leaf-to-root signals in wild tobacco and test for their ecological relevance in the field. The project will be integrated into our newly established group on root-environment interactions in tobacco, and may significantly contribute to our understanding of plant-insect interactions.

We look for students with a completed Master degree or equivalent who have a strong background in plant molecular biology, biochemistry, systems biology and/or ecology. Highly motivated candidates with solid training in other areas of biology are also encouraged to apply.

We offer an excellent research environment with enthusiastic scientists from different nationalities in the Department of Molecular Ecology (director: Prof. Ian T. Baldwin) at the Max Planck Institute for Chemical Ecology in Jena, Germany.

The deadline for applications is March 31, 2011. Interviews will start in April. The positions will be available from May 1st, 2011.

Please send your application including CV, letter of motivation and two references via e-mail to Dr. Matthias Erb (matthias.erb@unine.ch).

matthias.erb@unine.ch

Munster NGS Bioinformatics

WWU Münster Institute for Evolution and Biodiversity Evolutionary Bioinformatics

A highly motivated individual is sought for the following project:

Bioinformatic Analysis of NGS Whole Genome Data Taking advantage of next generation sequencing (NGS) we are aiming to understand genomic variations and their impact on fitness. The three-spined stickleback Gasterosteus aculeatus has become a model organism for evolutionary and behavioural ecology par excellence because of its wide distribution across the northern hemisphere, repeated and independent adaptation to rivers and lakes after the glacial period, the associated morphological changes such as loss of bony armour and a well annotated genome. Investigating genome architecture in a population sample we want to unravel genomic changes underlying adaptations and in particular to understand the role of structural variation and copy number variation. The great importance of structural variations in the genome has recently been shown in biomedical field. Here, findings from the stickleback model system will contribute to a better understanding of the evolution and fitness consequences of this type of variation in the genome.

The position holder will be given the opportunity to pursue a PhD project. Tasks include: â- Analysing and comparing genome assemblies obtained by Illumina and/or 454 â- Software development for downstream variation analysis â- Setting up databases to improve accessibility of the data â- Creating a web application for whole genome data visualization

Essential qualifications are: â- MSc (or equivalent degree) in computer science, statistics or bioinformatics with experience and/or desire to excel in a biological area â- Basic skills in statistics and/or programming â- Motivation and proven ability to carry out research independently â- Good communication skills, English

Contact: p.feulner@wwu.de until the 15.4.2011 (application should be send in a single pdf file, maximal 2 pages, including motivation, publications list, and degrees)

p.feulner@uni-muenster.de

NaturalHistoryMuseum London Supertrees

Applications are invited for a PhD studentship at the Natural History Museum, London, on maximum likelihood supertrees

The project will be based at the Natural History Museum, London, and at University College, London. The supervisors will be Drs Mark Wilkinson (mw@bmnh.org) and Peter Foster (p.foster2@gmail.com), Department of Zoology, The Natural History Museum, and Prof Ziheng Yang (z.yang@ucl.ac.uk), Research Dept. of Genetics, Evolution and Environment, UCL.

The project will involve computational phylogenetic methods development, specifically implementation and testing of new models for evaluating supertrees. More details are available on request from Peter Foster.

The studentship starts in October 2011, and is open to EU nationals. The closing date for applications will be 11 April, 2011. Please send your application (full academic CV including two referees and covering letter) to

Anna Hutson, Postgraduate Studies Administrator, The Natural History Museum, Department of Botany, Cromwell Road, London SW7 5BD

Or electronically to A.Hutson@nhm.ac.uk.

Peter Foster Natural History Museum, London

Peter Foster <p.foster2@gmail.com>

QueenMaryU BatSpeciation

Funded PhD - Start October 2011 or January 2012 “Hunting for speciation genes in bats”

Deadline 21st March 2010

I am seeking a highly motivated student to undertake a PhD that tackles a central question in evolutionary biology: how do new species form?

Growing evidence indicates reproductive barriers can be established by divergence at a few loci. The idea that only a few key genes can control speciation has profound implications for explaining how species might form without geographical isolation. The aim of this project is to discover $B!H(Bspeciation genes$B!I(B in echolocating horseshoe bats. These bats live in an acoustic world and emit calls in order to hunt, avoid obstacles and communicate. So selection pressures acting on the call frequency for a particular diet or habitat could also influence communication and vice versa. Call frequency divergence might thus be related to rapid speciation seen in this group. The project will combine laboratory work, fieldwork and computational analyses, so experience in one or more of these (and a willingness to learn) is essential. The student will also need to be able to work independently at times, as well as part of a team.

For further details including instructions on how to apply see: http://www.findaphd.com/search/showproject.asp?projectid=32227&inst=QLON-BiSc&searchtype=l&theorder=2&page=1

Stephen Rossiter <s.j.rossiter@qmul.ac.uk>

SimonFraserU HPA-Stress evolution

PHD OPPORTUNITY in HPA-STRESS PROGRAMMING & EVOLUTION, SIMON FRASER UNIVERSITY

GOAL: We are seeking to recruit a graduate student interested in pursuing a PhD on the early development of the hypothalamic-pituitary-adrenal (âstressâ) axis.

PROJECT: The stress axis plays a critical role in determining an individualâs ability to cope with challenges throughout the lifetime. However, the extent to which stress axis function is âcalibratedâ by prenatal stress at different gestational stages is unclear. This project involves the use of a unique longitudinal data set to explore the impact of stress experienced during the first six weeks of gestation on post-natal stress response in later life.

QUALIFICATIONS: We are seeking an individual with: â Excellent academic record â Background in evolutionary biology, physiology, genetics and/or epigenetics â An evident commitment and passion for science

START: ideally, September 2011

WE OFFER: annual stipend, research funds, training at the interface of evolutionary biology with physiology, development, genetics and epigenetics, innovative intellectual environment

LOCATION: Human Evolutionary Studies Program, Faculty of Health Sciences and Dept. of Biology, Simon Fraser University, Burnaby, BC, Canada.

PIs AND WEBSITES: Dr. Pablo A. Nepomnaschy and Dr. Bernard Crespi Dr. Pablo A. Nepomnaschy: http://www.sfu.ca/ ~ pan2/Home.html Dr. Bernard Crespi: http://www.sfu.ca/biology/faculty/-crespi/lab.html

APPLICATION: Please send a letter of intent and a CV to Katrina Salvante <kgsalvan@sfu.ca>

Bernard Crespi <crespi@sfu.ca>

SoutheasternLouisianaU ChloroplastGenomeEvol

Masters in Biology Project: Chloroplast Genome Evolution Rick E. Miller's Lab Southeastern Louisiana University

We invite a highly motivated graduate student (masters degree) to participate in a research project examining the molecular evolution of the chloroplast genome in morning glories. We are presently obtaining 30 whole-chloroplast genome sequences from an exemplar sample of morning glories (members of the tribe Ipomoeeae). Specifically, we are obtaining whole plastid sequences using both 454 and Solexa sequencing for the 160,000 bp morning glory chloroplast genome. We are carrying out both de novo and reference-based assembly. Then we are forming contigs using Sequencher and annotating the genomes with Dogma prior to submission to GenBank.

These results provide a wonderful opportunity to examine the molecular evolution of the 81 well-characterized genes of the chloroplast genome found in angiosperms, as well as molecular evolutionary analyses of indel hotspots and substitution patterns in non-coding regions.

This research is being carried out in collaboration with Jim Leebens-Mack at the University of Georgia. Other research in our lab includes the systematics of morning glories, molecular evolution of anthocyanin pathway regulatory genes, phylogeography of morning glory species, and additional studies in evolutionary ecology. Our lab includes masters students, but also an active group of undergraduate research assistants.

I am making this announcement at this time because an additional position has become available in our department, which will provide support through a teaching assistantship.

Hammond is located (on solid ground) about 50 miles north of New Orleans and east of Baton Rouge. Southeastern Louisiana University is primarily an undergraduate institution, but the Department of Biological Sciences has a strong group of research-oriented faculty. Our masters degree is an excellent stepping stone towards a Ph.D. or also is a good terminal degree, depending on your career considerations.

The application deadline date for regular admission to the department is 1 February, for students to begin in the Fall 2011, however, because of the recent opening we are extending the deadline until 1 April 2011. The admissions requirements are modest including a Bachelor's degree, a minimum GPA of 3.0, a minimum GRE score of 1,000 (verbal + quantitative).

For more information about the details of the graduate program, please consult our website about Graduate Degrees in the Biology Department.

http://www.selu.edu/acad_research/depts/biol/-grad_degree/index.html If you are interested in a applying for a masters degree in our lab.

PLEASE CONTACT: Dr. Rick E. Miller Department of Biological Sciences Southeastern Louisiana University Hammond, LA 70401 985 549-5556 Email: rickmiller@selu.edu http://www2.selu.edu/-Academics/Faculty/rickmiller/ Rick E. Miller, Ph.D. Department of Biological Sciences Southeastern Louisiana University Hammond, LA 70402

Biology Building Room 403 office/ 419 lab phone: (985) 549-5556 FAX: (985) 549-3851 email: rickmiller@selu.edu http://www2.selu.edu/Academics/Faculty/rickmiller/ rickmiller@selu.edu

Tuebingen Germany 2 MarineEvolutionaryEcol

Two Ph.D.-student positions are available at the University of Tuebingen funded by the VolkswagenStiftung. Apologies for cross-posting.

The project addresses context-dependent plasticity of sexual selection. We will study the plasticity and evolution of sex roles within and across populations with different environmental contexts. Our main study species is the common goby (Pomatoschistus microps) with exclusive paternal care, plastic sex-roles, and a mating system that is highly affected by its natural and social context such as by nest availability, predation risk, water temperature, operational sex-ratio, and mate competition. Coastal areas of the Baltic Sea provide a natural gradient in terms of biotic, abiotic, and community ecological factors. We will study how the environmental, ecological, and demographic context affects populations and the mating system. We will conduct experiments and population surveys to obtain relevant data.

Requirements: Applicants should have a keen interest in doing experimental work with small fish in the field, and in performing molecular analyses and behavioural assays in the lab. The ideal candidates for this project have a background in evolutionary ecology (or a related field), are highly motivated, creative and independent. A Diplom or MSc degree (or equivalent) in Biology, Ecology or a related discipline is required.

The new team will be part of Animal Evolutionary Ecology at the Institute of Evolution and Ecology at the University of Tuebingen. Regular visits of field sites and extended stays at research stations, mainly in Finland, Sweden and Germany during the field season (May-July) are essential. The working language in Tuebingen and at the field stations is English. However, for everyday life at the University and in Tuebingen (located in southern Germany, close to Stuttgart), some knowledge of German will be advantageous.

Both positions are fixed-term for 4 years. The salary and benefits are set according to the German salary scale TV-L E13 (50%). In case of equal quality of applicants, those with disabilities will be preferred. The University of Tuebingen aims to increase the representation of women in research and teaching and therefore encourages female scientists to apply.

Please send your application by email as one single pdf-file including 1) a letter of motivation, 2) CV, 3) name and email of at least two references who could be contacted, 4) short description of current and future research interests 5) a 1-page summary of your MSc project or undergraduate work and research experience to katja.heubel(at)helsinki.fi.

Review of applications will start from 15 April 2011 onwards, but candidates will be considered until the positions are filled. Start date: 1 August 2011 or on appointment. For more information, feel free to contact me!

Dr. Katja Heubel Advanced Fellow - VolkswagenStiftung, University Lecturer, Department of Biosciences, Ecology and Evolutionary Biology, University of Helsinki, Finland.

After 1.8.2011: University of Tuebingen, Department of Biology, Institute for Evolution and Ecology, Animal Evolutionary Ecology, Auf der Morgenstelle 28 D-72076 Tuebingen, Germany

links: http://www.evoeco.uni-tuebingen.de http://www.eve.uni-tuebingen.de http://www.volkswagenstiftung.de/funding/challenges/evolutionary-biology.htm l?L=1 http://luoto.tvarminne.helsinki.fi/english/index.htm http://www.eseb2011.de/tuebingen.htm http://www.helsinki.fi/people/katja.heubel/ Dr. Katja Heubel, Docent University Lecturer Ecology and Evolutionary Biology Department of Biosciences, PO Box 65 (Viikinkaari 1), FIN-00014 University of Helsinki, FINLAND

phone +358 9 191 57806 fax -57694

office location: Biokeskus 3, room 6403 email: katja.heubel@helsinki.fi http://www.helsinki.fi/people/katja.heubel/ Katja Heubel <katja.heubel@helsinki.fi>

UBristol EvolutionBehaviour

PHD STUDENTSHIP ON "THE EVOLUTION OF PSYCHOLOGICAL AND PHYSIOLOGICAL MECHANISMS FOR BEHAVIOUR"

Supervisors: Prof. Alasdair Houston, Prof. John Mc-

Namara & Dr Tim Fawcett Modelling Animal Decisions (MAD) Group, University of Bristol

We are seeking a talented and enthusiastic student for a PhD position in our group, as part of an exciting new ERC-funded project on 'The evolution of mechanisms controlling behaviour'. This is an ambitious, interdisciplinary project which aims to shed light on the internal workings of behaviour and lead to a better understanding of how evolution has shaped decision making in a wide variety of animals, from invertebrates to humans.

THE PROJECT

The PhD project will involve the development of mathematical and computational models of animal behaviour, based on evolutionary theory. A key part of the work will be to integrate mechanistic considerations into evolutionary models, in order to understand how behaviour is affected by constraints in evolved psychological and physiological systems. Within the general aims of the project, the candidate will have the freedom to develop the work along the lines that interest them most. The issues we are currently working on include:

- The evolution of irrational preferences. Animals (including humans) value rewards (food, money, etc.) in a subjective and sometimes inconsistent way. For example, gains and losses often seem to matter more than the animal's final state. We are using evolutionary models to try to explain this apparently irrational behaviour.

- The evolution of patience. In some situations animals act impulsively, seeking instant gratification, while in other situations they are willing to wait for a greater reward. We are trying to understand what ecological factors favour impulsive behaviour and what factors favour patience.

- The evolution of obesity. One hypothesis for the rise in obesity in the developed world is that our evolved foraging strategies no longer work well in environments where energy-rich food is readily available. We are using evolutionary models of dietary preferences to examine whether this is a plausible explanation.

- The evolution of emotions. Although animal behaviour is complex, it seems to be related to a small number of motivational drives, for example fear, hunger and sexual arousal. We are building models of the evolution of emotional states to help us understand why behaviour is organised in this way.

We collaborate closely with empirical biologists working on a range of different systems, but the PhD project will be theoretical. The major techniques we use include optimality theory, game theory, dynamic programming, genetic algorithms, neural networks and genetic programming. Training in these methods will be provided, but we are seeking a student with good skills in mathematics or computer science.

McNamara, J. M. & Houston, A. I. 2009. Integrating function and mechanism. Trends in Ecology & Evolution 24: 670-675.

THE WORKING ENVIRONMENT

The successful candidate will join a new, dynamic research group under the leadership of Profs Alasdair Houston and John McNamara, world leaders in theoretical approaches to studying animal behaviour. The Modelling Animal Decisions (MAD) group (www.bristol.ac.uk/biology/research/behaviour/mad) is based in the School of Biological Sciences and has strong links with researchers in Mathematics, Computer Science, Psychology, Philosophy and Animal Welfare. We have ongoing collaborations with experts elsewhere in Britain and throughout the EU, and there will be opportunities to travel to international workshops and conferences as part of the PhD project.

The University of Bristol is one of the top research universities in the UK and is the pre-eminent institute for mathematical approaches to studying animal behaviour. Students have access to world-class library and computing facilities and are immersed in a vibrant research environment, with several active seminar series, frequent visits from prominent international scientists and an active social scene. The School of Biological Sciences runs a special training scheme for graduate students, offering a variety of modules and workshops to improve skills in statistics, communication, collaboration, time management, peer review, public engagement and much more besides.

WHO WE ARE LOOKING FOR

We are seeking a student with good mathematical and/or computational skills. Applicants should have (or expect to obtain) a degree in Mathematics, Physics, Computer Science or a related discipline. We also encourage applications from Biological Sciences students whose degree includes a substantial (i.e. $> 30\%$) mathematical component. A keen interest in evolutionary biology is essential.

The studentship is open to all EU students. Those from within the UK need at least an upper second-class Bachelors degree before they can take up the position.

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UCL Belgium Cambridge ButterflyPheromones

We are looking for applicants for a PhD project about "The role of sex pheromones in reproductive isolation among /Heliconius/ butterflies". The project is a collaboration between Chris Jiggins and the /Butterfly Genetics Group/ in Cambridge, UK and Caroline Nieberding in the Académie Louvain (UCL), Belgium. Potential funding sources are available from Belgium starting October 1^st , 2011. There is also potential for collaboration with Luana Maroja, at Williams College, and Mathieu Joron at the Natural History Museum in Paris who are also beginning to explore pheromonal communication in /Heliconius/. The project will also benefit from the fact that Prof. P. Brakefield has recently moved to Cambridge, bringing considerable expertise in butterfly evolutionary genetics and pheromonal communication in particular.

/Heliconius/is a diverse neotropical genus famous for Müllerian mimicry, where unrelated species converge in their aposematic colour patterns to more efficiently advertise their unpalatability to predators. Sister taxa tend to belong to different mimicry rings and evidence suggests that shifts in colour pattern can cause both pre-mating and post-mating isolation, thereby promoting rapid speciation. These colour patterns are therefore a clear example of an ecological trait with a pleiotropic effect on mate choice and could be considered 'magic traits' (sensu Gavrilets). However, pheromones also play an important role in butterfly courtship but little is known about them in /Heliconius/. This project aims to characterise and explore the importance of pheromones in /Heliconius/ speciation. We postulate that reproductive isolation between sympatric related species of /Heliconius/ must involve olfactory communication, especially where such species share wing patterns due to mimicry. We anticipate that females recognize conspecific mating partners based on the differentiation of male sex pheromones (in composition, titres or ratios) used during courtship, between closely related species. Experiments will involve manipulation of butterfly phenotypes, behavioural experiments and chemical exploration of the chemical diversity present in /Heliconius/. Little is known about pheromonal communication in /Heliconius/, so there is enormous scope for this project to develop in different directions. Possible future avenues include studies of the genetic basis of pheromonal differences between populations, or the information content of pheromonal signals within species.

We are looking for a strongly motivated PhD candidate with a Msc in the broad field of Evolutionary Biology and Ecology. The successful applicant is expected to apply, with our full support, for a 4-year PhD grant delivered by the FNRS in Belgium, where chances to get funded will be high if training is seriously done. The deadline for the application is September 1^st , 2011 and will be followed by an interview within the next 8 weeks. Salary ranges between 1600-1800 euros netto per month plus benefits (health insurance,...) which are included in the Belgian system. Applications should be sent by email to Chris Jiggins (c.jiggins@zoo.cam.ac.uk) and Caroline Nieberding (caroline.nieberding@uclouvain.be) and should include the following: (1) a cover letter describing your research interests and qualifications, (2) a full CV, (3) contact information of minimum 2 referees. Informal inquiries are welcome. Applications will be reviewed directly until the position is filled.

Caroline Nieberding <caroline.nieberding@uclouvain.be>

UDusseldorf MolEvol SexGenes

UDüsseldorf_PhD_position-molecular evolution of sex determining genes in social hymenoptera (Heinrich-Heine University Düsseldorf, Department of Biology, Group of Evolutionary Genetics)

Application deadline: 30. April 2011

We are looking for a highly motivated PhD candidate to study the population dynamic and molecular evolution of sex determining genes in social hymenoptera (honey and bumble bees). Understanding the evolutionary forces and processes that have led to the fascinating (single locus) sex determining system in these bees will contribute to elucidate general principles in evolution. Sex determination in the honey bee Apis mellifera is governed by heterozygosity at a single locus harbouring the complementary sex determiner (csd) gene, which arose by a gene duplication before honey bee divergence. Bees heterozygous at csd are females, whereas homozygotes and hemizygotes (haploid individuals) are males. Diploid males occur when csd is homozygous and are lethal in Apis mellifera. Rare alleles thus have a selective advantage, are seldom lost by the effect of genetic drift, and are maintained over extended periods of time when compared with neutral polymorphisms.

The ideal candidate should have a Masters degree (or equivalent degree) and have a strong background in population genetics, including excellent skills in molecular lab work and major interest in bioinformatics. Previous experience with bees is beneficial. We offer a stimulating and dynamic working environment and excellent research facilities. Further information about the group, including latest publications (PNAS; Nature, PlosBiol) can be found under http://www.genetik.uni-duesseldorf.de/Gruppen/beye. The position (TV-L 13 65%) is funded by the Deutsche Forschungsgemeinschaft for three years. Applicants should send a cover letter, C.V., list of publications, a statement outlining past research experience and particular motivation for the position (max. 2 pages), and contact details of 2-3 referees to martin.hasselmann@uni-duesseldorf.de. Please contact me for any further questions and send in your application as a single pdf by 30. April 2011 latest. The candidate should be start working by mid of 2011.

– Dr. Martin Hasselmann Heinrich-Heine Universitaet Duesseldorf Assistant Professor Institut fuer Genetik Universitaetsstr. 1 Gebaeude 26.03, Ebene U1 Raum 68A 40225 Duesseldorf

Tel. : ++49-0211/8114808 Fax : ++49-0211/8112279 email: martin.hasselmann@uni-duesseldorf.de

http://www.genetik.uni-duesseldorf.de/Gruppen/-beye/Hasselmann Martin Hasselmann <Martin.Hasselmann@uni-duesseldorf.de>

ULausanne PopulationGenomicsDevo

A PhD position is open for a collaborative project between the labs of Prof. Alexandre Reymond (Genome Structure and Expression) and Prof. Marc Robinson-Rechavi (Evolutionary Bioinformatics). The project concerns the interface between Population Genomics and Developmental Biology. We will study how genome structural changes affect gene expression during mouse development, and possibly adaptation. The work will involve bioinformatics, as well as some molecular biology.

We are looking for an autonomous and ambitious student, with a strong motivation to understand fundamental questions in biology, and an open mind towards using computational and experimental tools towards this end. The ideal candidate will have basic training in biology, and a degree in bioinformatics or computer science.

The student will receive training in bioinformatics and in experimental biology, and participate in the activities of the new doctoral program in Population Genomics (http://www.unil.ch/pg/page75326.html).

Please send a CV and contact information of two references to: alexandre.reymond@unil.ch; marc.robinson-rechavi@unil.ch

Websites for additional information: http://www.unil.ch/cig/page8508_en.html http://bioinfo.unil.ch/ Marc Robinson-Rechavi Department of Ecology and Evolution Biophore 3219, University of Lausanne, 1015 Lausanne, Switzerland tel: +41 21 692 4220 fax: +41 21 692 4165 http://bioinfo.unil.ch/ Swiss Institute of Bioinformatics http://www.isb-sib.ch/groups/lausanne/eb-robinson-rechavi.html La liberte ne s'use que quand on ne s'en sert pas

marc.robinson-rechavi@unil.ch

ULaval FishPopulationGenomics

Ph.D. position in fish population genomics and conservation

I am currently searching for a Ph.D. candidate for conducting a research project on the population genomics in the American eel. Three specific research objectives are being achieved as part of this research program that involves several other academic researchers and government partners: i) to characterize the availability of marine and estuarine habitats in Canadian waters, ii) to test the existence of glass eel/elver ecotypes in fresh and marine water in the theoretical framework of conditional strategies, and iii) to document the genetic, physiological, and behavioural basis of the control of the expression of these ecotypes and their propensity to occupy different habitats. From an applied perspective, this project will provide knowledge for improving the conservation of the species and its sustained exploitation. From a fundamental point of view, the results will contribute to a better understanding of the mechanisms underlying the proximal and ultimate control of continental dispersion of eel and its consequences on adaptation to heterogeneous habitats.

The candidate will be specifically involved in the realisation of the objective dealing on population genomics and testing for the effect of natural selection at the molecular level associated with use of contrasted habitats. This will involved the use of next-generation sequencing methods, the development and genotyping of SNP markers, as well as bioinformatic treatment and analysis of large data base. The ideal candidate should thus possess strong skills in any of those applications, as well as a solid background in evolutionary biology and interests for conservation genomics.

To apply, please send a cover letter describing your research interests, a complete CV and names of three references by e-mail to Louis.Bernatchez@bio.ulaval.ca

To know more about;

Quebec City:

http://www.quebecregion.com/e/ Laval University: http://www.ulaval.ca/ Our laboratory: http://www2.bio.ulaval.ca/louisbernatchez/presentation.htm Opportunité dâun Ph.D. au QuÃ©bec en gÃ©nomique des populations et de la conservation des poissons.

Je suis Ã la recherche dâun(e) candidat(e) pour rÃ©aliser une thÃse portant sur la gÃ©nomique des populations dâanguille dâAmÃ©rique. Trois objectifs spÃ©cifiques seront rÃ©alisÃ©s dans le cadre de ce programme de recherche qui implique plusieurs chercheurs universitaires et partenaires gouvernementaux soient ; i) caractÃ©riser la disponibilitÃ© des habitats marins et estuariens dans les eaux canadiennes, ii) tester l'existence d'Ã©cotypes de civelles d'eau douce et marines dans le cadre thÃ©orique de la stratÃ©gie conditionnelle, et iii) documenter les bases gÃ©nÃ©tiques, physiologiques et comportementales du dÃ©terminisme de l'expression de ces Ã©cotypes et de leur propension Ã occuper diffÃ©rents habitats. Outre ses retombÃ©es appliquÃ©es pour amÃ©liorer la gestion et la conservation de lâespÃce, ce projet vise Ã approfondir les connaissances sur les mÃ©canismes sous-jacents au contrÃle proximal et ultime de la dispersion continentale de l'anguille et de ses consÃ©quences sur l'adaptation aux habitats hÃ©tÃ©rogÃnes.

LâÃ©tudiant recrutÃ© sera spÃ©cifiquement impliquÃ© dans la rÃ©alisation du troisiÃme objectif portant essentiellement sur la gÃ©nomique des populations et la mise en Ã©vidence au niveau molÃ©culaire de lâeffet de la sÃ©lection naturelle associÃ©e Ã lâutilisation dâhabitats contrastÃ©s. Ceci fera notamment appel Ã lâutilisation des techniques de sÃ©quenÃde nouvelle gÃ©nÃ©ration, au dÃ©veloppement et au gÃ©notypage de marqueurs SNP, ainsi quâau traitement bioinformatique de grandes bases de donnÃ©es. Le candidat idÃ©al devrait donc possÃ©der une solide expertise dans au moins une ou lâautre de ses applications de mÃme quâune solide formation en biologie Ã©volutive et un intÃ©rÃt marquÃ© pour la gÃ©nÃ©tique de la conservation.

Le poste est ouvert dÃs maintenant, mais pourra dÃ©buter jusquâen septembre 2011. Pour appliquer, faites parvenir une lettre de

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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

ULethbridge AvianPopulationGenetics

Population Genetics of North American Forest Birds

A graduate assistantship (M.Sc.) is available in the laboratory of Dr. Theresa Burg at the University of Lethbridge starting Sept 2011. I am looking for a highly motivated graduate student to work with me to study large-scale population divergence of birds. The project involves both laboratory and field-based research and the use of high-throughput DNA-based methodologies. Students must be able to work independently and as part of a group. Candidates should have a solid undergraduate background in evolution, and genetics. Prior research experience with molecular techniques and mistnetting are desirable but not required. Please consult the Graduate Studies website (http://www.uleth.ca/graduatestudies/) for admissions criteria, tuition fees and other expenses.

For more information please contact Theresa Burg at theresa.burg@uleth.ca. The deadline is April 11 or until the position is filled. Please send me a copy of your CV, transcripts and research statement, if you are interested.

Thanks

Theresa Burg

http://people.uleth.ca/˜theresa.burg
theresa.burg@uleth.ca

ULondon PlantMicrobeCoevolution

Hi Evol dir,

There is NERC-funded PhD studentship available at Royal Holloway University of London that will investigate the coevolution and evolutionary ecology of plant microbe interactions. There is increasing interest in the ability of root-associated bacteria to promote the growth of plants via improved nutrient uptake or suppression of pathogens. Applied crop research has indicated that these bacteria have the potential to improve crop yields, especially in developing countries where costs can limit the application of fungicides and fertilizers. The basic biology of many of these spore- formers is still relatively unknown, and this PhD aims to improves our understanding of how ecological factors and/or evolutionary relationships with host plants affect this symbiosis, and may ultimately help growers select strains appropriate to particular crops or soils. Please feel free to contact ben.raymond@rhul.ac.uk for further details. UK residency is a requirement for the full NERC funding, although EU residents are eligible for a fees-only award.

Dr Ben Raymond, NERC Advanced Research Fellow, Lecturer in Population Genetics, School of Biological Sciences, Royal Holloway University of London, Egham, Surrey. TW20 0EX

tel 0044 1784443547 Ben.Raymond@rhul.ac.uk

Ben Raymond <Ben.Raymond@rhul.ac.uk>

UNeuchatel PlantEvolutionaryGenomics

PhD Student in Plant Ecological Genomics at the University of Neuchatel, Switzerland

A PhD position is available in the Laboratory of Evolutionary Botany at the University of Neuchatel (Switzerland) to contribute to our ongoing projects on transposable elements, genome organization and speciation in Brassicaceae.

The PhD project aims at understanding the mechanisms of reproductive isolation in the alpine autopolyploid complex Biscutella laevigata. In particular, populations showing signature of local adaptation in the face of gene flow will be used to highlight genes and genetic architectures underlying adaptive responses to solar radiation.

We are seeking a highly motivated and independent student that has completed an MSc degree in evolutionary ecology or plant molecular genetics. You should be familiar with (i) field sampling and experimental design, (ii) molecular techniques and (iii) statistical analysis (skills in NGS bioinformatics would be an asset). Strong organizational and communication (English) skills are required. Interested candidates are encouraged to make informal contacts.

Motivated applicants should submit (i) a one-page letter that summarizes their research interests and experience, and their motivation for working on this project, (ii) CV, and (iii) contact information of 2-3 reference persons (all as one PDF) to: christian.parisod@unine.ch

Closing date is on May 1st, 2011. The position will begin June 1st, 2011. Yearly salary: CHF 38000 - 44000.

Dr Christian Parisod Evolutionary Botany University of Neuchatel Rue Emile-Argand 11 2000 Neuchâtel - Switzerland Phone: +41 32 718 2344, Fax: +41 32 718 3001 e-mail: christian.parisod@unine.ch http://www2.unine.ch/evobot/page29932.html Christian Parisod <christian.parisod@unine.ch>

UNewSouthWales DolphinPopulationGenetics

PhD Position Dolphin Population Viability Analysis

FORECASTING DEMOGRAPHY OF BOTTLENOSE DOLPHINS

A/Prof W Sherwin Evolution and Ecology Centre, University of New South Wales

With partners from Murdoch University we are funded to study ecology, threats, and genetics of Bunbury (WA) bottlenose dolphins. The PhD student at UNSW will use these data in existing or novel programs, to evaluate population viability with different management and threats. The work involves integration between demographic, ecological, and genetical approaches. There would be field-trips to Bunbury. You should be qualified in population ecology, with good numerical and computational skills. A knowledge of molecular ecology would be an advantage. Molecular ecology qualifications are desirable.

PROCEDURE

(1) DISCUSS: Email letter with CV, academic record, and details of two academic referees, to A/Prof Bill Sherwin (W.Sherwin@unsw.edu.au). For further information phone: +61-2-9385-2119. Your letter should include explicit explanation of how your results are sufficient to allow application for a SCHOLARSHIP at UNSW (see below for grades required). We cannot consider other applications.

(2) PhD M/Phil CANDIDACY APPLICATION: Requirements for PhD are BSc (Hons 1), MSc, or equivalent. For MPhil, requirement is BSc. Specific areas essential and desirable are shown for each project above. Solid research and communication skills. Full NSW driver license desirable. For exact timing and details www.grs.unsw.edu.au/homepage.html (3a) PhD SCHOLARSHIP APPLICATION - LOCAL: Citizens or permanent residents of Australia/NZ, apply for APA and UPA at UNSW. You will need to have completed a research degree (eg MSc or BSc Honours research year), with results which are equivalent to 85% or higher, in order to be competitive for these scholarships. Publications in ISI-listed international journals will help also. Applications are due 25 Mar 2011, for study commencing in Second Session in 2011. For exact application timing and details see www.grs.unsw.edu.au/-scholarships/local.html

(3b) PhD SCHOLARSHIP APPLICATION Â INTERNATIONAL: Applicants who are NOT- citizens or permanent residents of Australia/NZ, can apply for IPRS and UIPA at UNSW. In order to be competitive for these scholarships, you will need to have completed a research degree (eg MSc or BSc Honours research year), with results which are equivalent to 95% or higher. Note that a coursework MSc is NOT acceptable. Publications in ISI-listed international journals will help also. Applications are due 25 Mar 2011, for study commencing in Second Session in 2011. For exact timing and details see www.grs.unsw.edu.au/-scholarships/internationalschols.html (3c) M Phil SCHOLARSHIP APPLICATION. Local and international students can apply for a $4000 stipend form the EERC, UNSW. International students can apply for a tuition fee waiver scholarship, provided that they can formally guarantee the remainder of their own stipend www.grs.unsw.edu.au/scholarships/-internationalschols.html www.eerc.unsw.edu.au/-GradProgram.html Associate Professor WB Sherwin Co-coordinator, Genetics Plan Evolution & Ecology Research Centre Deputy Head, School of Biological Earth and Environmental Science, University of New South Wales, Sydney NSW 2052 Australia W.Sherwin@unsw.edu.au PH:61-2-9385-2119 FX: 61-2-9385-1558 http://www.bees.unsw.edu.au/-school/staff/sherwin/sherwinwilliam.html CRICOS provider code 00098G

William Sherwin <w.sherwin@unsw.edu.au>

UParis6 EvolutionOfAntCastes

GraduatePosition;UParis6.EvolutionOfAntCastes

PhD position (3 years starting September 1st 2011)

Equipe Evolution of Animal Societies, Laboratoire Ecologie & Evolution CNRS UMR 7625, Universit Pierre et Marie Curie, 7 quai Saint Bernard, 75005 Paris

Supervisors : Mathieu Molet and Thibaud Monnin

Contact : mathieu.molet@gmail.com; +33 1 44 27 26 94

Web site : http://ecologie.snv.jussieu.fr/socialite/ Anomalous queen-worker mosaics drive the evolution of novel phenotypes in ants

Studying the mechanisms that allow for the production, survival and selection of novel phenotypes is crucial to understand biodiversity. The classic evolutionary mechanism involves random mutations and selection. Molet, Wheeler and Peeters (2010) propose an extension, only available to polyphenic organisms, i.e. exhibiting phenotypic plasticity with discrete alternative forms, where traits from existing alternative phenotypes are recycled and recombined to generate novel mosaic phenotypes. Because these traits have already been tested by natural selection in the phenotypes where they normally occur, mosaics are likely to be viable. They can be selected because they result from variability in genes that control the sensitivity thresholds responsible for the polyphenism. Molet et al. (2010) also propose that in social taxa, anomalous phenotypes have higher probability of survival since the colony buffers them against the outside environment. Accordingly, we suggest that polyphenic and/or social organisms show an enhanced potential for evolving biodiversity.

Ants are an ideal model to test these two hypotheses. They live in societies where reproduction is not shared equally. Fundamental to this division of labour is an ancestral female polyphenism with two castes: winged queens specialized in colony founding and egg-laying cooperate with wingless workers that perform all other tasks. These two adult phenotypes are environmentally-determined during larval development. Ants produce rare anomalous phenotypes called intercastes that are intermediate between winged queens and workers. These intercastes can be the first step towards the numerous novel castes that have evolved in ants, such as wingless queens and soldiers.

The PhD student will investigate the production of intercastes in colonies of *Mystrium *and *Temnothorax*. Using ethological, morphometric and dissection methods, he/she will assess whether they are mosaics that survive in the colonies where they emerge, measure the costs that they may inflict on colonies, and test whether they can occasionally bring benefits to colonies by providing new functions or performing existing functions more economically. He/She will also expose colonies to various environmental conditions in order to reveal some parameters that can influence intercaste production.

The applicant should have a B.Sc. (Hons) and a good English level. He/She should have skills in several of the following area: ecology, evolution, ethology, morphometry, social insects. Fieldwork in France or other countries (Madagascar') will be planned.

Email motivation letter, CV, academic records, and details of two academic referees, to Dr Mathieu Molet (mathieu.molet@gmail.com). For further information phone: +33 1 44 27 26 94. Application deadline is May 1. Interviews will take place end of May.

Molet M., Wheeler D., Peeters C. (2010) Developmental mosaics, social buffering, and the evolution of novel castes in ants. Congress of the International Union for the Study of Social Insects, Copenhague, Danemark.

– Mathieu Molet mathieu.molet@gmail.com http://-www.mathieumolet.fr/ Laboratoire Ecologie & Evolution UMR 7625 Universit Pierre et Marie Curie 7 quai St Bernard bat A, 7me tage 75005 Paris, FRANCE Tel. +33 (0)1 44 27 26 94 Fax. +33 (0)1 44 27 35 16

Mathieu Molet <mathieu.molet@gmail.com>

UPotsdam SmallMammalDynamics

Biodiversity and Functional Ecology of Agricultural Landscapes

The University of Potsdam (UP) together with the Leibniz Centre for Agricultural Landscape Research (ZALF) and the Leibniz Institute for Zoo and Wildlife Research (IZW) offers

3 PhD positions

within the following topics: - Public Health: Density and spatial distribution of small mammals as hosts for ticks and of ticks as vectors for Lyme borreliosis, prevalence and diversity of tick-borne pathogens, spatiotemporal modelling of human infection risk in response to agricultural landscape structures (supervisors: J. Eccard, UP; F-R. Matuschka / D. Richter, CharitÃ©; B. Schröder, UP / ZALF) - Ecosystem services of bats with respect to agricultural landscape structures, Quantification of the economic benefits of bat species through consumption of agricultural pest insects. Acoustic monitoring of bats, spatial analysis of habitat use, insect diversity and diet analysis (supervisors J. Eccard, UP; C. Voigt, IZW) - Experimental assessment of establishment dynamics and genetic structure of plant and animal species in response to agricultural landscape structures; modelling of dispersal dynamics and interspecific interactions (supervisors: J. Joshi, UP; B. Schröder, UP / ZALF) All three projects offer a challenging scientific task in the stimulating environment of a research collaboration between UP and two Leibniz-Institutes. The projects combine a variety of different methods and techniques, and a broad range of training options will be available to the candidates.

Candidates should have a master degree or Diploma in Biology, Geoecology or Landscape Ecology and are expected to be highly motivated to perform both independent field and laboratory work. They must be team players for synergies in field work. At least one of the following expertises is required: experience in field work with small terrestrial mammals, bats or plants, modelling, spatial statistics. Experience in molecular biological methods is a benefit. Good English language skills and driverâs license are required.

The dissertations are funded through university stipends (until 12-2012) and followed by PhD positions at the Leibniz institutes (12-18 months). Candidates will participate in the Potsdam Graduate School and will be situated both at Potsdam Sanssouci Ecology Campus and the counterpart institutes. Field work will be performed at the research station of ZALF in Dedelow (Uckermark), laboratory work at UP and the cooperating institutes. For each position, please submit your application as a single pdf including CV, names and contact information of two references, and a letter of motivation to Prof. Eccard (mthrun@uni-potsdam.de). Please indicate the title of the position you are applying for in the subject line of your email. We will start reviewing the applications on May 1st, 2011 until positions are filled. The positions will be available from June 1st, 2011.

UP, ZALF and IZW are equal opportunities employers and place particular emphasis on fostering career opportunities for female scientists. Qualified women are therefore encouraged to apply.

For further information please contact Prof. Eccard, Animal Ecology, Frau Thrun, 0331-977-1920 University of Potsdam, Maulbeerallee 1, 14469 Potsdam, Germany

Prof. Dr. Jasmin Joshi

Biodiversity Research/Systematic Botany Institute of Biochemistry and Biology University of Potsdam

Maulbeerallee 1 D-14469 Potsdam

Germany Tel. ++49 331 977 4884 Fax ++49 331 977 4865 e-mail jjoshi@uni-potsdam.de e-mail jasmin.joshi@ieu.uzh.ch

Jasmin Joshi <jjoshi@uni-potsdam.de>

UQueensland ReefFish

Maybe the Best Biology PhD in the world The function of reef fish colour patterns: how did the coral trout get its spots?

Ok, you didn^{1}t get the OBest Job In The World^1 (www.islandreefjob.com), which involved snorkeling on the Great Barrier Reef, living for weeks on remote tropical islands, and spending hours watching brightly coloured reef fish.

So, why not come to The University of Queensland and do all that, and get a PhD?

We are looking for 1-2 outstanding PhD candidates to work on a project investigating the evolution and function of reef fish colour patterns.

Students will be based at The University of Queensland, Brisbane, Australia, in the Queensland Brain Institute and work in collaboration with researchers in the School of Biological Sciences, UQ and at the University of Bristol, UK. Supervisors will be Prof. Justin Marshall, Dr. Karen Cheney, Dr. Shelby Temple and/or Prof. Tom Cribb.

Applicants should have interests and preferably experience in neuroethology, neurobiology, sensory biology, fish behaviour, evolution of visual signals, phylogenetics and/or animal communication mechanisms. The PhD will include behavioural experiments, field observations, field spectrophotometry, retinal anatomy and/or microspectrophotometry.

The ideal candidate would be a qualified SCUBA diver, have experience in the field, and be prepared to spend time at field stations, such as Lizard Island (http://australianmuseum.net.au/-Lizard-Island-Research-Station) and Heron Island (http://www.science.uq.edu.au/facilities/heron-island).

Prospective students will be expected to secure either an: Australian Postgraduate Award (APA; for Australian citizens) OR an International Postgraduate Research Scholarship (IPRS; International students). N.B. to be competitive for an IPRS at least one publication, preferably as first author, may be required. For information on these awards go to: http://www.uq.edu.au/grad-school/ This PhD will provide excellent scope for integrative research, for unique skill acquisition, as well as for personal development. For further information please contact Karen Cheney (k.cheney@uq.edu.au) or Shelby Temple (Shelby.Temple@bristol.ac.uk)

To apply, please send a C.V. and covering letter outlining past research experience to Karen Cheney: k.cheney@uq.edu.au. Deadline is 15th April, 2011.

k.cheney@uq.edu.au

UTuebingen 2 MarineEvolutionaryEcology

Two Ph.D.-student positions are available at the University of Tuebingen, Germany funded by the VolkswagenStiftung. Apologies for cross-posting.

The project addresses context-dependent plasticity of sexual selection. We will study the plasticity and evolution of sex roles within and across populations with different environmental contexts. Our main study species is the common goby (Pomatoschistus microps) with exclusive paternal care, plastic sex-roles, and a mating system that is highly affected by its natural and social context such as by nest availability, predation risk, water temperature, operational sex-ratio, and mate competition. Coastal areas of the Baltic Sea provide a natural gradient in terms of biotic, abiotic, and community ecological factors. We will study how the environmental, ecological, and demographic context affects populations and the mating system. We will conduct experiments and population surveys to obtain relevant data.

Requirements: Applicants should have a keen interest in doing experimental work with small fish in the field, and in performing molecular analyses and behavioural assays in the lab. The ideal candidates for this project have a background in evolutionary ecology (or a related field), are highly motivated, creative and independent. A Diplom or MSc degree (or equivalent) in Biology, Ecology or a related discipline is required. The new team will be part of Animal Evolutionary Ecology at the Institute of Evolution and Ecology at the University of Tuebingen. Regular visits of field sites and extended stays at research stations, mainly in Finland, Sweden and Germany during the field season (May-July) are essential. The working language in Tuebingen and at the field stations is English. However, for everyday life at the University and in Tuebingen (located in southern Germany, close to Stuttgart), some knowledge of German will be advantageous. Both positions are fixed-term for 4 years. The salary and benefits are set according to the German salary scale TV-L E13 (50%). In case of equal quality of applicants, those with disabilities will be preferred. The University of Tuebingen aims to increase the representation of women in research and teaching and therefore encourages female scientists to apply. Please send your application by email as one single pdf-file including 1) a letter of motivation, 2) CV, 3) name and email of at least two references who could be contacted, 4) short description of current and future research interests 5) a 1-page summary of your MSc project or undergraduate work and research experience to katja.heubel[at]helsinki.fi.

Review of applications will start from 15 April 2011 onwards, but candidates will be considered until the positions are filled. Start date: 1 August 2011 or on appointment. For more information, feel free to contact me!

Dr. Katja Heubel Advanced Fellow - Volkswagen-Stiftung, University Lecturer, Department of Biosciences, Ecology and Evolutionary Biology, University of Helsinki, Finland.

After 1.8.2011: University of Tuebingen, Department of Biology, Institute for Evolution and Ecology, Animal Evolutionary Ecology, Auf der Morgenstelle 28 D-72076 Tuebingen, Germany

links: http://www.evoeco.uni-tuebingen.de http://www.eve.uni-tuebingen.de http://www.volkswagenstiftung.de/funding/challenges/evolutionary-biology.htm l?L=1 http://luoto.tvarminne.helsinki.fi/english/index.htm http://www.eseb2011.de/tuebingen.htm http://www.helsinki.fi/people/katja.heubel/ –

Dr. Katja Heubel, Docent University Lecturer Ecology and Evolutionary Biology Department of Biosciences, PO Box 65 (Viikinkaari 1), FIN-00014 University of Helsinki, FINLAND

phone +358 9 191 57806 fax -57694

office location: Biokeskus 3, room 6403 email: katja.heubel[at]helsinki.fi http://www.helsinki.fi/people/katja.heubel/ Katja Heubel <katja.heubel@helsinki.fi>

WesternKentuckyU ConservationGenetics

MS ASSISTANTSHIP in the Biology Department at Western Kentucky University, Bowling Green, Kentucky, USA.

I am seeking a motivated, qualified individual with appropriate prior experience in the fields of genetics and population biology to conduct independent research towards the completion of a Master^{1}s of Science Degree while acting as one of two graduate teaching assistants for our undergraduate Genetics course.

The successful candidate will conduct research in the areas of conservation genetics or evolutionary ecology of amphibians. Specific areas of research include 1) landscape genetics of tiger salamanders using microsatellite loci to evaluate the distribution of genetic variation and identify the interaction between geographic features and gene flow; and 2) analysis of hybrid zones using single nucleotide polymorphisms (SNPs) to describe genomic patterns of admixture and identify genes of ecological interest. Desirable skills include a familiarity with standard population genetic software (Structure, Fstat, Migrate, etc.) and experience with basic laboratory techniques (PCR, sequencing, etc.). While enrolled in the Master of Sciences in Biology program at WKU students are expected to develop, implement, and analyze independent research projects, prepare scientific manuscripts, and present research at regional and/or national meetings.

Teaching Assistant responsibilities for the Genetics course include: instruction of two 18-student laboratories once a week, preparation of laboratory materials, grading and evaluation of student performance, and weekly TA meetings with the course instructor. Instruction responsibilities include a brief pre-lab lecture describing concepts and protocols followed by hands-on demonstration of appropriate techniques. Prior teaching experience is not required. However, prior experience with basic molecular laboratory techniques such as preparation of aqueous solutions, DNA extraction, PCR, and gel electrophoresis is desirable.

A B.S. degree in biology, or closely related discipline is required. Additional requirements include: competitive GRE scores, prior independent research experience, demonstrated excellence in course work, excellent written and oral communication skills, and ability to work independently and as a team member. The successful applicant receives two years of TA stipend, a partial tuition waiver, and contributions towards health insurance benefits. For further details about this position please contact Dr. Jarrett Johnson: jarrett.johnson@wku.edu

To apply please submit a letter of interest, CV, unofficial transcripts and GRE scores, and contact information for three references to jarrett.johnson@wku.edu. Formal acceptance to the M.S program at Western Kentucky University is required. Review of applications will begin immediately (4/1/11) and will continue until a suitable applicant is selected.

jarrett.johnson@wku.edu

WestVirginiaU MicrobialEvolution

Graduate Positions in Microbial Evolution

Positions are available for Ph.D. students interested in exploring evolutionary questions using genomic and metagenomic data. Students will have the opportunity to express their computational skills in data mining of vast genomic datasets. Student research will involve computing on high performance clusters and on the cloud along with extensive training in programming, data analysis, mathematical modeling, communication skills, and teaching. For more information about the ongoing projects in the lab, please visit http://ecg.bio.wvu.edu . Summer support is available and this would supplement the compensation received during the academic year as a teaching assistant in the Department of Biology at West Virginia University. Information about the graduate program in biology, and how to apply, is available at http://www.as.wvu.edu/biology/graduate/programs.htm. Although official deadline for applications was January 1, 2011, applications for these positions will be considered on case-by-case basis for either Fall 2011 or Spring 2012 admission.

A successful applicant should have: (1) a bachelor's or master's degree in a relevant field of study (biology, bioinformatics, etc.); (2) a strong interest in molecular evolution and genomics; (3) a willingness to learn and apply computational techniques to large genomic datasets; (4) an interest in learning programming and incorporating it into their research; and (5) strong writing skills and a commitment to the effective communication of science to technical and non-technical audiences.

To learn more about these opportunities, please contact: Olga Zhaxybayeva Biology Department West Virginia University olgazh@mail.wvu.edu Phone: 304-293-5201 x 31531

olgazh@mail.wvu.edu

Jobs

Antwerp LabTech Conservation

The Centre for Research and Conservation (CRC) of the Royal Zoological Society of Antwerp (RZSA - KMDA) is searching for a Laboratory assistant (FTE 4/5 or 5/5)

The successful candidate shall be involved with applied sciences and other relevant activities of the Centre for Research and Conservation (CRC). The CRC is a research institute, part of the RZSA - KMDA subsidised by the Flemish Government. The institute is active in all aspects of the RZSA - KMDA (Zoo Antwerp, Wild animal park Planckendael, and Nature reserve De Zegge). The CRC also runs a number of in-situ conservation projects in Cameroon and Brazil, and is a research partner in other projects with an in-situ component. Scientific research is an integral component of the RZSA - KMDA mission statement and the activities of the CRC directly link to the societies objectives of environment and nature protection as well as education outreach.

The lab assistant shall become a member of the scientific team and will be expected to work in the DNA lab of the RZSA - KMDA. This person must have a thorough theoretical knowledge and essential minimum practical experience with DNA-isolation, PCR and capillary sequencing.

Job description:

. Technical - DNA isolation (hairs, blood, feathers,faeces) using commercial kits, and traditional technologies (chelex, phenol- chloroform etc) - Use of restriction enzymes - Marker and primer development (MtDNA, microsatellite, SNP) - PCR - including optimisation - Gel electrophoresis - Very good knowledge of using an ABI sequencer - for sequencing and genotyping including software analysis. - Data management and dissemination to research partners. - Very well developed organisation and time management skills - Very well developed ability to manage multiple projects according to established timelines.

. General: - Laboratory and inventory management including order placement. - Contributing to writing the method sections of peer-reviewed publications - Exisiting experience with next-generation sequencing technologies is an advantage

Essential requirements: - Interest in applied zoological science; - Diploma of a relevant training; - Practical experience as detailed above; - Eager to learn (apply new methods); - Computer skills (Word, Excel, PowerPoint); experience in (genetic) data analyses - Enterprising, self-acting, independent, efficient - Have a good knowledge of Dutch and English; - Be able to work independently but in a good collaboration with your colleagues; experience in in guiding students - Easy going and social

You'll report to the head of veterinary medicine and conservation biology.

Salary is determined by the RZSA under the classification of: Laboratory Technician.

The vacancy is immediately available. We offer a parttime (4/5) or a full time contract for an initial period of 1 year (trial period of 6 months) with a definite possibility of extension for an indefinite period.

You can respond to this vacancy by sending your letter of application, CV and list of publications to the address below. Explain in the letter why you are interested in this vacancy and your motivation to be involved in lab research at a zoo, a description of skills and qualities you'll bring to the position, and how you meet the criteria above.

Please send your written application before April 26 to: Greta Thewis, Human Resources Koninklijke Maatschappij voor Dierkunde van Antwerpen Koningin Astridplein 26 2018 Antwerpen, België Greta.Thewis@zooantwerpen.be

For more information you can also contact Peter Galbusera (peter.galbusera@kmda.org; telephone 03 202 4551). On the CRC website (http://www.onderzoekindezoo.be/) http://www.zooresearch.be/?lang=NL

Peter Galbusera <Peter.Galbusera@kmda.org>

Antwerp LabTech Conservation 2

The Centre for Research and Conservation (CRC) of the Royal Zoological Society of Antwerp (RZSA - KMDA) is searching for a Laboratory assistant (FTE 4/5 or 5/5)

The successful candidate shall be involved with applied sciences and other relevant activities of the Centre for Research and Conservation (CRC). The CRC is a research institute, part of the RZSA - KMDA subsidised by the Flemish Government. The institute is active in all aspects of the RZSA - KMDA (Zoo Antwerp, Wild animal park Planckendael, and Nature reserve De Zegge). The CRC also runs a number of in-situ conservation projects in Cameroon and Brazil, and is a research partner in other projects with an in-situ component. Scientific research is an integral component of the RZSA - KMDA mission statement and the activities of the CRC directly link to the societies objectives of environment and nature protection as well as education outreach.

The lab assistant shall become a member of the scientific team and will be expected to work in the DNA lab of the RZSA - KMDA. This person must have a thorough theoretical knowledge and essential minimum practical experience with DNA-isolation, PCR and capillary sequencing.

Job description:

. Technical - DNA isolation (hairs, blood, feathers,faeces) using commercial kits, and traditional technologies (chelex, phenol- chloroform etc) - Use of restriction enzymes - Marker and primer development (MtDNA, microsatellite, SNP) - PCR - including optimisation - Gel electrophoresis - Very good knowledge of using an ABI sequencer - for sequencing and genotyping including software analysis. - Data management and dissemination to research partners. - Very well developed organisation and time management skills - Very well developed ability to manage multiple projects according to established timelines.

. General: - Laboratory and inventory management including order placement. - Contributing to writing the method sections of peer-reviewed publications - Exisiting experience with next-generation sequencing technologies is an advantage

Essential requirements: - Interest in applied zoological science; - Diploma of a relevant training; - Practical experience as detailed above; - Eager to learn (apply new methods); - Computer skills (Word, Excel, PowerPoint); experience in (genetic) data analyses - Enterprising, self-acting, independent, efficient - Have a good knowledge of Dutch and English; - Be able to work independently but in a good collaboration with your colleagues; experience in in guiding students - Easy going and social

You'll report to the head of veterinary medicine and conservation biology.

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Please send your written application before April 26 to: Tim De Backer, Human Resources Koninklijke Maatschappij voor Dierkunde van Antwerpen Koningin Astridplein 26 2018 Antwerpen, België Tim.Debacker@kmda.org

For more information you can also contact Peter Galbusera (peter.galbusera@kmda.org; telephone 03 202 4551). On the CRC website (http://www.onderzoekindezoo.be/) http://www.zooresearch.be/?lang=NL

Peter Galbusera <Peter.Galbusera@kmda.org>

ArizonaStateU Undergrad ResAssist

Seeking Undergraduate Research Assistant for Study of Avian Coloration and Sexual Signaling

We are seeking a highly motivated and qualified undergraduate to participate in a Research Experience for Undergraduates (REU) opportunity, funded by the National Science Foundation, to study coloration and sexual signaling in birds. The research experience will involve up to 10 weeks of full-time work during the summer of 2011 (approx. June-August) at Arizona State University in Tempe, AZ. The REU student will work closely with Professor Kevin McGraw and Dr. Mat Giradeau (post-doctoral associate) on this project. The program includes a weekly stipend, and some travel funds may be available to help defray the cost of airfare to and from Arizona.

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

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

Interested students should submit the following application materials electronically (as attachments, preferably in a single PDF) to kevin.mcgraw@asu.edu by 25 March 2011:

i) curriculum vitae

ii) grades (unofficial transcripts are fine) and a list of relevant courses

iii) names and contact details for three references

iv) a cover letter that describes any previous research and a brief statement explaining your interest in obtaining research experience in these areas

Kevin McGraw <Kevin.McGraw@asu.edu>

Barnard ColumbiaU TeachingEvolution

*Term Assistant Professor and Adjunct(s) - Academic Year Aug 2011- May 2012

The Department of Biological Sciences at Barnard College, Columbia University, seeks a full-time Term Assistant Professor to teach five courses (one-year appointment, beginning August 2011). It also seeks one or more adjuncts (rank open) to teaching one or several courses.

Those hired will teach some combination of the following courses: Evolution, Ecology, Genomics & Bioinformatics, and Vertebrate (or Invertebrate) Biology; and Lab in Genetics, Lab in Ecology, and Lab in Cell Biology. Applicants should specify which position(s) and courses they seek. A Ph.D. and teaching experience are required. Applicants should send curriculum vitae, teaching statements, and three letters of recommendation to: biologyjob@barnard.edu. Review of applications will begin 15 April 2011. Barnard College is an Equal Opportunity Employer. Women and members of under-represented minorities are encouraged to apply.

Hilary Callahan Associate Professor, Associate Chair Department of Biological Sciences Barnard College, Columbia University 3009 Broadway New York, NY 10027 212-854-5405

* < http://www.imdb.com/name/nm3322957/- >*Brendan:You can't find out everything from books, you know. Aidan: I think I read that once. (from *Secret of Kells*)

HILARY CALLAHAN <hcallaha@barnard.edu>

BiKF Germany PlantBiogeography

The Biodiversity and Climate Research Centre (BiK-F) is a new interdisciplinary institute with the mission to carry out internationally outstanding research on the interactions of biodiversity and climate change on the organism level. It has been founded by the Senckenberg Gesellschaft fuer Naturforschung, the Goethe-University Frankfurt am Main, and other partners. The Centre is funded by the Federal State of Hesse through its Initiative for the Development of Scientific and Economic Excellence (LOEWE). It provides a new, dynamic research environment that integrates a variety of disciplines from both natural and social sciences. The Project Area A "Evolution and Climate" invites applications for the position of a

Postdoctoral Researcher Plant Biogeography/Molecular Clocks [Ref. #A29b]

The Department of Systematics, Evolution and Climate Change, lead by Prof. Alexandra N. Muellner (http://www.bik-f.de/root/index.php?page_id=262), is seeking a botanist with a research focus on plant evolution and historical biogeography. The successful applicant is expected to develop an extramurally funded research program, as well as collaborating with other staff members. The position entails basic teaching obligations.

Applicants should hold a Ph.D. in Botany or in another relevant subject and have a solid publication record. Preference will be given to applicants with skills in at least one of the following areas: historical biogeography, molecular clocks, ecological phylogenetics, evolutionary ecology. Competence in general biostatistical methods and knowledge of the Central European flora are an advantage. Excellent written and oral communication skills in English and the interest in joining a multidisciplinary team are required.

Salary and benefits are according to a public service position in Germany (TV-H E 13). The Research Centre BiK-F advocates gender equality. Women are therefore strongly encouraged to apply. Equally qualified severely handicapped applicants will be given preference. The contract shall start as soon as possible and will initially be restricted to three years. The duty station will be Frankfurt am Main, Germany. The employer is the Senckenberg Gesellschaft fUEr Naturforschung. Please send your application by e-mail attachment (pdf), mentioning the reference of this position (#A29b) and including a letter outlining your suitability for the position, a detailed CV, contact details of 2 referees and a copy of your PhD certificate before 10 March 2011 to: Prof. Dr. Dr. h.c. V. Mosbrugger, Scientific Coordinator Biodiversity and Climate Research Centre, Senckenberganlage 25, D-60325 Frankfurt am Main, Germany. E-mail to Service and Finances: recruiting@senckenberg.de, and cc to alexandra.muellner@senckenberg.de. For scientific enquiries please write to Prof. Dr. Alexandra N. Muellner (e-mail: alexandra.muellner@senckenberg.de).

Kind Regards,

Nicole Kurth Biodiversity and Climate Resarch Centre

recruiting <recruiting@senckenberg.de>

DukeU Undergrad AntBacteriaSymbiosis

Exploring an Ant-Bacterial Symbiosis Research Experience for Undergraduate (REU) opportunity Duke, summer 2011

To apply: Please send the items listed at the end to j.wernegreen@duke.edu **before March 17**.

Summary: We seek a highly-motivated undergraduate to join our lab this summer to study symbiotic relationships between ants and microbes. Working with Jen Wernegreen's lab at Duke University, the student will explore the ecology and evolution of an obligate mutualism between bacteria and ants of the tribe Camponotini.

Applicants should have a strong interest in ecology and evolution, symbiosis, microbiology, and/or insect physiology, some exposure to molecular biology, and possess a genuine drive to perform basic research. The project will combine local fieldwork around the Durham area, rearing of ants in the lab, as well as molecular biology approaches to quantify symbiont densities and gene expression patterns. The 10-week position will include a summer stipend, and if needed, travel and housing on Duke campus.

Eligibility: REU positions are available to U.S. citizens or Permanent Residents who are currently enrolled as undergraduates at U.S. colleges or universities. Freshmen, sophomores, and juniors are eligible to apply. (NSF stipulates that graduating seniors are not eligible for REU positions.)

Additional information: Please see http://fds.duke.edu/db/Nicholas/esp/faculty/jjw27 for more information about the lab and publications relating to the project. Please contact Jen Wernegreen (j.wernegreen@duke.edu) with any questions about the position or project possibilities.

To apply: Please email the items below to j.wernegreen@duke.edu before March 17. - A letter describing your interest in this fellowship, and your prior research experience(s) if any. - CV - Names and phone numbers of two references. - Transcript from undergraduate work so far. (Unofficial copy is fine.)

Jennifer Wernegreen <j.wernegreen@duke.edu>

Fisheries Seattle MolGenetics

Announcement for a permanent federal position available soon:

Research Molecular Geneticist, Genetics & Evolution Program, Conservation Biology Division, NOAA Fisheries, NWFSC, Seattle WA. Scientists in the Conservation Biology Division's Genetics and Evolution Program conduct research to support NOAA's mission of conservation and management of marine and anadromous organisms. Research activities include: assessing genetic and phenotypic variation to support conservation and recovery of listed species; analyzing composition of mixed fishery stocks (Genetic Stock Identification, or GSI); estimating reproductive success in wild or naturally spawning populations; characterizing components of adaptive evolution; determining the evolutionary consequences of inbreeding within and interbreeding among distinct populations; exploring how life histories respond to selection such as size-selective exploitation; and evaluating consequences of hatchery domestication and climate change. Current research projects include study sites from California to Alaska involving diverse marine organisms such as salmon and steelhead, killer whales, Pacific herring, hake, rockfish, eulachon, tunicates, abalone, corals and sponges. Primary activities involve population genetics, genomics, and quantitative genetics, as well as on providing genetic analysis of forensic evidence in support of NMFS Office of Law Enforcement activities.

The Genetics & Evolution Program is seeking a broadly trained molecular geneticist to assist with analysis of genetic data. The position will involve development of a research program that integrates molecular genetic and genomic approaches to characterize the amount, distribution, and functional significance of genetic variation within and among natural populations. This program will involve analytical methods from population genetics, molecular and gene expression techniques, dissection and mapping of genome regions, and identification of candidate genes. The incumbent is expected to be familiar with statistical approaches to analyze genomic variability. The incumbent will work in a broadly interdisciplinary environment with geneticists, fishery biologists, ecologists and other scientists. A strong theoretical background is required, as is the demonstrated ability to collaborate with experimentalists and resource managers on practical management and conservation issues. Expertise in analysis of DNA sequence data, comparative genomic analysis, and population genetics is essential. Documented experience with the development and dissemination of genomic analysis is also required. Training and work experience in population genetics and genomic identification of functionally important genes is highly desirable. Examples of relevant experience include, but are not limited to, working with marker-based genotyping, including a diversity of array-based SNP genotyping platforms; reduced-representation sequencing using next-generation sequencing technology; and whole-genome sequencing. Familiarity with DNA microsatellite variation in marine and anadromous fishes is valuable, as is an understanding of current methods in use in bioinformatics. The position will open on March 18 and close on March 28, 2011. Applicants must U.S. citizens and be available to travel to Seattle between April 1-14 for interviews. Applicants must apply online through USAJOBS (http://www.usajobs.opm.gov/); the announcement numbers are NMFS-NWC-2011-0041 for federal applicants and NMFS-NWC-2011-0042 for external applicants.

Jeff.Hard@noaa.gov

GeorgiaTech ResTechIV MicrobialGenomics

Research Technician in Marine Microbial Genomics

A Research Technician IV position is available in Frank Stewart¿s lab in the School of Biology at Georgia Tech. The Stewart lab studies the evolution, ecology, and physiology of marine microorganisms using the tools of genomics. Primary topics include metagenomic and metatranscriptomic analysis of microbial metabolism and taxonomy, and molecular analysis of bacteria-eukaryote symbioses. The Research Technician will work collaboratively with the PI and other lab members to manage the lab, perform field and benchtop research, and synthesize results for publication.

Responsibilities:

* Conducting experiments to support multiple research projects. Specific duties may include: field-based sample collection, DNA/RNA extraction and purification, PCR and RT-PCR, genetic manipulation of bacterial genomes, in situ hybridization, fluorescence microscopy, pulsed field gel electrophoresis, preparation of DNA libraries for high throughput sequencing analysis. *

Troubleshooting/optimizing protocols and developing new methods. * Managing data and running scripts via a command-line interface. * Assisting in drafting research papers and grant proposals. * Performing or overseeing routine lab management tasks, including cleaning/autoclaving, preparing media, ordering supplies and interacting with vendors, maintaining instrumentation, implementing laboratory safety standards. * Supervising and training lower-level technical and research personnel, including graduate and undergraduate students.

Qualifications:

Bachelor's Degree in Biology, Molecular Biology, Biochemistry or a related discipline AND three years of relevant research experience; OR, five years of relevant research experience; OR, Any equivalent combination of experience, training and/or education. Preferred qualifications include a Master's Degree.

Additional Qualifications:

* Laboratory experience required. * Proven expertise in molecular biology and microbiological techniques. * Good oral and written communication skills and excellent organizational skills. * Ability to work both independently and collaboratively. * Experience in bioinformatics or programming is highly preferred. * Experience with high throughput DNA sequencing is highly preferred.

The successful applicant will be enthusiastic, motivated by experimental and analytical challenges, and skilled in a diverse range of laboratory techniques. Salary will be commensurate with experience and will include fringe benefits. Additional information about the lab can be found at www.fjstewart.org. Informal inquiries about the position can be emailed to Frank Stewart (frank.stewart@biology.gatech.edu) and should include 'Research technician IV' in the subject line. Applications should be submitted through the Georgia Tech Office of Human Resources (http://careers.gatech.edu/career-paths) in response to position number 0164417. Applicants should include a cover letter (describing your interest in the position, work experience, and availability), CV, and contact information (name, email, phone number) for at least three references. Thank you for your interest we look forward to hearing from you.

Frank J. Stewart, Ph.D. Assistant Professor School of Biology Georgia Institute of Technology ES&T building, office #1242 311 Ferst Drive Atlanta, GA 30332-0230 office: 404-894-5819 www.fjstewart.org frank.stewart@biology.gatech.edu

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IowaStateU Bioinformatics

The Office of Biotechnology at Iowa State University is currently accepting applications for an Associate Scientist that will lead bioinformatics support and leadership in the field of Next-generation sequence analysis and will be expected to facilitate Next-generation sequence analysis by collaborating with faculty and scientists from Iowa State University, and other institutions. This position will also develop computational resources that will be available to the Iowa State University research community and to potential off-campus collaborators and customers; supervise and mentor postdoctoral scholars and graduate students with respect to sequence analysis; collaborate with Iowa State University researchers, faculty, and staff on proposals to granting agencies; and actively apply for external funding. The individual will be expected to publish results in scientific journals and present them at national and international meetings and conferences.

For details of the position and directions to apply, please see: www.iastatejobs.com/applicants/Central?quickFindy723 Questions can be directed to James Reecy, Director of the Biotechnology Council (jreecy@iastate.edu) or Anne Bronikowski, Ecology, Evolution & Organismal Biology (abroniko@iastate.edu)

abroniko@iastate.edu

Kadoorei 3 Conservation Botany

Kadoorie Farm & Botanic Garden Corporation

Notice of Vacant Post: Senior Conservation Geneticist

JOB SUMMARY Applications are invited for a permanent Senior Conservation or Population Geneticist position at Kadoorie Farm and Botanic Garden (KFBG) in Hong Kong. The general remit of the post is to improve the integration of genetic information into conservation programmes and to manage a Genetic Laboratory. The successful candidate will study the effect of habitat fragmentation on the genetic diversity and the adaptability of populations of South Chinese and Indochinese plants at various geographical and temporal scales. The obtained results will be used to develop a decision-making framework for integrating genetic information into conservation programmes. Key conservation genetics concepts and research findings should be summarised and communicated in user-friendly handbooks, scientific publications and online resources for conservation practitioners and conservation management.

Applicants should have a PhD in the field of population or conservation genetics. Strong communication skills (written and oral), advanced knowledge of population and statistical genetics, and computational skills are required. Additional knowledge in genomics, analysis of high-throughput sequencing data and computer programming (Perl/Python/R/) are a plus.

Daily duties will include managing the genetic laboratory and projects, supervising junior laboratory staff as well as analysing genetic samples and interpreting the results.

Application Method Interested parties should send a detailed CV, expected salary, and a short essay (describing relevant work experience and reasons for interest in the post) to:

Dr. Gunter Fischer, Head of Flora Conservation Department, Kadoorie Farm & Botanic Garden Corporation Lam Kam Road, Tai Po, N.T., Hong Kong Email: gfischer@kfbg.org

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Kadoorie Farm & Botanic Garden Corporation

Notice of Vacant Post: Botanist (Plant Identification and Records Officer)

JOB SUMMARY Applications are invited for a permanent Botanist position at Kadoorie Farm and Botanic Garden (KFBG) in Hong Kong. The general remit of the post is to identify specimens collected at field surveys in South China and Indochina, assist in herbarium management and to manage the specimen database. The successful candidate will conduct field work and participate in survey projects in Hong Kong, South China and Indochina, work on taxonomy and conservation status assessment of plant genera, handling and processing botanical information, conducting plant conservation research and providing capacity building.

Applicants should have a PhD in plant taxonomy, plant biodiversity and/or plant conservation. Strong communication skills (written and oral) and knowledge of the local flora are required. Additional knowledge in herbarium management software, phylogenetics, GIS and computer programming are a plus.

Interested parties should send a detailed CV, expected salary, and a short essay (describing relevant work experience and reasons for interest in the post) to:

Dr. Gunter Fischer, Head of Flora Conservation Department, Kadoorie Farm & Botanic Garden Corporation Lam Kam Road, Tai Po, N.T., Hong Kong Email: gfischer@kfbg.org

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Kadoorie Farm & Botanic Garden Corporation

Notice of Vacant Post: Botanist (Plant Ecology and Forest Restoration)

JOB SUMMARY Applications are invited for a permanent Botanist position at Kadoorie Farm and Botanic Garden (KFBG) in Hong Kong. The general remit of the post is to use the findings of research into the ecology of plants to conduct forest restoration projects. The successful candidate will conduct field work and participate in survey projects in Hong Kong, South China and Indochina, map forest ecosystems using fieldmap technology, develop an understanding of the life-cycle dynamics of plants to pinpoint which factors are causing population declines, conduct projects to understand biotic and abiotic habitat requirements of plants and conduct forest enrichment and restoration projects.

Applicants should have a PhD in plant ecology or forest restoration. Strong communication skills (written and oral) and knowledge of the local flora are required. Additional knowledge in herbarium management software, soil science, GIS and computer programming are a plus.

Daily duties will include managing our native tree nursery and supervising work teams and junior staff.

Interested parties should send a detailed CV, expected salary, and a short essay (describing relevant work experience and reasons for interest in the post) to:

Dr. Gunter Fischer, Head of Flora Conservation Department, Kadoorie Farm & Botanic Garden Corporation Lam Kam Road, Tai Po, N.T., Hong Kong Email: gfischer@kfbg.org

gfischer@kfbg.org

NESCent GMOD support

Are you fascinated by genomics and bioinformatics? Are you passionate about collaborative open-source software? Do you enjoy teaching and working with scientists?

The Generic Model Organism Database project (GMOD) is a collection of open source software tools for creating and managing biological, and particularly genomic, databases. GMOD has a large, highly distributed, and dynamic community of software users and developers.

The University of North Carolina at Chapel Hill has an opening for a GMOD user support specialist, to be based at the US National Evolutionary Synthesis Center (NESCent, www.nescent.org) in Durham, North Carolina, while serving the international community of GMOD users.

Job Description: The GMOD user support specialist will maintain online documentation; respond to mailing list help requests; present tutorials; organize short courses, conference sessions and other community building activities; survey user needs, and recruit members of the community to assist with these functions. The incumbent will collaborate closely with the GMOD Coordinator (Scott Cain, The Ontario Institute for Cancer Research) and other distributed personnel. See http://gmod.org/wiki/GMOD_Help_Desk for more background on the activities of the user support specialist. The salary range is $68,906 to $82,687, depending on qualifications, with a comprehensive benefits package.

Qualifications: Required qualifications include: excellent written and verbal communication skills; team orientation with strong interpersonal skills. Preferred qualifications include: an MS or PhD in biology, computer science or related field; three or more years of experience with web programming and relational database management systems; three or more years of experience with genome database administration or curation, preferably in a GMOD environment; at least one year of experience with web content management, ideally using MediaWiki; freedom to travel 5-15 weeks/yr.

To Apply: Please provide a cover letter and CV, including contact information for three references, to Hilmar Lapp, Assistant Director of Informatics, NESCent, at hlapp@nescent.org, and submit materials through http://bit.ly/h9l74r. For phone inquiries, please call 919.668.5288.

tjv@bio.unc.edu

NESCent UserInterface WebApplicationDeveloper

The National Evolutionary Synthesis Center (NESCent) seeks a creative and enthusiastic individual to design user interfaces and web applications for scientific applications. The incumbent will work as part of a small informatics team in close collaboration with domain scientists.

NESCent (http://nescent.org) is an NSF-funded center dedicated to cross-disciplinary research in evolutionary science. Our informatics team works closely with visiting and resident scientists to support their custom software and database development needs. All NESCent software products are open-source, and the Center has a number of initiatives to actively promote collaborative development of community software resources (http://informatics.nescent.org). Above all, we are enthusiastic about our work, about the mission of the Center, and about the contribution of informatics to that mission.

Job description: The incumbent will design and develop user interfaces and web applications for databases and other software tools for sponsored scientists and staff. The job responsibilities include all stages of the software development process, including requirements gathering, design, implementation, release packaging and documentation, as part of a small team (typically 2-3 individuals) following project management best practices. We expect the incumbent to present their work at conferences and contribute to publications with scientific collaborators; interact regularly with visiting and resident scientists, other members of the informatics team and Center staff; and generally serve as an expert resource for Center personnel. The position provides opportunities for professional development. Most informatics staff work at our Durham NC offices, located adjacent to Duke University, but we do support a wide range of technologies for virtual communication with off-site staff and collaborators.

Required Qualifications: * Demonstrated success collaborating with clients on custom software solutions * Experience with various stages of the software development cycle * Expertise in development and testing of user interface designs * Excellent communication skills, both virtual and face-to-face

Preferred Qualifications: * M.S. or Ph.D. in Computer Science, Bioinformatics or related field * Demonstrated interest in science, particularly biology * Expertise in dynamic and interactive web technologies (JavaScript, CGI) * Expertise in rapid application development and respective programming technologies and languages (e.g., modern scripting languages and web-application frameworks such as Python/Django, Ruby/Ruby-on-Rails, and Perl/Catalyst). * Expertise in graphic design * Expertise in data visualization and/or scientific data integration * Expertise in software usability design and assessment * Expertise in web service (SOAP, REST, XML, JSON) and semantic web technologies * Fluency in Java programming * Prior experience in relational database programming (PostgreSQL or MySQL) * Experience with open-source, and collaborative, software development

How to apply: Please send cover letter, resume and contact information for three references to Dr. Karen Cranston, Training Coordinator and Bioinformatics Project Manager (karen.cranston@nescent.org). Informal inquires or requests for additional information may be directed to Dr. Cranston by email or phone (+1-919-613-2275).

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Karen Cranston Training Coordinator and Informatics Project Manager nescent.org

Karen Cranston <karen.cranston@nescent.org>

OregonStateU Nematode EvolutionaryGenomics

The laboratory of Dee Denver at Oregon State University is searching for a Faculty Research Assistant (FRA) or Postdoctoral Scholar; position available 06/11 to investigate evolutionary genomic processes using Illumina high-throughput DNA sequence data. Experience in computer programming required, specific knowledge in Perl and R applications, Knowledge Unix/Linux operating systems preferred. BA/BS required for FRA applicants; PhD required for Postdoc applicants. Postdoc applicants would be expected to pursue independent funding before or during an initial one-year of support on the PI?s grant funds. Include cover letter of application, CV, and the contact information for three professional references (email addresses preferred). For full consideration apply by 4/15/11. OSU in an AA/EOE employer.

The Denver lab primarily studies genomic evolutionary processes in nematodes. We study the evolution of both mitochondrial and nuclear DNA in diverse interesting nematode genera including Caenorhabditis (includes the famous model C. elegans), Meloidogyne (plant parasites), Panagrolaimus (free living), Strongyloides (animal parasites) and Xiphinema (plant parasites). We are currently funded by NIH and USDA. We take advantage of the superb resources offered by the OSU Center for Genome Research & Biocomputing ? this facility offers Illumina/Solexa (new HiSeq2000 system in addition to the GAII) and Roche/454 sequencing.

Denver Lab website: http://denverlab.cgrb.oregonstate.edu/ For inquiries, contact Dee Denver: denver@cgrb.oregonstate.edu

Full job description and instructions for applying available at:

jobs.oregonstate.edu/applicants/Central?quickFindX186

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Dee R. Denver Assistant Professor Department of Zoology Oregon State University 3029 Cordley Hall Corvallis, OR 97331 PH: 541-737-3698 FX: 541-737-0501 http://denverlab.cgrb.oregonstate.edu/ denvedee@cgrb.oregonstate.edu

Rennes DynamicsDiversity

University of Rennes 1 will this year recruit a docent (permanent position, 196 teaching hours per year) in “Dynamics of diversity and the functional properties of communities”. Please find the job description below. It is in French, because teaching is in French. You shouldn’t apply if you cannot make yourself understood in French. And you do not have the right to apply if you do not have the French formal “Qualification” i.e. got your CV evaluated by a national committee months ago already.

Except of this - international applications are welcome. Funnily, French universities do not pay travel costs for candidates, but possibly we find solutions of needed.

Starting salary is 1800 Euros net and can increase to 3200 Euros. Starting salaries are OK to feed a family of three, and childcare is excellent and for free in France.

More about Ecobio at http://ecobio.univ-rennes1.fr/news.php - in a nutshell, there are about 60 permanent researchers in all fields of Ecology and Evolution, the unit was ranked “A” in the last evaluation and the strong points of the unit are among others in Community Ecology / Diversification / Invasion biology / Environmental, Ecological and Evolutionary Genomics / Landscape Ecology / Ecology of Stress / Ecological Engineering.

Deadline is 25.3., 16.00 and should be done online at https://www.galaxie.enseignementsup-recherche.gouv.fr/ensup/candidats.html . Best regards

Andreas Prinzing

Maître de Conférences ≪ Dynamique de la diversité et propriétés fonctionnelles des communautés ≫

Enseignement

Le Maître de conférences recruté assurera des enseignements en écologie générale, biogéographie, écologie des communautés végétale, en particulier au niveau L1 à L3. Ces enseignements seront complétés par des sorties et stages de terrain. Il devra également participer à l’encadrement des étudiants dans le cadre des stages de M1 et M2, notamment en ce qui concerne les formations professionnelles.

Recherche

Ce profil de recherche relève du champ thématique de l’écologie des communautés, et s’inscrit dans une approche fonctionnelle et évolutive de la dynamique de la diversité végétale.

Cet angle d’approche doit permettre d’identifier les contraintes écologiques qui pilotent les règles d’assemblage des espèces, en tenant compte des contraintes historiques, phylogénétiques.

Les propriétés fonctionnelles analysées en lien avec la structure et diversité des communautés végétales pourront être relatives à la capacité de réponse aux changements (résistance, résilience) et aux services rendus (cf. cycle de la matière et des nutriments, qualité agronomique et patrimoniale, ..).

Une des hypothèses de travail proposées pour comprendre les variations de diversité spécifique, évolutive et fonctionnelle avec les facteurs environnementaux reposent sur les contrastes de traits biologiques et de stratégies de vie. Considérer les interactions entre espèces ou groupes fonctionnels comme élément déterminant des patrons de diversité constitue une seconde hypothèse de travail que souhaite voir développer l’équipe d’accueil.

Une clé d’analyse essentielle des règles d’assemblages et de réponses des communautés aux facteurs environnementaux réside dans la prise en compte de la variabilité spatio-temporelle des assemblages et de leur fonctionnement. Les travaux développés devront en conséquence prendre en compte le contexte théorique lié aux méta-communautés et viendront ainsi renforcer les travaux en cours dans l’équipe quant aux complémentarités fonctionnelles entre habitats.

Le maître de conférence recruté devra situer ses travaux dans le cadre des problématiques de recherche de l équipe Structure et Dynamique de la Diversité de l UMR 6553 ECOBIO. Cette équipe s attache à i) mettre en évidence les patrons, processus et mécanismes écologiques et évolutifs impliqués dans la réponse des communautés et des populations aux contraintes environnementales et ii) apprécier les conséquences induites par les activités humaines ou contraintes naturelles sur les propriétés écosystémiques portées par les communautés. Les variables de forçage anthropiques prises en compte sont notamment les modalités de gestion des espèces et des espaces ; par suite, les résultats produits dans l équipe présentent une interface importante dans le cadre de la gestion des habitats, de la biologie de la conservation et de l écologie de la restauration.

contactes : gabrielle.thiebaut@univ-rennes1.fr (enseignement) et jean-sebastien.pierre@univ-rennes1.fr (recherche)

see also

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StAndrews ResTech Drosophila

Research Technician; Testing genetic models of same-sex sexual behaviour in Drosophila

Nathan Bailey and Mike Ritchie are seeking to appoint a Research Technician to provide research support in the Centre for Evolution, Genes and Genomics within the School of Biology at the University of St Andrews, Scotland. You will be required to organize, maintain and screen lines of the fruit fly Drosophila melanogaster, perform behavioural observations, assist with performing crosses and collect and maintain data to support the project. You should have a degree in a relevant biological field, and prior experience working with Drosophila melanogaster and/or a background in evolutionary biology or behavioural ecology is highly desirable.

The aim of this project is to empirically test evolutionary explanations for the persistence of same-sex sexual behaviour in animals.

Duration: 18 months. Start Date: 1st June 2011 or by negotiation.

Informal enquiries can be made to Nathan Bailey nwb3@st-andrews.ac.uk See also http://www.flexiblephenotype.org/ http://biology.st-andrews.ac.uk/ritchielab/ Further details and the application materials are available at: https://www.vacancies.st-andrews.ac.uk/welcome.aspx , Ref No. CD7979

Clunky direct link https://www.vacancies.st-andrews.ac.uk/ViewVacancy.aspx?enc=3DmEgrBL4XQK0+ld8aNkwYmM4/ymoCsgWgpnbrKtZIdoFpKHWTaiheGYCrYRkt+VynBCVXlEmisA/tolMY4szOogPLEASE NOTE THAT ALL APPLICATIONS MUST BE MADE THROUGH THE UNIVERSITY, NOT TO THE PIs

Mike Ritchie Acting Head School of Biology Dyers Brae House University of St Andrews St Andrews, Fife Scotland KY16 9TH

Phone: 0 (44 outside UK) 1334 463495 Fax: 0 (44 outside UK) 1334 463366

Websites: http://biology.st-andrews.ac.uk/ritchielab/ http://biology.st-and.ac.uk/supplemental/ritchie/papers.aspx mgr@st-andrews.ac.uk

UColorado ScienceTeachingFellow

Science Teaching Fellow

The Department of Ecology and Evolutionary Biology (EBIO), at the University of Colorado, Boulder, invites applicants for the position of Science Teaching Fellow to assist with enhancing teaching and learning in our undergraduate courses. Candidates should hold a doctoral degree in Ecology or Evolutionary Biology or a related field and have excellent organizational and interpersonal communication skills. However, their primary interest and at least some experience should be in science education. The successful candidate will work within the department and with other education specialists. Specific responsibilities will include working with EBIO faculty who teach our core undergraduate courses (Ecology, Genetics and Evolution) to specify an integrated set of specific learning goals for these courses; develop strategies for including more active learning; develop and validate assessments of student learning gains; and participate in the development of techniques, materials and practices for improving student learning in these courses.

The salary for this 1-year renewable (up to three years) appointment will be competitive and commensurate with experience. Applicants should submit a single pdf containing their CV, a statement of teaching philosophy, and the names and email addresses of three individuals who can serve as references to am@colorado.edu. To ensure full consideration, applications must be received by April 15, 2011.

The University of Colorado at Boulder is an Equal Opportunity/Affirmative Action Institution committed to cultural diversity and compliance with the Americans with Disabilities Act. Women and minorities encouraged to apply. We invite applications from qualified candidates who share our commitment to diversity. The University of Colorado conducts background checks on all final applicants being considered for employment.

Andrew Martin Dept of Ecology and Evolutionary Biology University of Colorado Boulder, CO 80309

Andrew Martin <Andrew.Martin-1@Colorado.EDU>

UGuelph ProjectManager Biomonitoring

Project Manager, Postdoc and Graduate Student positions available at Biodiversity Institute of Ontario, University of Guelph

Biodiversity Institute of Ontario based at University of Guelph, Canada, is leading a large-scale project in the use of Next Generation Sequencing for biodiversity analysis from various environmental samples. We are currently seeking applications for various positions:

1. Project Manager (based at University of Guelph, Ontario), starting May-June 2011. Qualifications: MSc or PhD in biology (or computer science), minimum 2 years of experience in large-scale project management and budgeting (accounting), articulate and well-organized. Being computer/web savvy is an asset as the project manager will be in charge of updating the project website. We would also consider exceptional candidates who would like to pursue an alternative career path in science management after their

PhD/postdoc. Duration: 3 years (initial contract for one year).

2. Postdoctoral Fellow (based at University of Guelph, Ontario, Hajibabaei group), starting July-September 2011. PhD in molecular evolution, phylogenetics, molecular ecology, population genetics, bioinformatics or related fields. Excellent theoretical knowledge and experience in comparative sequence data analysis for biodiversity, evolutionary or ecological analysis, preferably using NGS data. Experience in using Linux and Python (or similar scripting languages) and knowledge of R would be desirable. Duration: 3 years (initial contract for one year).

3. GIS Software Developer (based at Dalhousie University, Halifax, Nova Scotia, Beiko group), starting May-June 2011. BSc or MSc in Computer Science, Bioinformatics or a related field. The scope of the project would also permit an applicant with a PhD to carry out research in the context of a postdoctoral position. Must be proficient in Python and C++, and ideally experienced in OpenGL and graphical software development. Experience with previous development projects is essential. Duration: 3 years (initial contract for one year).

4. Postdoctoral Fellow (based at University of Guelph, Ontario, Hajibabaei group), starting June-Sept, 2011. PhD in biological sciences preferably in molecular ecology, phylogenetics or related fields with expertise in molecular method development/optimization. Experience in soil biodiversity/ecology is highly desirable. Duration: 2 years (initial contract for one year).

5. Graduate Student positions (MSc/PhD, 3 positions) based at University of Guelph, Department of Integrative Biology (2 positions) and Dalhousie University, Department of Biology (1 position). These positions involve the use of NGS data to address evolutionary and ecological questions in arthropod, plant and soil biodiversity. Graduate students will be supervised jointly by members of Biomonitoring 2.0 project and will gain insights in using NGS genomics approaches as well as bioinformatics tools to develop and explore their own hypotheses in ecology and evolutionary biology.

6. MSc Student position at the University of New Brunswick, Canadian Rivers Institute / Aurora Research Institute. This position will examine the use and application of Biomonitoring 2.0 techniques by local communities in Canada's North.

For each position, please submit your CV (including names and contact information of 3 references) and a cover letter to Dr. Mehrdad Hajibabaei (mhajibab@uoguelph.ca). Please indicate the title of the position you are applying for in the subject line of your email. We will start reviewing the applications on April 15, 2011.

Mehrdad Hajibabaei, PhD Assistant Professor Biodiversity Institute of Ontario & Integrative Biology University of Guelph Guelph, ON N1G 2W1 Canada Phone: 519-824-4120 x52487 Fax: 519-824-5703 Email: mhajibab@uoguelph.ca www.ibarcode.org/-hajibabaei www.biodiversity.ca www.dnabarcoding.ca < http://www.dnabarcoding.ca/ >

Mehrdad Hajibabaei <mhajibab@uoguelph.ca>

UKonstanz MolecularEvolution

UNIVERSITY OF KONSTANZ/GERMANY

ASSISTANT PROFESSOR/JUNIOR GROUP LEADER IN EVOLUTIONARY BIOLOGY (molecular evolution/comparative genomics or devo-evo)

A position as "Assistant Professor" (German government salary scale TV-L 13 or possibly Akademischer Rat) in the Department of Biology at the University of Konstanz in Germany is available from May 2011 on.

The person we are looking for should work in the fields of either molecular evolution, comparative genomics, and/or the evolution of developmental mechanisms. The position is for a Ph.D. biologist, ideally with prior postdoc experience in bioinformatics, or molecular and developmental biology. A total of three research groups, two of which are headed by Junior Group Leaders each representing their particular subdisciplines of evolutionary biology, make up the evolutionary biology group (Lehrstuhl Evolutionsbiologie) in the Department of Biology (http://www.evolutionsbiologie.uni-konstanz.de/index.php?section=10).

The taxonomic emphasis is open, however, work on fishes, particularly on cichlid or zebrafish model systems is desirable. Most of the ongoing evolutionary research in Konstanz deals with comparative developmental and molecular evolutionary/genomic aspects of the origin of adaptation and speciation in cichlid fish adaptive radiations. For publications of the lab see: http://www.evolutionsbiologie.uni-konstanz.de/index.php?section' Space in a modern animal care facility is available and the exclusive help of a part-time technician will be available to this new group. Excellent opportunities are available in terms of space, equipment, departmental facilities and annual financial support for research expenses. The lab has state-of- the-art facilities for molecular and developmental biology, including Illumina and Roche FLX Titanium next-generation sequencers at the Genomics Center Konstanz (http://cms.uni-konstanz.de/-en/genomics-center/).

The University of Konstanz and the Department of Biology are among the most highly ranked institutions in Germany and provide a lively and academically outstanding research environment. Konstanz is a lovely historic town located on Lake Constance on the border to Switzerland.

Appointments are initially for two to three years, and are renewable for up to six and potentially even ten years, with an annual gross salary (depending on prior experience) of about 58,800 Euros (about 73.000 US$). Habilitation is possible, and a modest amount of teaching (English or German) is required.

Additional information can be obtained from axel.meyer@uni- konstanz.de, (tel.+49 7531 884163, fax + 49 7531 883018) or from our www page.

http://www.evolutionsbiologie.uni-konstanz.de . Applications including a (short 2-3 page) statement of research interests, a full CV, and names and email addresses of 2-3 referees, should be emailed to axel.meyer@uni-konstanz.de. Applications should be received before March 30, 2011. The University of Konstanz is an equal opportunity employer.

Axel Meyer <axel.meyer@uni-konstanz.de>

ULeicester EvolutionBehaviour

Chair/Reader in the Neurobiology of Behaviour

Department of Biology

College of Medicine, Biological Sciences and Psychology

Ref: MBP00320

At Leicester we're going places. Ranked in the top 15 universities in Britain our aim is to climb further. A commitment to high quality fused with an inclusive academic culture is our hallmark and led the Times Higher Education to describe us as "elite without being elitist".

You will be an outstanding researcher with an international reputation in the causal mechanisms underlying animal behaviour, able to strengthen and expand our multi-disciplinary Neuroscience & Behaviour research theme (weblink). Current strengths include a wide range of behavioural and cognitive neuroscience, as well as auditory and motor physiology, all underpinned by fundamental studies of synaptic function and plasticity.

We are seeking candidates who have an interest in taking a "whole organism" approach to the neurobiological and/or genetic basis of behaviour, to integrate with existing expertise in proximate (electrophysiological, cellular and molecular) and ultimate (evolutionary, ecological) approaches to the study of behaviour.

Links will be encouraged with other College-wide research themes particularly Genome Science (weblink)

A Lectureship will also be offered in association with this post.

Closing date for applications 17th April 2011 See https://swww2.le.ac.uk/offices/personnel/ for further details

Prof Paul Hart Head, Department of Biology University of Leicester Leicester LE1 7RH UK

Phone: +44 (0)116 2523348 Fax: +44 (0)116 2523330 pbh@le.ac.uk

Fish and Fisheries Website: www.fishandfisheries.org Paul Hart <pbh@leicester.ac.uk>

UManchester EvolutionaryBiol

The Faculty of Life Sciences at The University of Manchester have a new fellowship extension scheme for Independent Research Fellows with substantive external funding to join the Faculty as Principal Investigators. For Fellows bringing in 4-5 years of external funding (on qualifying schemes) the Faculty will top up fellowships by 1 to 2 years additional support. This scheme reflects our desire to ensure that Fellows can perform to their full potential and develop highly competitive biology research programmes. The Faculty has an excellent track record in retaining fellows as permanent academic members of staff.

The world-class research in our Faculty is organised into 12 interconnected areas (http:/-/www.manchester.ac.uk/lifesciences/research/-researchgroups) and we are recruiting in any of these. The Faculty's research spans the entire spread of life sciences from molecules to cells to organisms and environmental sciences. We are interested in dynamic successful individuals with an outstanding record of achievement at the post-doctoral or junior investigator level. The Faculty offers a vibrant collaborative research environment, being one of the largest and most successful research organisations of its type in Europe. At the latest Research Assessment Exercise, it was ranked in the top three life science departments in the country. Investigators are housed in purpose-built laboratory and office space (most less than 7 years old) with access to superb state-of-the-art core facilities.

For further information or informal discussions please contact the relevant Research Group Leader or the Associate Dean for Research (Prof. Cay Kielty). More details, including relevant contact details, can be found at http://www.manchester.ac.uk/lifesciences/-research/fellows/ To be considered for this scheme, prospective fellows should send a brief curriculum vitae and one page summary of their research interests to fellowships.lifesciences@manchester.ac.uk

There are two deadline dates for applications to this scheme in 2011: 31st March 2011 and 30th September 2011.

Caroline.Aylott@manchester.ac.uk

UmeaU PaleoEvolution

Senior lecturer in paleoecology Umeå University, Sweden, is seeking a senior lecturer in paleoecology. The holder of the position should have one of two nonexclusive research profiles, both aimed at strengthening the integration between research in paleoecology, ecology and evolution in the research environment Ecosystem Change, which has been identified as a Strong Research Environment at Umeå University and includes ecologists, environmental scientists, evolutionary biologists, bio-mathematicians, and biogeochemists.

One possible research profile is in aquatic paleoecology to study lake-ecosystem dynamics across limnological and paleolimnological timescales (Holocene), integrating geochemical and ecological/evolutionary research. Here, we particularly encourage applications from scientists using up-to-date paleolimnological approaches such as molecular genetic, spectroscopic or biogeochemical methods. An alternative research profile is in evolutionary paleoecology to address evolutionary questions with paleoecological methods, to enhance the ongoing integration of paleoecology with research in evolution and biogeography, and in collaboration with researchers in macroevolution, macroecology, phylogenetics or population genetics.

The duration of a position as associate senior lecturer is four years of research, and can be expanded to five years with 20 % of teaching. At the end of the employment period, an associate senior lecturer owns the right to be examined for a permanent position as senior lecturer at Umeå University. The assessment criteria for such an examination are described in the corresponding job profile.

To be eligible, in the first place, for the position as associate senior lecturer you should have a PhD, or a corresponding degree, which is not more than five years old, in a relevant field such as ecology, evolutionary biology, environmental science or biogeochemistry.

An associate senior lecturer should primarily pursue research. The successful applicant is expected to create his/her own research group and to supervise graduate students as well as post-docs. He/she is also expected to attract research grants from external sources of funding and to have a vivid collaboration with scientists at both Umeå University and other universities. In the evaluation, particular emphasis will be given to scientific skills. Pedagogical and administrative skills and the ability to collaborate with other researchers in the Strong Research Environment will also be considered.

Further information about the position and how to apply can be found at http://www8.umu.se/-umu/aktuellt/arkiv/lediga_tjanster/312-224-225-11.html#eng Last day for application is April 26, 2011.

Roland Jansson, associate professor Dept. of Ecology and Environmental Science Umeå University SE-901 87 Umeå, Sweden phone: +46-(0)90-7869573 web: http:/-/www.emg.umu.se/english/about-the-department/-staff/jansson-roland roland.jansson@emg.umu.se

UVirginia GenomicsBioinformatics

Research Scientist

The Department of Biology at the University of Virginia invites applications for a Research Scientist position. The research will focus primarily on the genomic and bioinformatic resources to be used in the identification of sodium channel genes in reptiles. The position also involves analyzing and preparing materials for publication, data management and dissemination, and mentoring graduate and undergraduate students.

The completion of Ph.D. degree in Biology or a related discipline by appointment start date is required. Candidates must be proficient with maximum likelihood and mixed-model multivariate statistical analyses of quantitative genetic data. Candidates with a background in evolutionary biology and experience in the development of analytical mathematical models are preferred. Candidates must have effective oral and written communication skills.

To apply, please submit a candidate profile on-line and attach a cover letter, curriculum vitae, and the contact information for three references through Jobs@UVA (https://jobs.virginia.edu); search on posting number 0607344.

Review of applications will begin April 11, 2011; however, the position will remain open until filled.

Questions regarding this position should be directed to:

Dr. Edmund Brodie III bbrodie@virginia.edu

Questions regarding the Candidate Profile process or Jobs@UVA should be directed to:

Shawna Edinger 434-982-5615 se5k@virginia.edu

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

"Edinger, Shawna (se5k)" <se5k@eservices.virginia.edu>

UVirginia GenomicsBioinformatics 2

Research Scientist

The Department of Biology at the University of Virginia invites applications for a Research Scientist position. The research will focus primarily on the genomic and bioinformatic resources to be used in the identification of sodium channel genes in reptiles. The position also involves analyzing and preparing materials for publication, data management and dissemination, and mentoring graduate and undergraduate students.

A Ph.D. degree in Biology or a related discipline and at least three years post-doctoral experience is required. Candidates must be proficient with maximum likelihood and mixed-model multivariate statistical analyses of quantitative genetic data. Candidates with a background in evolutionary biology and experience in the development of analytical mathematical models are preferred. Candidates must have effective oral and written communication skills.

To apply, please submit a candidate profile on-line and attach a cover letter, curriculum vitae, and the contact information for three references through Jobs@UVA (https://jobs.virginia.edu); search on posting number 0607414.

Review of applications will begin April 15, 2011; however, the position will remain open until filled.

Questions regarding this position should be directed to:

Dr. Edmund Brodie III bbrodie@virginia.edu

Questions regarding the Candidate Profile process or Jobs@UVA should be directed to:

Shawna Edinger 434-982-5615 se5k@virginia.edu

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

"Edinger, Shawna (se5k)" <se5k@eservices.virginia.edu>

Vienna GroupLeader PopGenetics

Tenure-track group leader position available at the Institute of Population Genetics, Vetmeduni Vienna.

The research focus of the Institute of Population Genetics is to understand the genetics of adaptation. This central question in evolutionary biology is being tackled using a variety of approaches including experimental evolution, quantitative genetics, life history, evodevo, experimental population genetics, bioinformatics and statistics. While the workhorse in the institute is Drosophila (we host one of the largest collection of natural D. melanogaster populations), research at the institute also includes Arabidopsis, camels, cheetahs and lemurs among others.

To strengthen functional Drosophila genetics we are searching for a group leader to join the Institute of Population Genetics. The successful candidate will have a proven record of high quality research in functional Drosophila genetics, preferably with a proven ability to attract extramural funding. The specific research area of the candidate is not as important as a keen interest to take advantage of the expertise available at the institute.

The future post holder will have priority access to a state of the art core facility (including an Illumina sequencer), well-equipped laboratory space and facilities for fly work (including state of the art imaging equipment). The successful applicant will receive funding through the Vienna School of Population Genetics (http://www.popgen-vienna.at), which attracts an international body of graduate students.

In recent years Vienna has developed into one of the leading centers in population genetics and evolutionary biology (http://www.evolvienna.at) and is home to a high profile Drosophila research community and the VDRC Stock Center. In an addition to a stimulating scientific environment, Vienna also offers an extraordinary quality of living. Affordable housing, excellent public transport, great restaurants, a range of international schools, two operas, two music centers, many theaters and museums in combination with a pleasant climate make Vienna one of the most attractive cities in Europe.

The position is available from June 2011. The application should be emailed to christian.schloetterer@vetmeduni.ac.at as a single pdf containing CV, list of publications, a statement of research interests, and the names of three references with contact details. While the search will continue until the position is filled, applications should be received by April, 30 to ensure full consideration.

Christian Schlötterer Institut für Populationsgenetik Vetmeduni Vienna Veterinärplatz 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

Other

Access to C-fit7 package

Dear evoldir readers,

I would like to construct clines on morphometric traits across a hybrid zone. The C-fit7 package by Laurene Gay seems to do a very good job on this.: Comparing clines on molecular and phenotypic traits in hybrid zones: a window on tension zone models. Evolution, 62(11): 2789-2806. 2008 Unfortunatelly, the download link (http://www.cefe.cnrs.fr/ecogev/-siteGB/CFitpage.htm) is broken and I can't contact Laurene Gay. Does anybody has the package or knows how to get it?

Any help is appreciated.

Cheers, Markus

Dr. Markus Ritz Senckenberg Museum of Natural History Görlitz Am Museum 1 02826 Görlitz / Germany +49 3581 4760 5309

Markus Ritz <markus.ritz@web.de>

Ancestral genome program

Dear colleagues,

Are there some programs available to reconstruct the bacterial ancestral genome content? I am working on three marine bacterial taxa. They fall into three orders in Alphaproteobacteria. I want to reconstruct the genome content of their common ancestor, and am looking for a program that is particularly robust in differentiating gene loss and lateral gene transfer events, which are responsible for the sporadic distribution of gene families in these genomes.

Thanks,

Haiwei Luo Postdoctoral associate Department of Marine Sciences University of Georgia

hluo2006@gmail.com

Bayesian supertree question

Dear EvolDir members,

I would like to know if there is any program that allows me to make supertrees and supermatrices using maximum likelihood (ML) and/or bayesian inference algorithms. I found literature which discusses these algorithms applied to the development of supertrees from a theoretical point of view, but I am not able to find a program where the aforementioned algorithms are applied.

Thanks for your attention.

Kindly regards,

Enrique González-Tortuero Ctra. de Alcalá, 9 19174 Torrejón del Rey (Guadalajara, Spain)

enriquegleztortuero@gmail.com

Bayesian supertree question anwers

Dear EvolDir members,

I want to thank the participation of the people I have answered on this issue. At the request of a researcher, I will discuss the responses I received.

Another researcher told me the use of program BEST (http://www.stat.osu.edu/~dkp/BEST/introduction/) to make the supermatrices - and / or supertrees - by ML (maximum likelihood) or BI (Bayesian inference) algorithms. This program is used to estimate the distribution of nodes posterior of gene and species trees using multilocus molecular data. However, I do not see the relationship between this program (which is useful when you have information from many DNA sequences and you look for concatenate trees, if I understand correctly) and the elaboration of supertrees. Therefore, I encourage any reader to a real answer whether any relationship.

Except for this response, I gather that silence can mean that no such program. If indeed this is what happens, it would be interesting, with the help of a computer, see if you can pass these mathematical algorithms to a software package.

Thanks for your attention.

Kindly regards,

Enrique González-Tortuero Ctra. de Alcalá, 9 19174 Torrejón del Rey (Guadalajara, Spain)

enriquegleztortuero@gmail.com

Buccal swab sampling storage

Hi Evoldir

I'm beggining a new project implicating camaeleonidae sampling during long field period. Consequently I need to find the best way to sample cameleons in a non invasive way. I'm thinking of using buccal swabs.

My question is simple How should I store those buccal swabs during the field period in order to avoid DNA degradation ??

1_Adding acohol to the tube containing the buccal swab?? 2_adding some buffer in the tube???(edta, etc) 3_adding some dessicant (silicagel) in the tube??? 4_any other solution??? (even solution implincating other methods than buccal swabs are welcome)

knowing that samples are going to stay during 2 to 7 month at ambient tropical temperature before being bringing back to the lab.

If you have any experience with this kind of problems, I would be happy to hear your advices or to read the selected bibliography you suggest

Thanks a lot in advance

Jordi

Salmona Jordi PhD Student in Integrative Biomedical Science Population and Conservation Genetics Group Instituto Gulbenkian de Ciência Rua da Quinta Grande, 6/ Apartado 14 2781-901 Oeiras, Portugal Tel Portugal IGC : +351 214407669 Tel Portugal telemovel : +351 917980338 Tel Portugal home : +351 211953580 jordi.salmona@gmail.com http://compbio.igc.gulbenkian.pt/pcg/pcg_home.html http://www.igc.gulbenkian.pt/research/unit/88

China FieldStudy EvolGenetics

Please distribute to any undergraduates who might be interested:

Unique (and Low-Cost) Opportunity for Ten Undergraduates 2012 Ecological Genetics Field Study Abroad in China

Learn Chinese and Ecological Genetics at the University of Georgia

With funding from NSF's Partnerships for International Research and Education (PIRE) program, we are offering 10 undergraduates (U.S. citizens or permanent residents only) the opportunity to participate in a unique research abroad opportunity in China during the spring and summer of 2012. This is the 4th year of the program and students have found it to be enormously rewarding. This is likely to be the penultimate offering of this course.

The research focus of our PIRE grant is a forensic biogeographic study of species that are native to China and invasive in the southeastern U.S. as well as a growing number of species native to the southeastern U.S. and invasive in China.

Each summer, we run a 6 week field course where we visit biological communities throughout China. After the field course, students continue in short-term (3-4-week) research internships in our partner labs in China.

Students will need to be prepared to take full advantage of this experience. Therefore, during the spring semester, students must enroll at the University of Georgia (UGA) and take 3 courses; two in intensive elementary Mandarin Chinese and a laboratory course in genetics. No prior experience with Chinese language is required, although students should have had at least a course in introductory biology and preferably courses in ecology and evolutionary biology.

After 1 semester of Chinese, most of our students can operate quite well in China.

The cost to the student of the summer program is minimal: the grant covers travel to and within China, lodging and most meals. The student is responsible for health insurance, visa costs and personal expenses. Students are also responsible for the costs of enrolling at the University of Georgia for all required courses (12 credit hours) (all students are charged at the in-state tuition rate of ~$300 per credit hour plus fees).

The deadline for applications is April 29, 2011. Applications for the 2012 program are available on our website: http://www.genetics.uga.edu/pire/undergrad.html. We encourage any interested students to contact Dr. Mauricio for more information (mauricio@uga.edu).

Rodney Mauricio Program Director, UGA-China PIRE

Rodney Mauricio, Ph.D. Department of Genetics University of Georgia Athens, GA 30602-7223

Lab Web Page: http://www.genetics.uga.edu/mauriciolab=0APIRE Grant Web Page: http://www.genetics.uga.edu/pire

Constructing computer clusters

Anyone have experience converting a student computer lab into a cluster for parallelizing phylogenetic analyses and next-gen sequence assembly? Any suggestions?

Justen

jwhittall@scu.edu jwhittall@scu.edu

DataONE Summer Internship Opportunity

The Data Observation Network for Earth (DataONE) is a virtual organization dedicated to providing open, persistent, robust, and secure access to biodiversity and environmental data, supported by the U.S. National Science Foundation. DataONE is pleased to announce the availability of summer research internships for undergraduates, graduate students and recent postgraduates. Program Structure

Up to eight interns will be accepted in 2011, each paired with one primary mentor and, in some cases, secondary mentors. Interns need not necessarily be at the same location or institution as their mentor(s). Interns and mentors are expected to have a face-to-face meeting at the beginning of the summer, and interns are encouraged to attend the DataONE All-Hands Meeting in the fall to present the results of their work. DataONE will pay all necessary travel expenses. Schedule

- *March 15* - Application period opens - *April 8* - Deadline for receipt of applications at midnight Pacific time - *April 15* - Notification of acceptance. Scheduling of face-to-face kickoff meetings based on availability of interns and mentors - *May 23* - Program begins* - *June 27* - Midterm evaluations - *July 29* - Program concludes - *October 18-20* - DataONE All-Hands-Meeting, New Mexico (attendance encouraged)

* Allowance will be made for students who are unavailable during these date due to their school calendar. Eligibility

The program is open to all undergraduate students, graduate students, and postgraduates who have received their masters or doctorate within the past five years. Given the broad range of projects, there are no restrictions on academic backgrounds or field of study. Interns must be at least 18 years of age by the program start date, must be currently enrolled or employed at a university or other research institution and must currently reside in, and be eligible to work in, the United States. Interns are expected to be available approximately 40 hours/week during the internship period (noted below) with significant availability during the normal business hours. Interns from previous years are eligible to participate. Financial Support

Interns will receive a stipend of $4,500 for participation, paid in two installments (one at the midterm and one at the conclusion of the program). In addition, required travel expenses will be borne by DataONE. Participation in the program after the mid-term is contingent on satisfactory performance. The University of New Mexico will administer funds. Interns will need to supply their own computing equipment and Internet connection. For students who are not US citizens or permanent residents, complete visa information will be required, and it may be necessary for the funds to be paid through the students university or research institution. In such cases, the student will need to provide the necessary contact information for their organization. Project Ideas

Projects cover a range of topic areas and vary in the extent and type of prior background required of the intern. The interests and expertise of the applicants will, in part, determine which projects will be selected for the program. Off-list projects are also eligible, in which case potential applicants are strongly encouraged to contact the organizers and/or potential mentors with their ideas prior to applying. The titles of this years projects (see below for more detailed descriptions) are:

1. DATA MANAGEMENT: Best practices of data management for public participation in science and research 2. DATA MANAGEMENT: Online learning modules related to best practices throughout the data lifecycle 3. EDUCATION: Accessing and analyzing environmental data in the classroom 4. SOCIOLOGY OF SCIENCE: Understanding how scientists analyze data 5. DATA SCIENCE: How much ecological data is out there? 6. DATA SCIENCE: Tracking the reuse of 1000 datasets 7. PROGRAMMING: Subsetting and publishing scientific datasets 8. PROGRAMMING: Scientific workflow provenance repository and publishing toolkit 9. PROGRAMMING: Integrating loosely structured data into the Linked Open Data cloud 10. SCIENCE COMMUNICATION: Developing video animations for DataONE community engagement

To Apply

Application materials should be sent to internship@dataone.org by 11:59 PM (Pacific time) on April 8th, and should include a cover letter, resume and letter of reference all in *PDF* format. The applicant should send the cover letter and resume, while the letter of reference should be sent directly by its author.

1. The cover letter should address the following questions: - What DataONE Summer Internship projects are you most interested in and why? - What contributions do you expect to be able to make to the project(s)? - What background do you have which is relevant to the project(s)? - What do you expect to learn and/or achieve by participating?

— / —

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

Didymosphenia samples

All,

My collaborators (listed below) and I are requesting assistance in obtaining samples of Didymosphenia geminata to assist with our research project entitled: "Determining the ecological and evolutionary processes associated with distribution and behavior of the nuisance freshwater diatom Didymosphenia geminata".

The specific supporting objectives of this research are to utilize contemporary molecular genetic and genomic techniques to: a) assemble a de novo transcriptome of D. geminata; b) identify and apply a sufficiently large number of nuclear genes for phylogenetic, phylogeographic, and population-level delineation, and c) conduct genome-wide association studies via comparative functional genomic comparisons;

Ideally, we would like to have samples preserved in RNAlater which will allow extraction of RNA and DNA. If you are willing to assist us by sharing samples or would like to obtain a copy of the project proposal, please contact one of the team. We will provide all necessary preservation/storage materials and pay all shipping costs.

We are also researching the development of culture methods to identify conditions which will allow this diatom to be brought into the laboratory for extensive physiological research; and will be conducting water quality evaluations to determine the environmental conditions that lead to shifts in demographic and growth patterns resulting in population explosions (i.e., blooms).

Collaborators Michael R. Gretz, Professor, Biotechnology Research Center, Department of Biological Sciences, Michigan Technological University (MTU), 1400 Townsend Drive, Houghton, Michigan 49931-1295; Phone: (906) 487-3175; E-mail: mrgretz@mtu.edu

Leslie J. Matthews, Environmental Scientist; Water Quality Division, Department of Environmental Conservation, Vermont Agency of Natural Resources, 103 South Main Street, 10 North, Waterbury, VT 05671; Phone: (802) 241-3798; E-mail: leslie.matthews@state.vt.us

Marina Potapova, Phycologist, Herbarium Curator; Diatom Herbarium, Academy of Natural Sciences, 1900 Benjamin Franklin Parkway, Philadelphia, PA 19103-1101; Phone: (215) 299-1000; E-mail: potapova@ansp.org

Andy L. Rost, Graduate Research Assistant, University of Nevada, Reno, Desert Research Institute, Div. Earth and Ecosystem Sciences, 2215 Raggio Parkway, Reno, Nevada 89512; Phone: (775) 673-7633; E-mail: arost@dri.edu

Thank you for considering this request.

Fair Winds and Following Seas,

Tim L. King, Ph.D. U. S. Geological Survey Leetown Science Center Aquatic Ecology Branch 11649 Leetown Road Kearneysville, WV 25430 Phone: 304.724.4450 Facsimile: 304.724.4424 Mobile: 304.582.4622

“It is not the strongest of the species that survives, nor the most intelligent that survives. It is the one that is most adaptable to change.” Charles Darwin

tlking@usgs.gov

Eukaryote 18S primers

Dear EvolDir members,

I am looking for a set of eukaryote specific 18S (SSU) primers amplifying a fragment about 3-400 bp long (i.e. suitable for 454 sequencing). So far those here (of Stoeck et al.) appear to be the best published ones (of about 250 bp)

http://icomm.mbl.edu/microbis/project_pages/details/proposals/APP_proposal.pdf but I may well have overlooked something. If anybody could point me to such a well approved set (or recommend those above) working well on all eukaryotes, I would be very grateful.

Best regards

Christoffer Bugge Harder

University of Copenhagen

Christoffer Bugge Harder <cbharder@bio.ku.dk>

Evaluating fitness

Dear EvolDir members,

I would like to know if there is any program that allows me to evaluate the fitness between a phylogenetic model and data, especially to compare the model fitness of GTR model (Maximum likelihood inference) and CAT model (Bayesian inference).

Thanks for your attention.

Kindly regards,

Bojian ZHONG, Allan Wilson Centre, IMBS, Massey University

Bojian Zhong <bjzhong@gmail.com>

EvoDevo Funding Opportunity

Please note the upcoming deadline for research exchange grants from the Evo-Devo-Eco Network (EDEN) is April 30, 2011. EDEN is a program funded by the National Science Foundation Research Coordination (http://edenrcn.com/).

One of EDENs major goals is to enable graduate students, postdoctoral fellows, and faculty to undertake research exchanges in the field of Evo-Devo-Eco, in order to develop or share techniques, protocols and tools for use with emerging model systems.

This spring EDEN will award five research exchanges to be held in 2011-2012. Each exchange will consist of an award of up to $3,000 per researcher toward travel, lodging and subsistence costs. You can find out more about this program at http://edenrcn.com/funding/index.html. If you know of outstanding lab personnel who would be interested, please forward this announcement to them.

If you have not done so already, please consider “joining” EDEN by filling out a brief survey about your lab’s areas of expertise. You can complete the survey on our website at http://edenrcn.com/join/ or by clicking

http://www.surveymonkey.com/s/JoinEDEN This survey will allow your lab to be added to a searchable database of scientists, organisms and techniques that is available on the EDEN website (http://edenrcn.com/participating/). With this database, other researchers in development, evolution and ecology will be able to learn about your work, hopefully facilitating new and useful networks and collaborations.

Please feel free to email edenrcn@fas.harvard.edu with questions about the program, and forward this email to colleagues who you think would be interested in EDEN.

“Grants, EDEN” <edenrcn@fas.harvard.edu>

EvoDevo texts

Dear friends,

Some of my biology undergraduate students are interested in to read about Evo Devo ideas, history, theories, etc.

I would like please to receive suggestions about book chapters, articles with good examples and reviews about this subject!

Thanks for any help!

Prof. Dr. J. C. VOLTOLINI Universidade de Taubate - Departamento de Biologia Taubate, SP. 12030-010. E-Mail: jcvoltol@uol.com.br ECOTROP (CNPq): http://dgp.cnpq.br/buscaoperacional/detalhegrupo.jsp?grupo=1546205IMB87W7 Currículo Lattes: http://lattes.cnpq.br/8137155809735635 Orkut ("Ensino de Ciência"): http://www.orkut.com.br/Main#Profile?rl=ls&uid=17608429643840608483 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>

EvoDevo texts answers

Dear friends,

Thanks to 30 people who wrote me indicating books and videos to use with undergrad classes about Evo Devo and these are the most cited material:

—–

The most cited books:

Endless Forms Most Beautiful for Evo Devo. By Sean Carroll. http://www.amazon.co.uk/Endless-Forms-Most-Beautiful-Science/dp/1849160481/ref=sr_1_1?ie=UTF8&qid01065731&sr=8-1. It would be a good introduction to get students interested. Very accessible.

>From DNA To Diversity: Molecular Genetics and the Evolution of Animal Design, 2nd ed. Carroll, Grenier, Weatherbee. 2005. Blackwell Publishing.

Wallace Arthur "Evolution. A developmental approach", which was just published by Wiley-Blackwell.

Hall BK, Olson WM: Keywords and Concepts in Evolutionary Developmental Biology. 2003:476.

—–

Other books:

There is a very nice chapter on the topic written by John True in Futuyma's textbook, Evolution (2nd edition).

"The Origin of Animal Body Plans" by Wallace Arthur

The evolution of developmental pathways. Wilkins.

Wray, G. A. 2010. Embryos and Evolution: 150 years of reciprocal illumination. In: Evolution Since Darwin: The Firt 150 Years, pp. 215-239, in M. A. Bell, D. J. Futuyma, W. F. Eanes, and M. A. Bell. Sinauer Associates, Sunderland.

Developmental plasticity and evolution. West-Eberhard. (lots of overview material)

Ontogeny and Phylogeny. Gould. (not exactly up to date, it's from 1977)

Evolution - The Extended Synthesis IT Press, 2010 http://mitpress.mit.edu/catalog/item/default.asp?ttype=2&tid173 Evolution, Development, and the Predictable Genome. David L. Stern (Author) http://www.amazon.com/Evolution-Development-Predictable-Genome-David/dp/1936221012/ref=sr_1_6?s=books&ie=UTF8&qid01078243&sr=1-6 Gilbert & Epel's "Ecological Developmental Biology: Integrating Epigenetics, Medicine, and Evolution

The shape of life. Raff

—–

VIDEOS:

"Ghost in Your Genes" (http://www.amazon.com/Ghost-Your-Genes-Nova/dp/B000XBPDYY/ref=sr_1_1?ie=UTF8&s=dvd&qid01077278&sr=8-1) "What Darwin Never Knew" both produced by the television show NOVA.

PBS video: http://www.pbs.org/wgbh/nova/body/epigenetics.html http://www.pbs.org/wgbh/nova/body/rnai-explained.html http://www.pbs.org/wgbh/nova/body/rnai.html http://www.hhmi.org/biointeractive/rna/rna_interference/01.html http://www.nature.com/focus/rnai/animations/index.html http://learn.genetics.utah.edu/content/epigenetics/rats/ —–

Website:

On ENSI site, there is a very nice Threespine Stickleback lesson that introduces elements of evo-devo: http://www.indiana.edu/ ˜ ensiweb/lessons/stickleback.html —–

Thanks for all of you and....... we need a website to organize references, links of videos and also a library of slides. We are always discussing about research but we need a place to centralize all material!

Prof. Dr. J. C. VOLTOLINI Universidade de Taubate - Departamento de Biologia Taubate, SP. 12030-010. E-Mail: jcvoltol@uol.com.br ECOTROP (CNPq): http://dgp.cnpq.br/buscaoperacional/-detalhegrupo.jsp?grupo46205IMB87W7 Currículo Lattes: http://lattes.cnpq.br/8137155809735635 Orkut ("Ensino de Ciência"): http://www.orkut.com.br/-Main#Profile?rl=ls&uid608429643840608483 Fotos Artísticas: http://voltolini.album.uol.com.br/texturas . 'Siamo tutti angeli con un'ala e possiamo volare soltanto se ciabbracciamo'

jcvoltol@uol.com.br

Evolution 2011 UndergraduateDiversity DeadlineExtended

Application Deadline Extended! Undergraduate Diversity at the Evolution meetings 2011

We have extended the deadline for our NSF-funded program for bringing talented and diverse undergraduates to the Evolution meetings this June 17-21 in Norman, Oklahoma. The application deadline is now Tuesday, March 15th.

For the ninth year in a row we will fly a cohort of 25 undergraduates from throughout the US and Puerto Rico to present a poster at the meetings, receive mentoring from graduate students, postdocs and faculty, and participate in the Diversity Social as well as a career-oriented 'Undergraduate Futures in Evolutionary Biology' panel and discussion. The program covers the costs of travel, registration, food and accommodation at the meetings.

The application deadline has been extended to March 15th, but admissions will be reviewed as they are received, and so the earlier you apply, the better. Applications are welcomed from all undergraduates, and the admissions goal is to create a diverse pool of students. An overview of the program and student eligibility can be found at:

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

www.nescent.org/Evolution2011_application Applications consist of a short statement of interest, a letter of recommendation and the title and abstract of the poster to be presented.

In addition, we will be soliciting names of graduate students, postdocs and faculty members who would like to serve as mentors during the meetings. 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 Richard Kliman <rmkliman@cedarcrest.edu> if you are interested in serving as a mentor.

For inquires contact one of the organizers:

Scott Edwards - sedwards@oeb.harvard.edu Richard Kliman - rmkliman@cedarcrest.edu Jory Weintraub - jory@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 Skype: jory.weintraub Web: www.nescent.org

Jory Weintraub <jory@nescent.org>

EvolutionTeaching YouTube

Evolution Academy http://www.youtube.com/-watch?v=_8h0rB8f99w Wide attention was given (New York Times, February 7) to the article by Berkman and Plutzer in the Science Educational Forum (January 28). This noted that creationism was being defeated in the courtroom, but not in the classroom. The proposed remedy was that college level education for future teachers include a mandatory course on evolution. To assist this, I have posted 12 short "Evolution Academy" videos on YouTube. These are modelled on the highly successful educational videos of the Khan Academy that are attracting world-wide attention (http://www.khanacademy.org/) and have won Gates Foundation support. My qualifications for this task include (i) my textbook Evolutionary Bioinformatics the second edition of which has just been released (Springer, New York), (ii) my revision of a chapter in Lewin's Genes X, and (iii) biographies of early evolutionists (William Bateson and George Romanes). You may visit my web-pages on evolution at http://post.queensu.ca/ ˜ forsdyke/evolutio.htm or inspect video titles at http://post.queensu.ca/-˜ forsdyke/videolectures.htm Donald R. Forsdyke

Department of Biochemistry, Queen's University, Kingston, Canada K7L3N6

Donald Roy Forsdyke <forsdyke@queensu.ca>

EZVision information

I want to migrate to a non-toxic dye for gel visualization and Ive heard about EZ-Vision. I would like to know if anybody is using it or has used it and what are the opinions about this reagent.

Thanks so much,

LYDA RAQUEL CASTRO, Ph.D Profesor Asistente Programa de Biologia Dir. Grupo de investigacion en evolucion y sistematica molecular Universidad del Magdalena Santa Marta, Colombia (575) 4301292 ext 273

lydaraquelcastro@hotmail.com

France VolFieldAssist TurtleEvolution

Field assistant in evolutionary ecology of European pond turtles

We are looking for a voluntary field assistant to participate in a conservation project on European pond turtles (Emys orbicularis) from mid April to mid July 2011 at the Research Station Petite Camargue Alsacienne in France (www.camargue.unibas.ch).

The work will include caring for the about 80 pond turtles living in the station's outdoor enclosures, capturing the turtles, observing breeding behaviour, locating nests and collecting eggs for artificial incubation in the lab. The applicant is expected to stay for the entire field season from mid April until mid July. Applicants should preferably have some knowledge of French or German. The work is planned as a student internship, thus applicants must be students.

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

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

PD Dr. Valentin Amrhein Zoological Institute University of Basel

valentin amrhein <pca.recherche@orange.fr>

Freeware Hsu correction

Dear Evoldir community,

I am looking for an alternative way to perform Hsu (1996)'s correction in resampling procedures (exactly: to correct resampling procedures for a skewed distribution and different sample sizes) - it is implemented in the software Genstat which I do not want to buy just for that. If anyone of you has heard about an alternative software or has written some R code/skript or something like that, I would be happy for any suggestion.

Thanks to all of you, Cheers, Katharina

katharina.keil@uni-muenster.de

Genepop matrix

Dear community,

I was wondering if anyone could send me a well-working matrix for analysing binary (0/1) DNA markers at GenePop software. We are trying to analyze by Mcheza software positive selection occuring along an ISSR dataset. Talking with Tiago Antão (Mcheza's dad) he said me that a well-working matrix prepared for Genepop is the unique way to make our dataset working fine at Macheza.

So if anyone could help us I will be glad for that. Thanks in advance.

Rodrigo A. Torres, PhD Laboratório de Genômica Evolutiva e Ambiental Departamento de Zoologia, UFPE Brazil

"Rodrigo A. Torres" <rodrigotorres@ufpe.br>

Genetics Awards

The American Genetic Association grants awards each year to AGA members for support of special events that further the purposes of the Association.

Eligible events include specialized workshops open to AGA members in areas of great current interest and short courses in some aspect of organismal genetics, but any event that would advance the purpose of the AGA is eligible for support. Awards are usually between $5,000-$20,000.

We encourage members to think creatively about the types of events they could offer with support from the AGA. However, these funds are not intended to provide awards such as travel support to attend outside meetings or workshops not organized by the applicant(s).

The Council has a particular interest in assisting students and emerging researchers to attend such events.

Funding of any event does not mean it will become a permanent, ongoing commitment from the AGA, and we encourage proposals for first time events.

Applicants must be current members of the AGA. To become a member or to view application guidelines, please visit http://www.theaga.org . The Council will review all applications received before Monday, May 2, 2011, and make award decisions at its annual meeting in July 2011.

Best wishes

Anjanette Baker Managing Editor, Journal of Heredity American Genetic Association 2030 SE Marine Science Drive Newport, OR 97365

mailto:agajoh@oregonstate.edu

AGA Annual Symposium 2011: Genomics & Biodiversity Guanajuato and Irapuato, Mexico 23-26 July 2011 for details, please visit: http://www.theaga.org/ agajoh@oregonstate.edu

Haplodiploid method

Dear Evoldir community,

I am interested in examining some quantitative genetic parameters for highly variable color patterns used for recognition in paper wasps. To this end, I have records of phenotypes for >1500 wasps from a pedigreed wild population. Ideally, I would like to use the 'animal model' to examine this question but all of the currently available packages for such analysis assume diploidy (and wasps are haplodiploid). Does any know of a method for adapting existing methods to this problem? I am also open to collaboration if someone would be interested in working on this issue.

Best Mike Sheehan mic@umich.edu

Ecology and Evolutionary Biology University of Michigan

Michael Sheehan <mic@umich.edu>

Invasive species

Dear Colleagues,

One of the world's largest demographic surveys of an invasive species is looking for new and returning collaborators. The Global Garlic Mustard Field Survey is now beginning its third field season with demographic data and seed collections from over 150 populations across Europe and North America – more than any published study of which we are aware. This year we are working to double that number and we are particularly keen to increase collaboration in under-sampled regions. For previous sample sites and preliminary results, see the map at www.GarlicMustard.org < http://www.garlicmustard.org/ >

The project is an international collaboration aimed at obtaining much-needed data on the abundance and distribution of /Alliaria petiolata/ (Garlic Mustard). It involves a very basic protocol that standardizes sampling across sites, and takes place in late spring/early summer making it ideal for incorporation into field courses, nature surveys, and long-term monitoring and management efforts. The estimated duration of sampling for a team of two people is 3-6 hours per population.

Academics who contribute to this endeavor will have the opportunity to contribute to manuscripts resulting from the work. Sampling protocol and additional information are available at the following website: www.GarlicMustard.org < http://www.garlicmustard.org/ >. Please contact us directly if you would like to participate or if you have any questions or concerns.

North-American**Coordinator Dr.Robert Colautti Biology Department Duke University* rob.colautti@duke.edu

Eurasian Coordinator Dr. Oliver Bossdorf Biology Department University of Bern bossdorf@ips.unibe.ch

Seed Collections Coordinator Dr. Steven Franks Biology Department Fordham University franks@fordham.edu

rob.colautti@duke.edu

Lepidoptera samples

Hello EvolDir,

As part of a collaborative group of researchers I am working on insects of conservation concern, specifically I am screening North American Lepidoptera that are of conservation concern for the endosymbiont Wolbachia. We are seeking additional material for this screening, specifically Lepidoptera that are listed at the state or federal level.

Please contact me if you are willing to share materials or discuss any details. I can send you pre-paid shipping materials or reimburse you for your expenses. Thank you.

Chris Hamm Department of Entomology Michigan State University chamm@msu.edu

chamm@msu.edu

Likelihood Bayesian software question

Hi everyone

I have a quick question about current software usage regarding likelihood and Bayesian model selection, being absent from this type of discussion for sometime. In the past I have developed some simple graphical interfaces (MrMTgui and modelpie) for programs like ModelTest and MrModelTest, that had some traction in the community. But with the not-so-recent advent of jModelTest, I was wondering if there is still some penetration of this type of simple GUIs, especially for Mr/ModelTest and if the community would actually use newly updated interfaces, apart from jModelTest availability.

Lastly, I have been looking for new command-line applications that would require a similar approach in order to reach a larger userbase, something simple that can benefit of a GUI that allows researchers to be more comfortable with the software.

Any comments, ideas, opinions, please send me an email at nuin AT genedrift DOT org.

Thanks a lot for the attention

Paulo Nuin

nuin@genedrift.org

Linux Easypop software

Dear all,

I was wondering if someone in the evoldir community has compiled the foward individual based pop gen simulation program “easypop” for Linux. On its website, downloads are only available compiled for Windows and MacOS. I would really like to have this software on Linux. The alternatives, which I found so far, are not doing what I like to have. My main interest is to be able to set the starting population to “maximum diversity”. Other such simulation programs start with monomorphic populations, usually. But I am studying a fixation process under a certain scenario, and easypop seems the best option to me (so far).

If you have further suggestions for other software, I’d also be happy to hear from you.

Cheers, Robert

robert.kraus@wur.nl

Linux Easypop software answers

Dear all,

last week I posted a request for a Linux version of the simulation program easypop (see original post below). I didn't find anyone who could provide such a version. However, I got several replies suggesting to use Wine to emulate windows and then run the windows easypop version. That shuuld work (it did for others), although I haven't had the time to try it. Thanks also to messages from authors of other such simulation programmes! It seems like one of those at least may help me.

Cheers, Robert

Dear all,

I was wondering if someone in the evoldir community has compiled the foward individual based pop gen simulation program "easypop" for Linux. On its website, downloads are only available compiled for Windows and MacOS. I would really like to have this software on Linux. The alternatives, which I found so far, are not doing what I like to have. My main interest is to be able to set the starting population to "maximum diversity". Other such simulation programs start with monomorphic populations, usually. But I am studying a fixation process under a certain scenario, and easypop seems the best option to me (so far).

If you have further suggestions for other software, I'd also be happy to hear from you.

Cheers, Robert

robert.kraus@wur.nl

Marine Gastropod Samples

Dear colleagues,

I'm a PhD student at University of the Azores. I work with molecular population genetics and phylogeography of littoral marine gastropods present Azores Islands.

I would be very grateful if you could help me to get (or indicate people able to help me) samples of the following locations/species:** - *UK:* *Gibbula magus* and *Melarhaphe neritoides*; - *Bay of Biscay:* *Bittium latreillii* and *Melarhaphe neritoides*; - *Italy:* *Bittium latreillii*, *Gibbula magus* and *Melarhaphe neritoides* ; - *Greece:* *Bittium latreillii*.

Thank you, Ricardo Cordeiro

Email: rjpcordeiro@gmail.com

Institutional Address: Departamento de Biologia, Universidade dos Açores Rua da Mãe de Deus, Apartado 1422 9501-801 Ponta Delgada Azores, Portugal

rjpcordeiro@gmail.com

NESCent WorkingGroup CallProposals EvolMedicine

Request for proposals for working group on Evolutionary Medicine curriculum

NESCent (The National Evolutionary Synthesis Center) is sponsoring a range of targeted activities in the general area of Evolutionary Medicine. As part of this program, NESCent is seeking to support a Working Group focusing on the development and implementation of model curricula and curriculum materials in Evolutionary Medicine to support teaching of undergraduates, and students in medicine, nursing, public health and medical research. The resources developed should show how evolutionary principles play an important role in understanding health and disease, and ideally, should span a wide breadth of medical disciplines.

NESCent Working Groups involve small groups of scientists (10-12 participants) collaborating intensively on the analysis or synthesis of data, models or both, to address a major question in evolutionary science. The working groups will typically meet 3-4 times over two years, with each meeting lasting 3-5 days. Meetings will be held at NESCent in Durham, North Carolina. Support includes travel, lodging and per diem.

Proposals are due by April 1st, 2011.

For more information, including details on the proposal process and requirements, please see http://www.nescent.org/evomedcurriculum . Jory P. Weintraub, PhD Assistant Director, Education and Outreach National Evolutionary Synthesis Center (NESCent) 2024 West Main St., Suite A200 Box 104403 Durham, NC 27705 Phone: 919.668.4578 Fax: 919.668.9198 Email: jory@nescent.org Skype: jory.weintraub Web: www.nescent.org

Jory Weintraub <jory@nescent.org>

New Drosophila stocks

The /Drosophila/ Species Stock Center at UCSD would like to announce the availability of three new genomic DNA packs for the /D. melanogaster/, /D. virilis/, and /D. mojavensis/ species groups. We also have genomic DNA now available for some of our most popular species including /D. miranda/, /D. eugracilis/, /D. santomea/, /D. teissieri/, and the Hawaiian species /D. soonae/, /D. eurypeza/, and /D. mimica/. To see a complete list of genomic DNA available please go to https://stockcenter.ucsd.edu/index.php?table=GenomicDNA . _We also have several __recent additions to the living collection:_ 1 wild-type strain of /D. suzukii/ (donated by T. Markow): stock number 14023-0121.218 3 inbred strains of /D. pseudoobscura/ (from M. Noor): stock numbers 14011-0121.215 through 14011-0121.217 3 wild-type strains of /D. pseudoobscura/ (from W. Anderson): stock numbers 14011-0121.218 through 14011-0121.220 3 isofemale lines of ///D. pseudoobscura/from Tucscon, Arizona, available until 3/30/2011 (donated by T. Markow): stock number 14011-0121.214A 19 isofemale lines of D. affinis, 18 from North Carolina and 1 from New York, available until 3/30/2011 (donated by B. Longdon): stock number 14012-0141.12A

More details available on the /Drosophila/ Species Stock Center Website at https://stockcenter.ucsd.edu/info/welcome.php – Maxi Polihronakis Richmond, PhD Drosophila Species Stock Center University of California, San Diego 9500 Gilman Drive # 0116 La Jolla, California 92093-0116

Section of Cell and Developmental Biology Division of Biological Sciences Muir Biology, Rm. 2125 or 2208 Phone: 858-246-0350

Maxi Polihronakis Richmond <mpolihronakis@ucsd.edu>

New evolution teaching video

Dear Folks,

following the line of work that our group began two years ago we have added a new video that we believe can help in tasks related to teaching evolution. You can see it at: http://vimeo.com/20236511 or at

http://webs.uvigo.es/plantecology/divulgacion.en.html The new video (The hypothesis of burglar alarm) illustrates the adaptive advantages of bioluminiscence for a group of algae.

This video was created for free use as teaching material. If anyone is interested, can download a version freely.

I hope you enjoy it.

PD: We appreciate that this information will be spread where you consider being helpful.

Luis Navarro

–

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

Luis Navarro <lnavarro@uvigo.es>

Phyloinformatics NESCent SummerCode

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

PHYLOINFORMATICS SUMMER OF CODE 2011

http://informatics.nescent.org/wiki/Phyloinformatics_Summer_of_Code_2011 The Phyloinformatics Summer of Code program provides a unique opportunity for undergraduate, masters, and PhD students to obtain hands-on experience writing and extending open-source software for evolutionary informatics under the mentorship of experienced developers from around the world. The program is the participation of the US National Evolutionary Synthesis Center (NESCent) as a mentoring organization in the Google Summer of Code(tm) (http://code.google.com/soc/).

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

NESCent is particularly targeting students interested in both evolutionary biology and software development. Initial project ideas are listed on the website. These range from visualizing viral epidemics to 3D protein structure evolution, rich annotation for TreeBASE content, exposing phenotype observations to the Encyclopedia of Life, to enhancing R packages for phylogenetic analysis. All project ideas are flexible and many can be adjusted in scope to match the skills of the student. We also welcome novel project ideas that dovetail with student interests.

TO APPLY: Apply online at the Google Summer of Code website (http://socghop.appspot.com/), where you will also find GSoC program rules and eligibility requirements. Each organization has a slightly different application format, and ours is at http://bit.ly/-PhyloSoC2011-apptemplate. The 12- day application period for students opens on Monday, March 28th, and runs through Friday, April 8th, 2011.

INQUIRIES: phylosoc {at} nescent {dot} org. We strongly encourage all interested students to get in touch with us with their ideas as early on as possible. Working closely with potential mentors to develop your project proposal greatly increases your chance for acceptance. Do not underestimate the amount of time it takes to develop a competitive proposal.

2011 NESCent Phyloinformatics Summer of Code: http://informatics.nescent.org/wiki/-Phyloinformatics_Summer_of_Code_2011 Google Summer of Code FAQ: http://socghop.appspot.com/-document/show/gsoc_program/google/gsoc2011/faqs

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Karen Cranston and Hilmar Lapp National Evolutionary Synthesis Center http://nescent.org hlapp@nescent.org

Positive selection software

Dear community, hello you all!!!

Please does anyone remmember along OUT2010 an anoucement for a software to measure positive selection for binary DNA markers? I have used such software to test its applicability but unfortunately I lost the link to download the software. I am not sure also if it is working in a online plataform or something similar. Anyway if some of you could help me I will be glad for the that.

Thanks in advance, Rodrigo A .Torres, D. Sc. Laboratório de Genomica Evolutiva e Ambiental Universidade Federal de Pernambuco Brazil

“Rodrigo A. Torres” <rodrigotorres@ufpe.br>

Positive selection software answers

Dear Robert and community,

Regarding my last post related to that software for measuring positive selection at binary DNA markers, I have found it. Please consult Mcheza workbench software at http://popgen.eu/soft/mcheza/ . Best regards, Rodrigo A .Torres, D. Sc. Laboratório de Genomica Evolutiva e Ambiental Universidade Federal de Pernambuco Brazil

Rodrigo Augusto Torres <rodrigotorres@ufpe.br>

Primate opsin sequences

Dear all,

I am preparing a bioinformatic/evolution activity for teachers and students to be contributed to the DNA to Darwin project (http://www.dnadarwin.org/). My goal is to have the participants analyse set of opsin sequences to point out the evolutionary convergence and gene duplication and divergence events. I wanted to replicate the phylogenetic trees as in, for example, David Hunt’s old paper (Hunt et al, Vision Res 1998), however, most of the sequences reported there (and later on in the literature) are not available publicly and/or in digital format.

I was hoping that someone would save me the need to manually re-type the sequences from the paper... To be able to make a decent tree I am only missing sequences of medium- and long-wave-sensitive opsins from the chimpanzee and howler monkey. I would be very grateful if someone would send them to me.

Thanks a million, Jarek

– Jarek Bryk | www.evolbio.mpg.de/~bryk Max Planck

Institute for Evolutionary Biology August Thienemann Str. 2 | 24306 Plön, Germany tel. +49 4522 763 287 | bryk@evolbio.mpg.de

Jarek Bryk <bryk@evolbio.mpg.de>

RAxML visitor program

Dear Community,

The Exelixis Lab (home of RAxML) traditionally focuses on method development and computer science aspects in evolutionary bioinformatics. Therefore, we solicit applications for three-month research visits by biology PhD students who face interesting methodological problems with their data such that we can work together toward solving these problems. We will cover travel costs and offer an internship of 500 EUR per month for housing in Heidelberg. Note that, our lab has recently moved to the Heidelberg Institute for Theoretical Studies http://www.h-its.org/. If you are interested, please send a one page description of your methodological problem, a CV, and your list of publications to Alexandros.Stamatakis@h-its.org by May 15.

All the best,

Alexis

– Dr. Alexandros Stamatakis

Group Leader: Scientific Computing Group (Exelixis Lab & HPC Infrastructure) Heidelberg Institute for Theoretical Studies (HITS gGmbH)

Schloss-Wolfsbrunnenweg 35 D-69118 Heidelberg Germany

Tel: +49 162 8541515 (Mobile) +49 6221 533240 (Office) Fax: +49 6221 533298 Skype: stamatak Email: Alexandros.Stamatakis@h-its.org WWW: http://wwwkramer.in.tum.de/exelixis/ http://www.h-its.org/english/research/sco/index.php Amtsgericht Mannheim/HRB 337446 Managing Directors: Dr. h.c. Klaus Tschira/Prof. Dr.-Ing. Andreas Reuter

Alexandros Stamatakis <alexandros.stamatakis@gmail.com>

Rhododendron samples

Dear EvolDir members

I am working on the evolution of the breeding system in /Rhododendron/, and I am looking for samples (leaves or DNA) of different species. I would be very grateful if someone could help me to get the samples of the following rhododendron species:/Rhododendron lapponicum, R. ponticum, R. semibarbatum, R. championae, R. hongkongense, R. moulmainense, R. farrerea, R. dayaoshanense, R. westlandi, R. calendulaceum, R. ovatum,/ /R. williamsianum, R. myrtifolium (/also known as/R. kotschyi).

/Many thanks

Nathalie

– Nathalie Escaravage Laboratoire Evolution et Diversité Biologique Université Paul Sabatier/CNRS 5174 Bâtiment 4R3 118 route de Narbonne 31062 TOULOUSE cedex 09 France

Nathalie Escaravage <nathalie.escaravage@cict.fr>

R package DEMEtics

Dear all,

We are happy to announce the release of the R package DEMEtics_0.8-3.

It allows to evaluate the genetic differentiation between populations based on Gst and D values.

The degree of genetic differentiation between populations is often measured by the fixation index Gst (Nei, 1973). Recently, Jost (2008) showed that Gst values do not reflect genetic differentiation and suggested calculating D-values instead. To verify this far-reaching statement, we programmed this R package and compared Gst versus D values of two artificial populations with known genetic divergence. The insights of this approach are published in Gerlach et al. (2010).

DEMEtics allows to calculate the fixation index Gst and the differentiation index D pairwise between or averaged over several populations according to the formulas given in Jost (2008). P-values, stating the significance of differentiation, and 95 percent confidence intervals can be estimated using bootstrap resamplings.

It can be downloaded from the following webpage: http://cran.r-project.org/web/packages/DEMEtics/index.html To cite the package 'DEMEtics' in publications use:

Gerlach G., Jueterbock A., Kraemer P., Deppermann J. and Harmand P. 2010 Calculations of population differentiation based on Gst and D: forget Gst but not all of statistics! Molecular Ecology 19, p. 3845-3852.

References

Jost, L. 2008 Gst and its relatives do not measure differentiation. Molecular Ecology 17, 18, p. 4015-4026.

Nei, M. 1973 Analysis of gene diversity in subdivided populations. Proceedings of the National Academy of Sciences of the United States of America 70, 12, p. 3321-3323.

Alexander-Jueterbock@web.de

SaoPaulo UNESP VisitingEvolutionTeacher

Urgent: Open position for visiting Teacher in University in a Brazilian University (University of the State São Paulo State/UNESP), for collaborations in Projects on Genetics and Evolution in Insects , mainly Drosophila or Heteroptera (Triatominae and Pentatomidae) Period: 30 days (the visit should occur until November/2011 Place: University of State São Paulo/Brazil (UNESP) located in São José do Rio Preto, SP http://www.ibilce.unesp.br/ Interested parties should submit a letter of interest and curriculum vitae via email to Lilian Madi-Ravazzi (lilian@ibilce.unesp.br)

APPLICATINS WILL BE ACCEPTED UNTIL APRIL 03, 2011 Question regarding the position can be directed to Dra. Lilian Madi-Ravazzi, Coordinator of the Genetics Pos-graduation Program , UNESP,IBILCE, lilian@ibilce.unesp.br

Profa.Dra.Lilian Madi-Ravazzi Coordenadora da Pós-graduação em Genética UNESP/IBILCE Rua Cristovão Colombo, 226 CEP: 15054-000 São José do Rio Preto/SP/Brasil

Lilian Madi-Ravazzi <lilian@ibilce.unesp.br>

SMBE2011 HomePage Server Transfer

Dear Evoldir people,

As many of you are aware, the northeast part of Japan was hit by a series of earthquakes. Kyoto is located in western Japan, and thankfully was left unscathed. The schedule for the SMBE2011 Kyoto Conference is unaffected. However, periodical electricity shutdown will take place every day, including Mishima City where this meeting homepage server is located. We therefore copied files of this website in private server located outside Japan (http://smbe2011.com). Original site (http://smbe2011.lab.nig.ac.jp/) will continue to be used.

Chair, SMBE2011 Domestic Organizing Committee

Saitou Naruya Professor, Division of Population Genetics, National Institute of Genetics Professor (concurrent), Department of Genetics, School of Life Science, Graduate University for Advanced Studies Professor (concurrent), Department of Biological Sciences, Graduate School of Science, University of Tokyo Council Member (concurrent), Japan Science Council

Home Page: sayer.lab.nig.ac.jp/˜saitou/ Postal address: Mishima, 411-8540, Japan TEL/FAX +81-55-981-6790/6789 Email: nsaitou@genes.nig.ac.jp

Saitou Naruya <nsaitou@genes.nig.ac.jp>

Softare fastsimcoal 1 1

fastsimcoal ver 1.1

fastsimcoal is a new and entirely rewritten, continuous-time version of the coalescent simulation program simcoal2

While preserving all the simulation flexibility of simcoal2 and keeping the same input files, fastsimcoal is now implemented under a much faster continous-time sequential Markovian coalescent (SMC) approximation, allowing it to efficiently generate genetic diversity for different types of markers along large genomic regions (i.e. >100Mb), for both present or ancient samples.

It includes a parameter sampler allowing its integration into Bayesian or likelihood parameter estimation procedure.

fastsimcoal can handle very complex evolutionary scenarios including an arbitrary migration matrix between samples, historical events allowing for population resize, population fusion and fission, admixture events, changes in migration matrix, or changes in population growth rates. The time of sampling can be specified independently for each sample, allowing for serial sampling in the same or in different populations.

Different markers, such as DNA sequences, SNP, STR (microsatellite) or multi-locus allelic data can be generated under a variety of mutation models (e.g. finite- and infinite-site models for DNA sequences, stepwise or generalized stepwise mutation model for STRs data, infinite-allele model for standard multi-allelic data).

fastsimcoal can simulate data in genomic regions with arbitrary recombination rates, thus allowing for recombination hotspots of different intensities at any position. It also allows one to define specific recombination distances between simulated markers.

Windows, Linux and MacOS X executable versions of fastsimcoal are available on http://cmpg.unibe.ch/-software/fastsimcoal/ together with example files, benchmarks, and a detailed pdf user manual.

– 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 From January to July 2011: Sainte-Justine Hospital Research Center, room B-454 3175 Cote Sainte-Catherine Montreal, PQ Canada H3T 1C5 Tel: +1 514 345 4931 (Ext 7521)

Laurent Excoffier <laurent.excoffier@iee.unibe.ch>

Software multicore TreeFinder

A new TREEFINDER version is online at:

www.treefinder.de TREEFINDER is a software to compute phylogenetic trees from molecular sequences.

New features include:

- support for multicore processors - parallel bootstrapping - parallel model selection - TL extended for parallel programming - more protein models: FLU, mtZOA, EX.., EHO.., EXEHO.. - convenient installer for Windows

On multicore processors, bootstrapping and model selection are now many times faster than with the old version.

There are versions for Linux and Windows, but not yet for Mac OS. On Macs with Intel processors one may try the Linux version, perhaps with Linux running from an USB or live CD.

I could have done much more, of course, and I could have done it earlier. But I am not very much motivated because I am still not being paid for my work.

Instead, they prefer supporting cheap and flexible scientists, people who accept the miserable salaries and move away from their home places, people who are good at doing what they are told. They prefer supporting people who are very much different from me, I feel being discriminated! And besides I doubt that such a science can do what it promises. There is no innovation without freedom. I don't want such science.

I think that that the academic system as well as other institutions have become part of a social engineering machinery that tries to breed a profitable global society by systematically replacing unprofitable people with profitable people. Profitable from the perspective of the rich who pay our politicians, but it is a way of life that most of us don't want. It is now high time for REAL democracy, especially in the so-called "free" world. I want a real choice. I want the possibility to vote against a system that denies me a fair income and makes me leave my home place - or replaces me with cheap foreigners, if I don't agree. I want the possibility to vote against a world in which most of the property belongs to a very small minority of rich people on which we others depend. Democracy cannot work if property is too ununiformly distributed. It is necessary to limit private property, worldwide.

I am slowly continuing the TREEFINDER project mainly for political reasons, to present a parallel and independent small science that proves the established science incompetent or at least unwilling to do do what they are supposed to.

Gangolf Jobb

Gangolf Jobb <gangolf.jobb@treefinder.de>

SouthAfrica VolunteerFieldAssist MammalEvolution

Volunteers needed as field assistants for the project:

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

Open positions from July 2011 onwards

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

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

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

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

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

Costs: Students have to arrange their transport to the field site themselves. Per month, an amount of Rand 1000 (around 150 US$, 110 Euro) must be paid for accommodation at the research station. For students with their own undergraduate project, a fee of Rand 1250 (approx. 190 US$, 140 Euro) per month applies. Students must buy their own food etc in Springbok (costs of about R 2250, approx. 340 US$ or 250 Euro/month). Including extras (going out for dinner; shopping), you should expect costs of about 550 US$, 450 Euros per month. Students get an invitation letter which they can use to apply for funding in their home country (eg. DAAD in Germany, SANW in Switzerland).

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

When and how long: At the moment we are looking for volunteers for the period July / August to November / December. Volunteers are expected to stay at least 2 months, but longer periods of up to 6months are preferred.

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

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

Dr. Carsten Schradin

Research Assistant, Department of Animal Behavior,

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

Tel: +41 - (0)44 635 5486

Honorary Associate Professor at the School of Animal, Plant and Environmental Sciences,

University of the Witwatersrand, South Africa.

WORKING AS A FIELD ASSISTANT IN GOEGAP NATURE RESERVE

A report by Romy Höppli, student at the University of Zurich, who staid in Goegap June to August 2008

Blue skies without a single cloud for six weeks rocky mountains with little vegetation yellow, orange and pink fields of flowers in whatever direction you look small mammals, lizards and birds in our front yard and Mountain Zebras, Springbok and Ostrich right next door...

This was my time at the Succulent Karoo Research Station in Goegap Nature Reserve in South Africa! During six weeks from the beginning of July until the middle of August I've been living here, studying mice, experiencing nature like never before and being part of a small community where there was always something to laugh and joke about!

After arriving in Goegap, right the next morning my scientific adventure in South Africa began: Setting and checking traps, nest observations and radio-tracking were our daily routine. While I got bitten by the mice quite often in the beginning and my right middle finger was scarred all over, I improved quickly shaking the mice out of the traps, weighing them and checking the number of the ear tag. Other duties like cleaning the cages of the mice in the captive colony, washing the dirt from probably several months out of the traps, painting the new Wendy House and putting in a floor

— / —

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

Teaching evolutionary epigenetics

Dear friends,

I will teach a class about epigenetics to my biology students and I would like to receive suggestions about a good introductory text or article and movies if possible.

I was looking in google but some texts and movies are very specific!

Thanks for any help!

Prof. Dr. J. C. VOLTOLINI Universidade de Taubate - Departamento de Biologia Taubate, SP. 12030-010. E-Mail: jcvoltol@uol.com.br ECOTROP (CNPq): http://dgp.cnpq.br/buscaoperacional/detalhegrupo.jsp?grupo=1546205IMB87W7 Currículo Lattes: http://lattes.cnpq.br/8137155809735635 Orkut ("Ensino de Ciência"): http://www.orkut.com.br/Main#Profile?rl=ls&uid=17608429643840608483 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>

Tree of life

The Assembling, Visualizing and Analyzing the Tree of Life (AVAToL) activity supports novel and transformative approaches to the development of an integrated and robust tree of life, as well as visualization and analysis on a dynamic tree of life. This will take place through the Ideas Lab project development and review process. The goal of this activity is to identify opportunities for investment to significantly advance the state-of-the-art in tree construction, visualization, and analysis across the tree of life. Participants selected through an open application process will engage in an intensive five-day residential workshop to generate project ideas through an innovative, real-time review process. New multidisciplinary teams will form during this workshop to engage in creative problem solving directed at outstanding problems concerning the tree of life. Multidisciplinary integrative approaches calling for communication and interaction among diverse scientists are key to the success of the approach. For example, in addition to those working in systematics and phylogenetics, AVAToL might benefit from mathematicians and computer scientists to contribute algorithms and models, bioinformaticians or genomicists to contribute data pipelines and novel molecular characters, or statisticians and artists with an interest in novel methods of visualization and interactive use of the tree of life. Therefore, members of the systematics research community, bioinformaticians, genomicists, morphologists, paleontologists, computer scientists, statisticians, mathematicians, educators involved in training the next generation of researchers, and representatives of any other disciplines that might contribute important ideas are all strongly encouraged to apply.

For more information see: http://www.nsf.gov/funding/pgm_summ.jsp?pims_id=503629&org=BIO&from=home Tim Collins Emerging Frontiers Office of the Assistant Director Directorate for Biological Sciences National Science Foundation Tel. 305-348-1730 (Miami) e-mail tcollins@nsf.gov

TreeOfLife CommunitySequencing

Dear Colleagues,

We are pleased to announce a community-based sequencing service for annelids within the framework of the recently awarded NSF AToL Grant "WormNet II - Assembling the Annelid Tree of Life". The project is intended to resolve phylogenetic relationships among closely related annelid species and to investigate genetic diversity within selected species and complexes of cryptic species. The service is available at no charge to researchers who can supply appropriately preserved material.

What we offer: * Sequencing of the two mitochondrial markers cytochrome c oxidase subunit I (COI) and 16S ribosomal RNA for approximately 3000 annelid samples, supplied by the community over a five-year period. Samples may consist of whole specimens, tissue samples or cleaned PCR products. Species not represented in GenBank will have priority. * Databasing of collection information and sequence data in a centralized databank at Auburn University * Collaboration on data analysis and publication * Deposition of voucher material in museum collections, if applicable

Interested parties are requested to supply a short description of the intended project, including the approximate number and type of samples, preservation method, permit requirements and status, shipping needs and logistics, plans for deposition of voucher material in museum collections (if not done by processing lab) and expected time frame for processing, data analysis and publication. A sample proposal is pasted below. Details of authorship of any resulting publications will be negotiated on a case-by-case basis. A Memorandum of Understanding between the party supplying the samples and the processing lab will outline the responsibilities of each party. Interested researchers should contact:

Anja Schulze, Texas A&M University at Galveston; Email: schulzea@tamug.edu Or: Frank Anderson, Southern Illinois University; Email: feander@siu.edu

Sample Proposal: My Ph.D. student is currently working on a morphological data set for the eunicid polychaete genus Palola. As the species in this genus are morphologically very similar we need to add molecular data to analyze the phylogeny of the genus. We have a total 40 specimens fixed and preserved in 95% ethanol which we think represent five different species. The specimens were collected in Belize, Panama, Palau and the Federated States of Micronesia in 2008. Copies of the respective collection and export permits will be provided. We will send whole specimens by regular mail in small amounts of ethanol. We have not made arrangements for deposition of voucher material in museum collections and would appreciate if you could assist us in this matter. We request the COI and 16S sequence data by Sept. 2011 because the student has to submit a manuscript draft by Dec. 2011. We may also require assistance with data analysis.

Anja Schulze, Ph.D. Assistant Professor, Marine Biology Texas A&M University at Galveston 200 Seawolf Parkway OCSB Bldg 3029, Rm 258 Galveston, TX 77553 Phone: 409-740-4540 Fax: 409-740-5001

schulzea@tamug.edu

UBristol VolunteerFieldAssist ClimateAdaptation

Volunteer field assistant in flowering traits and climate change, Bristol University, UK

We are looking for a motivated, hard-working volunteer to assist with fieldwork on Avon Wildlife Trust nature reserves around Bristol, UK. This NERC-funded project explores the ecological and evolutionary responses of plant-pollinator networks to climate change. It is a great opportunity to be involved in exciting research in evolutionary ecology, and would suit someone considering further study or research in this area. The applied aspect of the project, and its association with the Avon Wildlife Trust, also provides an excellent opportunity for people looking for experience in the conservation sector.

The role of the volunteer will be to assist with the collection of floral trait data and observations of floral abundance and pollinator visitation to the cowslip (Primula veris).

Requirements: * An interest in ecological and evolutionary scientific research, and natural history and conservation. * Enthusiasm for, and willingness to spend long days working outside in British weather conditions. * Ability to work carefully and meticulously, with close attention to detail.

Previous fieldwork experience and a valid driving license would also be an advantage.

Assistance is required from April - June 2011. Costs associated (travel, lunch etc.) with the field work will be covered. Although this is a casual position, applicants must be reliable and committed to their role.

For further information about this position, or to apply, please email Charlotte Bickler before 21st March charlotte.bickler@bristol.ac.uk.

Dr Jon Bridle School of Biological Sciences University of Bristol Bristol BS8 1UD

Office B70, Lab B38/9 Tel. 0117 928 7482 Fax. 0117 331 7985

jon.bridle@bristol.ac.uk http://www.bristol.ac.uk/-biology/research/ecological/genetics/ Jon Bridle <jon.bridle@bristol.ac.uk> Jon Bridle <jon.bridle@bristol.ac.uk>

UPGMA teaching example

I recently replaced the flawed example of a UPGMA distance calculation on the UPGMA Wikipedia page that was causing problems with teaching. The new link goes to page created and hosted By Rich Edwards and steps through the process in a clear way for students.

In case someone messes with the Wikipedia page again, the new link is http://www.southampton.ac.uk/~re1u06/teaching/upgma/ Cheers, Joel

Dr. Joel Parker School of Biological Sciences University of Southampton Life Sciences Building (B85) Highfield Campus Southampton SO17 1BJ

Phone: +44 023 8059 9007 Fax: +44 023 8059 4269 Email: jdparker@soton.ac.uk Website: http://www.personal.southampton.ac.uk/jdparker/Webpage/

“Parker J.D.” <J.D.Parker@soton.ac.uk>

Visualizing popgen processes

Dear evoldir members,

I would like to demonstrate some population genetics processes to the general audience. I think that some simulation/animation will be extremely useful for that. e.g. the spread of a beneficial mutation in a population, or drift etc. Do you know any animation/simulation tool that can be helpful for that?

best, pavlos

Pavlos Pavlidis <pavlidis@zi.biologie.uni-muenchen.de>

Visualizing popgen processes answers

Dear Evoldir members,

I would like to thank you for the replies I received. I have compiled a list of tools that can be used teaching purposes, animations etc of population genetics processes in the following link: http://www.bio.lmu.de/ ~ pavlidis/home/?Population_Genetics_Visualization_Tools In case that I will receive more replies I will update the list.

All the best pavlos

Pavlos Pavlidis

Scientific Computing Group (Exelixis Lab & HPC Infrastructure) Heidelberg Institute for Theoretical Studies (HITS gGmbH)

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Tel: +49 163 677 3137 (Mobile) +49 6221 533264 (Office)

Skype: idaios Email: pavlos.pavlidis@h-its.org WWW: http://bio.lmu.de/ ~ pavlidis/ Amtsgericht Mannheim/HRB 337446 Managing Directors: Dr. h.c. Klaus Tschira/Prof. Dr.-Ing. Andreas Reuter

Pavlos Pavlidis <pavlidis@zi.biologie.uni-muenchen.de>

Walter Fitch dies

Dear Brian,

very sad news came via email (see below), which is certainly worth posting at EvolDir... currently I do not remember the address to post it directly.

Best wishes, Heiko

From: Brandon Gaut <bgaut@uci.edu> Date: March 10, 2011 11:23:16 AM PST To: bio-all@department-lists.uci.edu Subject: Walter Fitch

Dear Colleagues -

I am sorry to report that a beloved member of our campus community, Dr. Walter Fitch, passed away in his sleep this morning at his home in University Hills. We will miss him dearly as a friend, as a colleague, and as a towering intellectual presence.

Walter was born in San Diego in 1929, and earned his Ph.D. in Comparative Biochemistry from the University of California, Berkeley in 1958. He was a postdoctoral scholar at both Stanford and University College (London) and held full professorships at the University of Wisconsin and the University of Southern California. He came to UC Irvine in 1989 as a Distinguished Professor and later became the Chair of the Department of Ecology and Evolutionary Biology.

Walter was a founding father of the field of molecular evolution, and established methods for constructing phylogenetic trees from amino acid and nucleic acid sequences. He also made contributions to virology, the origin of life, taxonomy, genetics and molecular biology. For his work he was elected to the National Academy of Sciences, the American Academy of Arts and Sciences and the Linnean Society (England). He founded the Society for Molecular Biology and Evolution and was the editor-in-chief of its journal, Molecular Biology and Evolution for its first 10 years. He contributed mightily not only to the intellectual process but as a mentor to young scientists.

Walter is survived by his beloved wife, his four children and several grandchildren. Funeral arrangements are pending.

Sincerely,

Brandon Gaut Professor & Chair Department of Ecology and Evolutionary Biology

Heiko Schmidt <heiko.schmidt@univie.ac.at>

Xenostrobus securis samples

Dear EvolDir members,

I'm currently studying phylogeography of Western Mediterranean populations of Xenostrobus securis (Lamarck, 1819).

In order to correctly reconstruct the relationships among recently established populations in the Western Mediterranean and to disentangle historical and contemporary factors, I would need to analyse samples from the original speciesâ range, which includes brackish-waters of South-Western Australia and New Zealand. Moreover, samples form Japan would also be crucial to make an attempt to reconstruct the routes of colonisation of this invasive species.

I wonder if there is any EvolDir member from South-Western Australia, New Zealand and Japan who can send me samples of X. securis from his territory, or at least the contact of any person and/or institution that could help me in gathering samples.

Tahnk you,

Michele Barbieri

– Michele Barbieri Ph.D. UniversitÃ di Pisa Dipartimento di Biologia UnitÃ di Biologia Marina ed Ecologia Via Derna 1, 56126, Pisa - Italy (I) Tel: +39 050 2211447 Lab: +39 050 2211407 Fax: +39 050 2211410

mbarbieri@biologia.unipi.it

Zootaxa editor needed

Dear Colleagues,

Due to increasing academic duties I must give up as Associate Editor for Terrestrial Adephaga of the journal Zootaxa. During one and a half year it has been a very positive experience and thus I would like to encourage you to accept this position and pay an excellent service to the scientific community. To date, all received manuscripts have been accepted and prepared for the Editorial Office, so there is no pending matter for the next Editor. Anyway, I may send any information about procedures, amount of work (about eighteen manuscripts per year), etc., to interested people in covering this position.

Please have a look on Zootaxa's home page to see further details (http://www.mapress.com/zootaxa/). There is no page charge and the journal publishes at high speed approved papers.

Best regards.

Would you mind to inform me how to proceed for posting? Cheers

– Prof. José Serrano Catedrático de Zoología Facultad de Veterinaria, Universidad de Murcia. Campus de Espinardo. 30071 Murcia (España)

jserrano@um.es

PostDocs

Berlin Metagenomics

Post-doctoral Researcher – Environmental Metagenomics

Leibniz-IGB, Berlin, Germany

The Leibniz-Institute of Freshwater Ecology and Inland Fisheries (IGB) in Berlin invites applications for a post-doctoral researcher in environmental metagenomics. The successful candidate will conduct research on climate-driven changes to microbial communities in water and sediments using experimental mesocosms and natural ecosystems and state-of-the-art genomic facilities. The start date is negotiable and funding is available for up to 3 years.

The position requires a PhD in biology, microbiology, aquatic ecology or a related field; experience with molecular techniques in metagenomics or similar using second-generation sequencing, and a good command of written and spoken English. For additional information, please contact Dr Michael T. Monaghan (monaghan@igb-berlin.de).

Applicants should submit a CV with publications, a cover letter highlighting your experience and research interests, and the contact details of two or more referees to monaghan@igb-berlin.de by 15 April 2011.

monaghan@igb-berlin.de

BielefeldU EvolutionaryBiology

Research Associate Position, Bielefeld University, Evolutionary Biology

Applications are invited for a *Research Associate *position in the *evolutionary biology* group at Bielefeld University, Germany. The position is available in June 2011 and is initially for 3 years, with the possibility of an extension for up to 3 additional years.

We are looking for a highly motivated young scientist with a PhD in evolutionary biology or related fields and preferentially with post-doc experience to form her/his own research group in the field of evolutionary biology. We especially welcome applications from researchers that have experience in one of the following areas: sexual selection, sperm competition or acoustic communication. Candidates should have a proven record of research and publication and should be willing to attract their own funding.

The successful candidate is expected to take part in teaching evolutionary biology (4 hours per week during the semester) and in supervising both undergraduate and graduate students. Starting date is negotiable (any time from June 2011 onwards).

Payment is based on the German TVL E 13 scale (approx. 40,000 per year depending on experience). Bielefeld University is an equal opportunity employer and encourages disabled persons to apply. Disabled applicants with suitable qualifications will be preferentially considered. The university also aims at increasing the number of women in fields where they are underrepresented, and therefore encourages them to apply. Given equal qualifications and skills between top ranked applicants, women will be preferentially considered.

Applications should be sent as a single pdf by e-mail and should include a CV, a list of publications and a research statement, including research plans. Please give names and e-mail addresses of two or three academic referees who are willing to write a letter of recommendation. Applications received before the application deadline will be given full consideration.

Applications and inquiries should be sent until March 28, 2011 to:

Professor Dr. Klaus Reinhold Evolutionary Biology Bielefeld University 33501 Bielefeld Germany

e-mail: Klaus.Reinhold“at”uni-bielefeld.de

Tel.: #49-521-106-2721

Klaus Reinhold <klaus.reinhold@uni-bielefeld.de>

CNRS Gif sur Yvette DrosophilaPheromones

Postdoctoral Fellow LEGS (Laboratory of evolution, genome and speciation) CNRS Location: Gif sur Yvette, France URL: http://www.legs.cnrs-gif.fr/ Start Date: ASAP Duration: 22 months Description: Regulation of Drosophila pheromone biosynthesis by mating and hormonal conditions

One post-doctoral position is open to work on Drosophila pheromone regulation at the LEGS. The position is founded by an ANR grant and is available for 22 months. In Drosophila, pheromones are important for mating and reproductive isolation. They are regulated by hormones and neurotransmitters and seem also to be regulated by mating. We have characterized the main biosynthesis genes. However, little is known on their regulation. We will study pheromone production in species of the melanogaster subgroup by gas chromatography and the expression of the biosynthesis enzymes will be measured by quantitative PCR.

Candidates should be highly motivated and have a strong background in molecular biology. Experience in drosophila genetics will be a plus. Candidate must have excellent analytical skills, strong interpersonal and communication skills.

Qualified candidates should send their curriculum vitae and arrange for two letters of recommendation to be sent to Claude Wicker-Thomas (wicker@legs.cnrs-gif.fr) LEGS, CNRS, Bâtiment13, Avenue de la Terrasse, 91198 Gif sur Yvette Cedex France. Deadline for application is September 1, 2011. Starting date is negotiable. The review of applications will begin immediately and applicants are strongly encouraged to submit applications as soon as possible.

Contact: Claude Wicker-Thomas Email address: wicker@legs.cnrs-gif.fr UPR 9034 Laboratoire Evolution, Génomes et Spéciation (LEGS) Bât. 13, CNRS Avenue de la Terrasse 91198 Gif sur Yvette Cedex Tel: 33 (0)1 69 82 37 08 Fax: 33 (0)1 69 82 37 36

Claude Wicker-Thomas <Claude.Wicker-Thomas@legs.cnrs-gif.fr>

CornellU BeePhylogeneticsGenomics

Postdoctoral Position Available in Bee Phylogenetics/Genomics V A postdoctoral position is available to investigate the utility of next-generation sequencing to develop phylogenetic data sets for bees at the family level. The position will begin as soon as a qualified applicant is found and is available for one year with the possibility of extension. Qualifications: a Ph.D. in entomology, genetics, molecular biology, or comparative genomics; demonstrated expertise in collecting and analyzing large, next-gen data sets, including 454 and/or Illumina. Preference will be given to applicants with prior experience preparing transcriptome samples for 454 and/or Illumina sequencing. Bioinformatic skills are essential, especially in assembly, annotation, and alignment, and phylogenetic analysis of next-gen data. The successful candidate will be expected to provide assistance to others in the lab in both transcriptome sequencing and analysis of transcriptome data. The position will be based in the Department of Entomology, Cornell University, Ithaca, NY. To apply, send curriculum vitae, statement of interest and qualifications, names and contact info for three references, and up to three relevant publications to: Dr Bryan N. Danforth bnd1@cornell.edu. Applications will be received until a suitable applicant is found. See http://www.danforthlab.entomology.cornell.edu/ for more information.

Bryan N. Danforth, Professor Department of Entomology 3124 Comstock Hall Cornell University Ithaca, NY 14853-0901 phone: 607-255-3563/FAX: 607-255-0939 email: bnd1@cornell.edu NEW lab website: http://www.danforthlab.entomology.cornell.edu/ NEW CU Insect Collection website: http://cuic.entomology.cornell.edu/ Bryan Nicholas Danforth <bnd1@cornell.edu>

CzechRepublic PhylogeneticAnalysis

Postdoctoral Research Fellow in Tropical Ecology University of South Bohemia - Department of Zoology Novotny-Basset Lab, Czech Republic Salary: Euro 27,000 - 31,000 pa Limit of tenure: up to three years

We are seeking a highly motivated and productive postdoctoral researcher to join our international team studying plant-insect food webs in tropical forests. The successful applicant will develop ecological, statistical, molecular or phylogenetic analyses of large data sets on plant-insect food webs. In addition, s/he will be able to develop an independent project, use our excellent tropical field research facilities in Papua New Guinea and collaborate closely with our partners at the University of Minnesota and the Smithsonian Institution. S/he will also contribute to the design of further studies of food webs, help apply for grant support and mentor graduate students. Information on our research team: http://www.entu.cas.cz/png/cv-novotny-vojtech-lab.html To apply, or informally enquire about the position contact Prof. Vojtech Novotny (novotny@entu.cas.cz).

Review of applications will begin on April 15th and will continue until the position has been filled. The position will open on 1st October 2011.

Location: Ceske Budejovice, Czech Republic

George Weiblen <gweiblen@umn.edu>

HarvardU ComparativeGenomics

Postdoctoral Position in human comparative regulatory genomics at Harvard Medical School.

A position is available for a highly motivated and productive postdoctoral researcher in the group of Barbara Stranger at Harvard Medical School, in the Division of Genetics at Brigham and Women's Hospital in Boston, MA, USA. The specific project is flexible, but will involve high-throughput sequencing technology to study transcriptional regulation and genome polymorphism data in humans. Current research in the lab includes (1) transcriptional network and pathway analysis; (2) comparative and evolutionary genomics, especially genome evolution, sequence features, and SNP patterns; (3) functional genomic data integration, management, and extensive data mining; and (4) detection of disease susceptibility genes/networks.

Our group shares space and weekly lab meetings with those of Paul de Bakker, Robert Plenge, Phil de Jager, and Soumya Raychaudhuri, and is part of the Program of Medical and Population Genetics at the Broad Institute of Harvard and MIT. We participate in a wide variety of academic programs and interactions with colleagues across many disciplines from multiple outstanding institutions in the Boston scientific community.

MINIMUM QUALIFICATIONS:

- A Ph.D. in bioinformatics, computer science, genomics, population genetics, or other relevant fields of biology.

- Research experience (with strong first-author publications) in computational genomics, molecular evolution, population genetics, or a closely-related field.

- Strong analytical, quantitative and computational/programming skills, ideally in C or C++ as well as in scripting languages such as perl, matlab, and R. Should be comfortable in a linux/unix environment, with large data sets, computer clusters, and databases.

- Fluency in probabilistic modeling and computational statistics.

- Ability to conduct independent cutting-edge research

PREFERRED QUALIFICATIONS: Experience in analysis of DNA-seq, RNA-seq, and/or CHiP-seq data, as well as experience constructing complex biological networks. Candidates with a multidisciplinary background, spanning both life sciences and computer sciences are especially encouraged to apply.

POSITION AVAILABLE: As soon as possible. Funding is available for a minimum of 1 year, and may be extended upon mutual agreement. Preference will be given to candidates with a high probability of applying for (with the help of the PI) and obtaining independent funding; NIH-NRSA fellowship, NSF Postdoctoral fellowships, or other funding agencies.

The position will remain open until filled. Informal inquiries are welcomed, prior to formal application. To formally apply, please send the following as a PDF (other file formats will not be opened) to Barbara Stranger (bstranger at rics dot bwh dot harvard dot edu):

1. A curriculum vitae including the names of 3 referees willing to provide a letter of recommendation upon request.

3. A brief statement of how your research goals fit with research on the human transcriptome

4. A brief statement of interest, ideas, and qualifications for independent fellowship and/or grant applications

Barbara E. Stranger, PhD Division of Genetics/Department of Medicine Harvard Medical School/Brigham and Women's Hospital 77 Avenue Louis Pasteur New Research Building, Room 0168B Boston, MA 02115 USA

http://strangerlab.bwh.harvard.edu/
bstranger@rics.bwh.harvard.edu

InstEvolution Haifa ComputGenomics

A Postdoctoral and Ph.D. positions in Computational Genomics and Phylogenetics are available at the Institute of Evolution at the University of Haifa. The research projects will be done in collaboration with the Phylogenetics and Computational Genomics lab of Dr. Sagi Snir. The positions are targeted to two projects:

1. The project is focused on large scale phylogenetics reconstruction by means of the supertree method. The project is based on algorithmic and computational/mathematical tools for piecing together the tree of life. We represent trees in a special graph and apply specific graph algorithms such as MaxCut on this graph. Preliminary results show advantages over existing methods. As these tasks are computationally hard, we employ probabilistic approaches to obtain the results. We investigate both theoretical and practical questions associated with this approach.

2. Detection and analysis of horizontal gene transfer (HGT) in prokaryotes. HGT is a major factor in prokaryotic evolution and plays a significant role in developing antibiotic resistance. We have developed several novel methods to detect HGT where existing methods fail. The methods use evolutionary signals, unique to HGT, that are detected by non trivial statistical approaches.

Both projects are funded by highly competitive grants that provide high fellowships.

The successful candidates must have familiarity with computational/mathematical biology. Essential requirements include proficiency in computer-programming skills, such as C/C++/Java and scripting languages (e.g. Perl, Phyton), demonstrated ability in applying the devised algorithms. Duties of the role will include algorithm development, implementation and testing by simulation and application on real biological data.

The Institute of Evolution is world leading in broad aspects of evolution, both theoretical and practical. The young team of Dr. Snir is characterized by works with both algorithmic and evolutionary appeal with ample collaboration with other leading labs around the world.

Applicants should send a CV, a statement of research interests and the names and contact information for 3 references. Review of the applications will start immediately until positions are filled. The initial contract is for the postdoc is one year with possibility of extension. For Ph.D. students, the contract is for three years with possible additional year extension.

Please send applications by email to:

Sagi Snir, Ph.D. Sagi Snir Department of Evolutionary and Environmental Biology and The Institute of Evolution, University of Haifa Mount Carmel, Haifa 31905 ISRAEL Tel: (972) 4 828-8774 Email: ssagi@research.haifa.ac.il

sagi.snir@gmail.com

IST Austria Speciation

A postdoctoral position is available, for research into the genetics of speciation in Antirrhinum. The project focusses on a hybrid zone between subspecies that differ in floral morphology: plants are genotyped for major genes that determine flower pattern, and for multiple microsatellite markers. The aim is to find why the subspecies remain distinct, and how they diverged from eachother.

This is a joint project between Nick Barton at the Institute of Science and Technology, Austria, and Enrico Coen, at the John Innes Institute in Norwich (http://rico-coen.jic.ac.uk). The postdoc would be based at IST; she/he would be primarily responsible for experimental design and data analysis, and would also take part in fieldwork.

The Institute of Science and Technology is a new multidisciplinary research insttitute, located in the Wienerwald, just outside Vienna (www.ist-austria.ac.at). There are close links with other population genetics groups at the University of Vienna and at the Veterinary University (www.univie.ac.at/evolvienna/) .

The position will be available for three years; the salary scale starts at euro 44,982 p.a. Applicants should have a Ph.D. in a relevant area, with good quantitative and computing skills, and an interest in evolutionary biology. For further details, please contact nick.barton@ist.ac.at. Applications should be sent by April 24th, and should include a CV, a statement of research interests, and names of referees.

Nick Barton

IST Austria Am Campus 1 Klosterneuburg 3400
'phone: (43)2243 9000 3001 www.ist-austria.ac.at
Nick.Barton@ist.ac.at

IST Austria TheorySelection

A postdoctoral position is available, for research at the interface between evolutionary biology and computer science. The position is funded by an ERC Advanced Grant “Limits to selection in biology and in evolutionary computation”, and addresses a variety of questions: How efficiently can natural selection accumulate and maintain information? How can we detect and quantify this process, through observations of DNA sequence variation? What is the relation between the concepts of fitness, information, and entropy? How can we optimise the performance of computational methods that are based on selection?

The Institute of Science and Technology is a new multidisciplinary research insttitute, located in the Wienerwald, just outside Vienna (www.ist-austria.ac.at). The Institute has strong computer science groups, and there are close links with other population genetics groups in Vienna (www.univie.ac.at/evolvienna/) .

Applicants should have a Ph.D. in a relevant area (including computer science, mathematics, statistical physics, and population genetics), with strong mathematical and computing skills, and an interest in fundamental research. For further details, please contact nick.barton@ist.ac.at. Applications should be sent by April 24th, and should include a CV, a statement of research interests, and names of referees.

Nick Barton

IST Austria Am Campus 1 Klosterneuburg 3400
'phone: (43)2243 9000 3001 www.ist-austria.ac.at
Nick.Barton@ist.ac.at

JagiellonianU EcologyEvolutionaryBiology

2 POST-DOC POSITIONS IN ECOLOGY AND EVOLUTIONARY BIOLOGY AT THE INSTITUTE OF ENVIRONMENTAL SCIENCES, JAGIELLONIAN UNIVERSITY, KRAKOW, POLAND

The leading Polish institute in: Behavioral ecology, Evolutionary genetics and life histories, Physiological and bioenergetics, Ecotoxicology and industrial pollutants, Ecosystem ecology, environmental education and management

is opening applications for

20-month fellowship programme for strongly motivated scientists with a PhD degree in Biology, Ecology or related field, with net-fellowship 3200 PLN per month plus social benefits, realized in one of the research groups at the Institute of Environmental Sciences and a monthly internship at the universities in Europe and the U.S.

Application deadline: 29 April 2011

Detailed information about the positions, containing profile of the applicant and the application instructions are available at: www.eko.uj.edu.pl/ecology Candidates are required to contact IES Staff to discuss potential research project prior to the application. For more information about the Institute visit: www.eko.uj.edu.pl –

ecology@uj.edu.pl

Lyon EvoDevo Bioinformatics

Post-doctoral position for a Bio-informatician

A full time postdoctoral position for a bio-informatician is available in the Laboratory of Evolutionary Developmental Genomics (LEDG) at the Institute of Functional Genomics, Lyon (IGFL) -France. The successful candidate will lead and coordinate the de novo assembly of at least one water strider genome and contribute to functional and evolutionary genomics analyses. In addition, the candidate is expected to help organize and analyze comparative transcriptomics sequence data obtained by next generation sequencing technology.

The general objective of the LEDG is to combine developmental genetics, transcriptomics, genomics, proteomics, and evolutionary ecology for the study of animal diversity. The successful candidate is encouraged and will have the opportunity to learn and conduct gene function analysis experiments to validate comparative genomics/transcriptomics findings.

Water striders are semi-aquatic bugs Va monophyletic group of predatory hemipterans that have proven to be suitable for integrative studies. This is a species-rich group with a large morphological diversity, particularly in their appendages, which are shaped by adaptation to locomotion on the water, co-evolution of the sexes, or prey-predator interactions. In addition to being models for evolutionary ecology and population genetics, we have established RNA interference (RNAi) technique for gene function analysis, both for single and multiple gene knockdowns and across multiple species. Some details can be found in our first publication by Khila et al. 2009, PLoS Genetics.

The position is within the IGFL of Lyon (http://-igfl.ens-lyon.fr/), a young but vibrant institute sponsored by Universite Claude Bernard, INRA, ENS, and CNRS. Lyon is the second biggest town in France, with a much more affordable cost of life compared to Paris, but with just as much charm.

A PhD degree in Genetics/Genomics, Bioinformatics/Computational Biology, or related disciplines is required. Experience with genome assembly and annotation, genomic data mining, sequence analyses are highly desirable. Experience with basic molecular techniques is a plus. Salary is guaranteed for 1-2 years and is defined by CNRS standards. The position may start as early as June, but no later than October 2011.

Please email a cover letter, CV, and names and contact info of three references to Dr. Abderrahman Khila at Abderrahman.khila@ens-lyon.fr

"Abderrahman Khila, Dr" <abderrahman.khila@mcgill.ca>

MaxPlanck 3 EvolutionaryOntology

The Laboratory of Evolutionary Biodemography within the Max Planck Institute for Demographic Research

(MPIDR) is seeking to recruit:

Post-doctoral fellow in DEVELOPMENTAL BIOLOGY Post-doctoral fellow in EXPERIMENTAL INVERTEBRATE BIOLOGY Post-doctoral fellow in EXPERIMENTAL PLANT BIOLOGY

For a project investigating the evolutionary and genetic basis of mortality patterns during ontogenesis. For scientific background on this project, please see: http://rspb.royalsocietypublishing.org/content/278/1707/801 Job Description The fellow will join an interdisciplinary project including demographers and evolutionary biologists investigating patterns of mortality over age and stage during development. Areas of research include how age patterns of genetic expression can predict developmental mortality and the role which sexual reproduction and recombination play in developmental mortality. These fellowships do not require teaching.

The developmental biologist should have a strong background in developmental biology and genetics of drosophila.

The experimental invertebrate biologist will design and conduct experiments with facultative asexual reproducers, (e.g, hydra and monogonont rotifers). Choice of species is open to discussion.

Candidates in experimental plant biology will design and conduct common garden experiments with facultative apomicts.

Required Qualifications Applicants should have a Ph.D. or expect to have a Ph.D. at latest by October 2011.

Background in demography is not required for this position, but a willingness to apply biological thinking and methods to investigating demographic patterns is.

Applications should be received by April 30th, 2011. Applications should include a letter outlining your research background and agenda, a CV including information about your education, a list of publications, and the contact details of 3 academic references. In order to apply please email these documents to applonotog@demogr.mpg.de

The Max Planck Society is committed to employing more handicapped individuals and especially encourages them to apply. The Max Planck Society wishes to increase the share of women in areas where they are underrepresented, and strongly encourages women to apply.

Levitis@demogr.mpg.de

MaxPlanck Biostatistician

The Laboratory of Evolutionary Biodemography and Laboratory of Statistical Demography within the Max Planck Institute for Demographic Research (MPIDR) is seeking to recruit a

Post-doctoral fellow in biostatistics, mathematical biologist or evolutionary demography

Job Description

The fellow will join a funded interdisciplinary project including demographers and evolutionary biologists investigating pre-adult mortality patterns. The fellow will participate in developing methods to link age- specific mortality to age-specific dynamics of gene expression, and other projects beyond the typical bounds of statistical demography. Areas of research include comparative analysis of mortality patterns in humans and non-humans, and characterization of the functional form of mortality decline over age between conception and maturity in a wide range of populations. The fellowship does not require teaching.

For background on the biological aspects of this project, please see: http://rspb.royalsocietypublishing.org/content/278/1707/801

Required Qualifications

Applicants should have a Ph.D. or expect to have a Ph.D. at latest by October 2011. Candidates should have a strong background in statistics, including model identification, and should be prepared to create innovative methods for unusual datasets and questions. Background in demography is not required for this position, but very strong quantitative skills and a willingness to apply demographic thinking and methods to biological questions are. Applications should be received by April 30th, 2011. Applications should include a letter outlining your research background and agenda, a CV including information about your education, a list of publications, and the contact details of 3 academic references.

In order to apply please email these documents to applontog@demogr.mpg.de

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Levitis@demogr.mpg.de

MaxPlanckInst ModellingAging

The Max Planck Research Group "Modeling the Evolution of Aging" within the Max Planck Institute for Demographic Research (MPIDR) in Rostock, Germany, is seeking to recruit Two Post-docs who are excited about uncovering fundamental principles and unifying theory of what determines the trajectories of life from birth to death across the diversity of species. Our interdisciplinary team is developing new concepts, measures, and models of aging in a comparative framework to shed light on the physiological and environmental determinants of why some organisms age and others do not, and how, for different species, aging trajectories are linked to the length of life. Approaches * Mathematical framework of Demography * Theory underlying life history biology, population ecology and evolution * Models of epidemiology and life cycle optimization approaches Skills * Curious, creative, independent team worker * Background in demography, biology, math/stats, biophysics, or other strong quantitative background with burning interest in questions of evolutionary biodemography * Fluent in a programming language, preferably R or Matlab * Fluent in English (spoken and written) Some key readings * Baudisch, A. (2011). The pace and shape of ageing. Methods in Ecology and Evolution. DOI: 10.1111/j.2041-210X.2010.00087.x < http://dx.doi.org/10.1111/j.2041-210X.2010.00087.x > * Rebke, M., Coulson, T., Becker, P. H. & Vaupel, J. W. (2010) Reproductive improvement and senescence in a long-lived bird. Proceedings of the National Academy of Sciences 107, 7841-7846 * Metcalf, C. J. E. & Pavard, S. (2007) Why evolutionary biologists should be demographers. Trends in Ecology & Evolution 22, 205-212 The Max Planck Society is committed to employing more handicapped individuals and especially encourages them to apply. It wishes to increase the share of women in areas where they are underrepresented, and strongly encourages women to apply. Please send your application by e-mail to Dr. Annette Baudisch, at applirgmea@demogr.mpg.de. PDF files are preferred.

"Papenhagen, Ute" <Papenhagen@demogr.mpg.de>

MaxPlanckInst Ploen MouseAdaptation

Postdoc for behavioural genetics and adaptation of house mice

Max-Planck Institute for Evolutionary Biology, Ploen, Germany Group of Diethard Tautz

We will soon open a new facility that allows setting up seminatural enclosure experiments with house mouse populations at a large scale. Experiments will include the analysis of the genetic basis of mate choice, the role of imprinting in environmental adaptations, as well as studies on the fitness effects of adaptive trait alleles. We seek a postdoc who is interested to join such experiments.

Generally we are using natural populations of the house mouse to study the genetic basis of adaptations. We are employing high level genomic approaches with in-house facilities for microarrays, high throughput genotyping, and next generation sequencing to detect and functionally characterize genes involved in recent adaptations. We have an unique collection of house mouse populations and pursue a large variety of projects.

Owing to its history as a limnological institute, we are located in a small town in the middle of a beautiful lake district. Our directly neighboring larger towns are Kiel and Lübeck, and Hamburg is approx. 70km away. We are allied with the University of Kiel and have a joint international graduate school in evolutionary biology.

Further information on the institute can be found at: http://www.evolbio.mpg.de/english/index.html The position is suitable for persons who have finshed a PhD in behavioural ecology or a general topic in evolutionary biology. Payment will be on the basis of a taxfree stipend, initially for two years and extendable for a third year.

Applications should be sent to tautz@evolbio.mpg.de and include a complete CV, publication list, letter of motivation and contact information for three references.

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

MissouriBotanicGarden FernPhylogeny

Applications are invited for a postdoc position to study the phylogeny of the fern genus Polystichum(Dryopteridaceae).This study is led by Libing Zhang(Missouri Botanical Garden) with collaboration from Xinfen Gao(Chengdu Institute of Biology, Chinese Academy of Sciences).

The postdoc will be responsible for generating DNA sequences, developing low-copy nuclear markers, traininggraduate students in the lab, analyzing data, and co-authoringmanuscripts. Applicants should have a strong molecular systematicsexperience, preferably also including cloning skills. Experience in ferns is not required. The postdoc iswelcome to work on his/her own projects in addition to the study ofPolystichum. The position is for one year with possible extension depending on performance and funding availability.

The postdoc will be based at the Chengdu Institute of Biology, Chinese Academy of Sciences (http://www.cib.ac.cn/blue_cib/index.html). The city, Chengdu (http://en.wikipedia.org/wiki/Chengdu), over 2,500 years old, is rich in culture and well-knownfor the food (Sichuan cuisine) and is close to the Himalayas. It was recently named China's 4th-most livable city byChina Daily.The salary of the position is comparable withthat of an assistant professor in Chengdu. The flights to and back from Chengdu after theposition ends will be paid. Free housing in Chengdu is provided. The start date isflexible. Applicants should email ashort cover letter, cv, and names and contact information of threereferences to Libing.Zhang@mobot.org by 17 March2011.

– Li-Bing Zhang Missouri Botanical Garden. Box 299, St. Louis, Missouri 63166 Tel: +1-314-577-9454; Fax: +1-314-577-9596 mobot.org/MOBOT/Research/curators/zhang.shtml

Libing Zhang <gonggashan@gmail.com>

Netherlands 2 EvolutionaryBiol

Starting May 1st 2011, the Netherlands Centre for Biodiversity Naturalis has positions available for:

One Research Fellow in Botany One Research Fellow in Marine Zoology

For 36 hours a week

We seek to attract Research Fellows to support our research themes, namely "Morphology and evolutionary developmental genetics", "Phylogenetics and horizontal genomics", "Biogeography" and "Global Change Biology". You are an energetic and enthusiast scientist with a proven track record and a clear view on how your research program will contribute to the future success of NCB Naturalis. You are eager to join our new institute, to cooperate with the existing staff of NCB Naturalis, to study the NCB Naturalis natural history collections, and to use the new scientific infrastructure. Developing active interactions between NCB Naturalis and our partners in biodiversity research as well as acquisition of externally funded projects are essential. You are expected to teach at the undergraduate and graduate levels and to represent NCB Naturalis in societal and scientific communities.

Requirements You have a PhD degree in systematics, evolutionary biology, geology, or other relevant discipline and at least two years, and preferably not more than six years, of experience at the postdoctoral level. You have excellent teaching and communications skills in English, both written and verbal. Furthermore, you have an excellent scientific track record (given the point in your career) and are involved in innovative and multidisciplinary research projects in biodiversity research, operating in an international scientific network. You are able to engage in collaborative networks with students and university partners as well as existing NCB Naturalis research staff.

Depending on the research theme, desired qualifications may include: * Ample experience with modern molecular techniques, advanced microscopy techniques, GIS applications and/or web-based taxonomy. * Experience with research popularisation. * Interest in the applications of systematic research in conservation, environmental management and species identification services.

We offer A fulltime contract (36 hours per week) for four years. A competitive salary up to a maximum of circa EUR 59,000 gross per year depending on experience and qualifications, including holiday allowance (8%). All our employees are incorporated into a pension fund.

Procedure You are invited to submit your application including your curriculum vitae, a clearly focused research program of maximum four pages (containing a four year working plan, a proposed budget, a complete list of publications*, your H-index, up to five keywords describing the research area, a statement of teaching interests and the names and e-mail addresses of at least three persons that can be contacted for reference (and who have agreed to be contacted) before March 14th 2011 by e-mail to; sollicitaties@ncbnaturalis.nl, or by mail; Naturalis, HR department, PO box 9517, 2300 RA Leiden, the Netherlands.

For more information on the current research and facilities, see the websites of the founding partners of the NCB Naturalis, on www.naturalis.nl - www.nhn.leidenuniv.nl - www.science.uva.nl/zma - www.bis.wur.nl/UK/Organisation/Herbarium Any additional information can be requested from: Prof.Dr. E.F. Smets, scientific director Netherlands Centre for Biodiversity Naturalis E-mail: erik.smets@ncbnaturalis.nl Phone: +31 71 5687 713

* Use the following categories: sci publications (incl. citations and IF); publications in non-sci journals; publications in books or proceedings; other relevant publications.

“Hoeksema, B.” <Bert.Hoeksema@ncbnaturalis.nl>

Netherlands SpeciesDiversity

The focus of NCB Naturalis is biodiversity. NCB Naturalis curates a collection of 37 million specimens; this is one of the world’s largest natural history collections. We present the history of our planet and the diversity of life on Earth with permanent and temporary exhibitions, educational programmes and websites. Our research and education are maintained at a high academic level. NCB Naturalis is appealing to a wide audience, attracting over 250,000 visitors and 5 million hits to its website annually. Co-operation with international institutions, including three renowned Dutch universities, and the outstanding collections, are all factors that attract hundreds of visiting scientists every year. Expectations and ambitions for the next few years are high. We will develop new exhibitions and plan to integrate several collections. NCB Naturalis will invest significantly in infrastructure for collections and research, including new buildings. In short, we are a developing, world-class institution, and present this exciting opportunity for you to help us achieve our ambitions and meet our challenges.

NCB Naturalis has a position available for a

Postdoctoral Researcher

36 hours a week

For a project entitled: Determinants of species diversity at 14 spatial scales in tropical micro snails from endangered limestone habitats

This project is part of an ongoing research programme on biodiversity dynamics on isolated limestone outcrops in Southeast Asia. The successful applicant will carry out the first-ever study of species diversity in a tropical land snail community that makes full use of the advantages of working with this animal group. He/she will sample, process, and taxonomically identify communities of land snails at standard plots covering a wide range of spatial scales, leading to a species-area-curve that is generated by different processes in different parts of the curve. Fitting observed species-abundance-distributions to known models, in combination with assessments of local niche differentiation, will allow the following questions to be answered: (1) which model best explains the shapes of the species-abundance distributions found at each of the spatial scales simultaneously? (2) is habitat differentiation or niche differentiation demonstrable at the smallest of spatial scales? (3) what are the spatial scales at which speciation contributes to patterns of species diversity?

We seek an enthusiastic researcher with a PhD in terrestrial invertebrate ecology and/or community ecological theory (or similar experience), a good track record in publishing in leading ecological or evolutionary journals, and an ability and willingness to spend up to two months per year in the field.

offer A fulltime contract (36 hours per week) for three years. A competitive salary up to a maximum of circa EUR 38,000 gross per year depending on experience and qualifications, including holiday allowance (8%). All our employees are incorporated into a pension fund.

Procedure You are invited to submit your application including your curriculum vitae, a complete list of publications*, and the names and e-mail addresses of at least three persons that can be contacted for reference (and who have agreed to be contacted) before 20 April 2011 by e-mail to: sollicitaties@ncbnaturalis.nl, or by mail: NCB Naturalis, HR department, PO box 9517, 2300 RA Leiden, the Netherlands. We aim to fill the position before July 1st, 2011.

Information

A link to a full description of the project can be found on http://science.naturalis.nl/schilthuizen

Any additional information can be requested from: Prof. Dr. Menno Schilthuizen Netherlands Centre for Biodiversity Naturalis E-mail: menno.schilthuizen@ncbnaturalis.nl Phone: +31 71 5687 769

* Use the following categories: sci publications (incl. citations and IF); publications in non-sci journals; publications in books or proceedings; other relevant publications.

For more information on the current research and facilities, see the websites of the founding partners of the NCB Naturalis, on www.naturalis.nl - www.nhn.leidenuniv.nl - www.science.uva.nl/zma - www.bis.wur.nl/UK/Organisation/Herbarium Prof. Dr. Menno Schilthuizen Netherlands Centre for Biodiversity 'Naturalis' P.O. Box 9517; 2300 RA Leiden; the Netherlands tel. (+31-0)-71-5687769; mobile: (+31-0)-6-22030313; home: (+31-0)-71-7370103 E-mail: menno.schilthuizen@ncbnaturalis.nl; schilthuizen@yahoo.com Webpage: http://science.naturalis.nl/schilthuizen

Other affiliations:

* Professor for Insect Biodiversity (Uyttenboogaart-Eliasen Endowed Chair); University of Groningen, the Netherlands

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Nordic TundraDynamics

3-5 Post Doc and 3-5 PhD positions open at a new Nordic Centre of Excellence âHow to preserve the tundra in a warming climateâ (NCoE Tundra)

NCoE Tundra is a new Nordic Centre of Excellence during 2011-15, funded by NordForsk, under the scheme Top-level Research Initiative (TRI). Our scope is to study the interaction between the ecological phenomenon of top down impacts in food webs and climate-vegetation interactions, and to integrate this perspective with the man-managed reindeer husbandry and the SÃmi culture dependent on it. Ultimately, we wish to learn how the top-down impact of reindeer can be optimally applied to the prevention of shrub encroachment and woodland expansion, and the resulting negative impacts of these processes on global climate and biodiversity. In the present project, we will approach the system of ecologic, climatologic, and socio-economic issues by means of an integrated, co-Nordic CoE project, gathering young specialists already working on different aspects of the above problem into an integrated Co-Nordic team.

The project consists of Work Packages (listed below), each of them dealing with their own specific questions. More information (including more detailed instructions for applications) can be found in our website (www.ncoetundra.utu.fi). The duration of positions is two years, with an option of two years of extension (2+2). Note that since one of the aims of the NCoE is to promote Nordic co-operation, post docs and PhD students will not carry their research in the country of their citizenship (i.e. a Finnish citizen cannot be placed in Finland).

Application deadline 15th of April 2011. All applications should be sent to the following address: ncoe.tundra@gmail.com

For queries on the different WPs, please contact the leaders and/or co-leaders listed below:

WP 1 Predation and the dynamics of arctic-alpine food webs (Prof. Erkki Korpimäki, Univ. of Turku, ekorpi@utu.fi, Assoc. Prof. Tarja Oksanen, Univ. of Turku, tarjamaarit.oksanen@gmail.com)

WP 2 Impact of vertebrate herbivory on tundra vegetation (Assoc. Prof. Johan Olofsson, UmeÃ Univ., Johan.Olofsson@emg.umu.se)

WP 3 Impact of grazing on the dynamics of rare arctic-alpine plants (Prof. Lauri Oksanen, Univ. of Turku and Finnmark Univ. College, lauoks@utu.fi, lauri@hifm.no, Prof. Lars Ericson, UmeÃ Univ., lars.ericson@emg.umu.se

WP 4 Moth-reindeer-birch dynamics in northernmost Fennoscandia (Prof. Pekka Niemelä, Univ. of Turku, pnieme@utu.fi, Prof. Rolf Anker Ims, Univ. of Tromsö, rolf.ims@uit.no)

WP 5 Large scale impacts of herbivory on vegetation (Senior Res. Bernt Johansen, NORUT-IT, bernt.johansen@itek.norut.no)

WP 6 Ecology and socio-economy of reindeer herding systems (Prof. Bruce C. Forbes, Univ. of Lapland, bforbes@ulapland.fi, Assoc. Prof. Tove Aagnes Utsi, Finnmark Univ. College, tove.utsi@hifm.no)

WP 7 interaction between vegetation and climate (Prof. Jouni Pulliainen, Finnish Meteor. Inst., jouni.pulliainen@fmi.fi)

WP 8 Abiotic processes, spatial information (GIS), synthesis and policy recommendations (Prof. Lauri Oksanen, Univ. of Turku, lauoks@utu.fi and Prof. Jukka Käyhkö, Univ. of Turku, jukkay@utu.fi)

Elina Koivisto <elina.koivisto@utu.fi>

Norway 4PDF 8PhD CodEvolution

8PhD_4Postdoc_NordicCountries_AtlanticCod_Ecology_Economy_Evolution

8 PhD- and 4 Postdoc positions are now available at The Nordic Centre for Research on Marine Ecosystems and Resources under Climate Change (NorMER) V A Nordic Centre of Excellence.

Research areas: Ecology, Evolutionary biology and Economy

NorMER (www.normer.org) is a new Nordic Centre of Excellence funded by Nordforsk, on behalf of the Top-Level Research Initiative (TRI). NorMER consists of 45 researchers from 10 research units situated within all of the Nordic territories: Norway, Sweden, Finland, Aaland, Denmark, Faroes, Greenland and Iceland. This collaborative project combines the expertise of internationally recognized research teams to implement a multidisciplinary research strategy to explore the biological, economic, and societal consequences of global climate change on fisheries resources in the Nordic region, with a primary focus on the Atlantic cod. NorMER will achieve this through a unique program of primary research, for which the members will collaborate in training a total of 15 new PhD students (8 announced in 2011, 7 in 2012) and 5 Postdocs (4 announced in 2011, 1 in 2012) through joint projects that integrate biology, economics, industry and policy.

All 12 positions are announced here: http://www.vacancies.normer.org/. Applicants from all countries are encouraged to apply. We also encourage all candidates to apply for more than one position, if possible.

Application deadline: 30th March 2011. Expected start date: 1st August 2011 For questions about the network, please contact normer-post@bio.uio.no

– Regards,

Olaf Kristian Sund Higher Executive Officer

Olaf Kristian Sund <o.k.sund@matnat.uio.no>

OregonStateU Nematode EvolutionaryGenomics

The laboratory of Dee Denver at Oregon State University is searching for a Faculty Research Assistant (FRA) or Postdoctoral Scholar; position available 06/11 to investigate evolutionary genomic processes using Illumina high-throughput DNA sequence data. Experience in computer programming required, specific knowledge in Perl and R applications, Knowledge Unix/Linux operating systems preferred. BA/BS required for FRA applicants; PhD required for Postdoc applicants. Postdoc applicants would be expected to pursue independent funding before or during an initial one-year of support on the PI?s grant funds. Include cover letter of application, CV, and the contact information for three professional references (email addresses preferred). For full consideration apply by 4/15/11. OSU in an AA/EOE employer.

The Denver lab primarily studies genomic evolutionary processes in nematodes. We study the evolution of both mitochondrial and nuclear DNA in diverse interesting nematode genera including Caenorhabditis (includes the famous model C. elegans), Meloidogyne (plant parasites), Panagrolaimus (free living), Strongyloides (animal parasites) and Xiphinema (plant parasites). We are currently funded by NIH and USDA. We take advantage of the superb resources offered by the OSU Center for Genome Research & Biocomputing ? this facility offers Illumina/Solexa (new HiSeq2000 system in addition to the GAII) and Roche/454 sequencing.

Denver Lab website: http://denverlab.cgrb.oregonstate.edu/ For inquiries, contact Dee Denver: denver@cgrb.oregonstate.edu

Full job description and instructions for applying available at:

jobs.oregonstate.edu/applicants/Central?quickFindX186

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Dee R. Denver Assistant Professor Department of Zoology Oregon State University 3029 Cordley Hall Corvallis, OR 97331 PH: 541-737-3698 FX: 541-737-0501 http://denverlab.cgrb.oregonstate.edu/ denvedee@cgrb.oregonstate.edu

Oxford Vietnam EvolutionEpidemiology ZoonoticPathogens

The Oxford University Clinical Research Unit in Vietnam —

The Oxford University Clinical Research Unit (OUCRU) in Ho Chi Minh CIty, Vietnam aims to have a positive and significant impact on global health and, in particular, the prevention, diagnosis and treatment of infectious diseases. This is achieved through an integrated, long-term clinical and laboratory research programme, including capacity building and training in Vietnam and other countries in the region. The programme is currently implemented by a dedicated team of 200 scientists, technical and administrative staff in Vietnam and other countries in Asia. The research programme focuses on clinical trials, central nervous system infections, dengue fever, enterics, malaria, respiratory infections, tuberculosis and zoonoses with units in Vietnam, Indonesia, China and Nepal. In Ho Chi Minh City, OUCRU operates from within the Hospital of Tropical Diseases and comprises state-of-the-art laboratory facilities, including a containment suite for BSL3 microbiology and virology, and Special Animal Pathogen Operations level 4 (SAPO4).

For more information please visit: www.oucru.org Post Description —

OUCRU has an ongoing collaboration with the Academic Medical Centre of the University of Amsterdam, the Netherlands and this post has been created by a collaborative project on antimicrobial resistance in agriculture and its potential effects on humans. The project is funded by ZoNMW/WOTRO (the Netherlands), however, the post holder is also expected to participate more broadly in the diverse research activities of OUCRU.

The successful candidate will be an independent postdoctoral researcher who will help OUCRU develop new research initiatives on zoonotic diseases and the animal-human interface. Initial responsibilities will be to oversee and coordinate a project on antimicrobial drug resistance and antibiotic usage in small scale poultry production units in southern Vietnam, with specific focus on antibiotic resistant non-typhi Salmonella and E. coli in poultry and humans.

Responsibilities and Duties — Post holder will report to Dr Juliet Bryant (jbryant@oucru.org), head of zoonosis research at OUCRU.

Duties will include:

1. oversee and coordinate implementation of the Antimicrobial Resistance (AMR) project research; 2. supervise a PhD student and Research Assistant for project-related activities; 3. manage project activities including animal and human sampling, and laboratory analyses; 4. coordinate and support surveys among farmers and veterinary drug sellers; 4. coordinate data management and supervise data analysis; 5. contribute to the publication of research findings in high quality journals 6. ensure optimal communication between research partners collaborating in the project

Selection Criteria — We are seeking a highly motivated and independent researcher with commitment to working on zoonotic and animal diseases, particularly those impacting food animal production.

Essential

1. A PhD and substantial research experience in one of the following areas: epidemiology, applied microbiology or microbial ecology, animal science, virology, vaccinology, mathematical modeling, or evolutionary biology 2. A strong publication record with documented examples of work at the level of first author in a leading refereed journal 3. Ability to work effectively independently, as part of a team and in a multicultural environment 4. Proven interest in agriculture sciences, veterinary epidemiology and/or zoonotic diseases 5. Experience conducting research on infectious diseases 6. Ability to manage the day-to-day running of a research project including assisting and guiding the work of junior researchers and PhD students 6. Proven communication skills including the ability to present work at international symposia and to a non-specialist audience

Desirable

7. Previous experience conducting research in an international environment, preferably in Asia or in developing countries; 8. Experience working in an infectious diseases diagnostic or research laboratory 9. Experience contributing to the development of new research projects and/or areas of research 10. Fieldwork work experience, particularly in surveillance or outbreak response

Salary — University of Oxford (UK) grade 7, 29,099 - 35,788 GBP per annum, depending on experience.

Duration — Three years.

Contact — Dr Juliet Bryant, jbryant@oucru.org mboni@oucru.org

StAndrews PredictingEnzymeFunction

Postdoctoral Research Fellow: Machine Learning Approaches to Predict Enzyme Function

£29,972 pa

http://www.jobs.ac.uk/job/ACI857/research-fellow-in-chemistry/ This project is being undertaken by Dr John Mitchell's research group in the modern Biomedical Sciences Research Complex. This computational project is sponsored by the Biotechnology and Biological Sciences Research Council (BBSRC). In this work, we will use machine learning methods to predict the catalytic functions and chemical mechanisms of enzymes. The key idea in our work is to identify the reaction mechanism, if any, catalysed enzymatically by a protein structure. The possible reaction mechanisms considered are the 300 or so distinct entries in our database MACiE. Our principal machine learning method is Random Forest, simply a forest made out of many different randomly created decision trees. After predicting the reaction mechanisms, we will apply chemoinformatics, docking and virtual screening to suggest substrates for the enzyme reactions identified.

We seek to appoint a highly computer literate postdoctoral scientist with a PhD in the Life, Chemical, Physical, Computer or Mathematical Sciences. Knowledge of, and experience in, at least one of the following areas is required for this position: bioinformatics, chemoinformatics, machine learning, computational chemistry, biological or pharmaceutical chemistry. A high level of computer literacy is expected and experience of scientific computing, preferably including some programming skills, would be an advantage. The position is available for three years from 1 June 2011, or as soon as possible thereafter.

Informal enquiries to Dr John Mitchell, jbom@st-andrews.ac.uk

Closing Date: 11 April 2011 Interview Date: Week commencing 25 April 2011

Please apply online at https://www.vacancies.st-andrews.ac.uk/welcome.aspx Please quote ref: JC7960

– Dr John Mitchell Biomolecular Sciences University of St Andrews North Haugh St Andrews Scotland KY16 9ST United Kingdom +44-(0)1334-467259

jbom@st-andrews.ac.uk

StAndrews SexualSelection

The evolution of gene expression in response to sexual selection.

A three year postdoctoral research assistant position is available to work with Mike Ritchie at the University of St Andrews (Scotland) on a NERC-funded research project, collaborative with Rhonda Snook of the University of Sheffield and Andy Cossin at the University of Liverpool. The project involves next-generation sequencing approaches to examine the evolution of fly populations under experimentally manipulated sexual selection regimes.

The candidate needs to have a PhD in a relevant subject, Evolutionary Biology or Genetics. Experience with basic molecular genetics is essential and with Drosophila and/or bioinformatics desirable. The candidate will co-ordinate this collaborative research project and take the lead in data collection, collation and analysis, in collaboration with researchers or technicians in the other laboratories.

Duration: 36 months. Start Date: 1st June 2011 or by negotiation. Appointment subject to UK work permit requirements.

Informal enquiries can be made to Mike at mgr@st-andrews.ac.uk http://biology.st-andrews.ac.uk/ritchielab/ Further details and the application materials are available at: https://www.vacancies.st-andrews.ac.uk/welcome.aspx , Ref No. JC7978

Clunky direct link: https://www.vacancies.st-andrews.ac.uk/ViewVacancy.aspx?enc=mEgrBL4XQK0+ld8aNkwYmAnOqoJIvp8sIBBYfSiya9JEHSlD3mAa NOTE THAT ALL APPLICATIONS MUST BE MADE THROUGH THE OFFICIAL UNIVERSITY CHANNELS, NOT TO MIKE RITCHIE.

Mike Ritchie Acting Head School of Biology Dyers Brae House University of St Andrews St Andrews, Fife Scotland KY16 9TH

Phone: 0 (44 outside UK) 1334 463495 Fax: 0 (44 outside UK) 1334 463366

Websites: http://biology.st-andrews.ac.uk/ritchielab/ http://biology.st-and.ac.uk/supplemental/ritchie/papers.aspx Michael Ritchie <mgr@st-andrews.ac.uk>

StanfordU EvolutionaryGenomics

Stanford University, Evolutionary genomics

A postdoctoral position is available in the lab of Hunter Fraser. The lab will combine experimental and computational approaches to studying the evolution of gene expression within and between species. Our long-term goals are to better understand 1) how new mutations affect gene expression; 2) what selective pressures act on these mutations; and 3) how changes in gene expression contribute to the evolution of other phenotypes. The project details are flexible, but may focus on analyzing genome-wide gene expression (RNA-seq) data from multiple species. Preference will be given to candidates with a strong background in computational biology, molecular evolution, and statistics. ÂFamiliarity with analysis of high-throughput sequencing data or quantitative/statistical genetics is a plus.

Stanford is an extremely stimulating environment, with many labs engaged in research on evolution and genomics. There is plenty of opportunity to interact with other labs, for example in the weekly evolutionary genomics joint lab meeting that includes labs from several departments. To apply, please email a CV, brief description of research experience and interests, and contact information for at least two references to hbfraser[at]stanford.edu. The position can begin immediately. ÂSalary and benefits are very competitive. For further information please see the labâs website, http://www.stanford.edu/Ëhbfraser/ . Hunter Fraser Assistant Professor Department of Biology Stanford University Stanford, CA hbfraser[at]stanford.edu

Hunter Fraser <hbfraser@stanford.edu>

Stuttgart CropPlant PopGenet

The research group âCrop Biodiversity and Breeding Informaticsâ invites applications for the position of a

RESEARCH ASSOCIATE (Senior Postdoc)

We are looking for a highly motivated scientist who wants to develop his or her independent research program in population or quantitative genetics of crop plants and their wild ancestors. We are particulary interested in a scientist with an interest in exploring new approaches to investigate genetic and phenotypic diversity in crop plant domestication and adaptation, and to utilize this diversity in breeding methods such as genomic selection.

Candidates with a Ph. D. degree and possibly some post doc experience in plant breeding, bioinformatics, population genetics, quantitative genetics or evolutionary biology are welcome to apply. Background knowledge in computer programming and statistical analysis are required. Previous experience with modern genomics is highly advantageous. We expect candidates to have a record of publications and to be willing to attract their own funding from national and international sources.

The successful applicant will be initially appointed for three years with the possibility of extension for another three years. The starting date can be as early as 1 June 2011. Salary will be according to the German government salary scale (TV-L E13) and depends on previous experience, age and marital status. The position involves 4 hours of teaching during the semester (entirely in English), and the supervision of Ph.D., graduate and undergraduate students. There is the possibility to obtain the Habilitation. The University of Hohenheim is an equal opportunity employer. Women and members of minority groups are strongly encouraged to apply.

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. Our research group is member of the Hohenheim Competence Center of Plant Breeding with a critical mass of researchers working on European and tropical crops, which provides ample opportunities for collaboration. Further information 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 18 April 2011 as a single PDF document to Bärbel Hessenauer (baerbel.hessenauer@uni-hohenheim.de).

Dr. Karl Schmid Professor of Crop Biodiversity and Breeding Informatics 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.schmid@uni-hohenheim.de>

UAlberta BeetlePopulationGenomics

Post-Doctoral Position: Population Genomics of the Mountain Pine Beetle System

Department of Biological Sciences - University of Alberta

Position duration - until September 30, 2012

Closing date - open until filled

The Department of Biological Sciences has an opening for a Post Doctoral Fellow in the area of Population Genomics. You will become an integral member of a fast moving, multidisciplinary team researching the Mountain Pine Beetle (MPB) infestation in Western Canada. This research will be conducted in the laboratory of Dr. Felix Sperling and will involve collaboration with other project researchers.

The main focus of the project will be to detect possible signatures of genetic selection by analysis of a large single nucleotide polymorphism (SNP) dataset generated for mountain pine beetles collected in different localities of the leading edge of the current outbreak. Similar data are being generated for the pine host and fungal associates of mountain pine beetle, and the candidate may have the opportunity to be part of the team that examines relationships between the three datasets.

The successful candidate will possess a doctoral degree in population genetics, quantitative genetics, molecular biology, bioinformatics, or a closely related field. Knowledge and experience in single nucleotide polymorphisms (SNPs), manipulation of large datasets, association and QTL analyses, and statistics (particularly spatial analyses) is preferred. Related experience with programming language (i.e. Ruby, Perl, Python, Java), insects and/or plants would be useful. You will be responsible for:

1) Association analysis of mountain pine beetle and potentially of interacting biological organisms using identified SNPs;

2) Preparation of manuscripts on this research.

Interested individuals should submit an application package (cover letter and curriculum vitae) and arrange to have three sealed letters of reference forwarded to the address below. In accordance with University of Alberta Policy, applicants should have no more than three years' post doctoral experience. Salary is commensurate with experience. Electronic applications are preferred.

Matt Bryman - Project Manager

The Tria Project: Genomics enhanced forecasting of lignocellulose feedstock for bioenergy

CW 405 Biological Sciences Building

University of Alberta

Edmonton, AB T6G 2E9

Email: mbryman@ualberta.ca

We thank all applicants for their time and effort, but only those selected for an interview will be contacted.

Additional Information

Dr. Felix Sperling is a Professor in the Department of Biological Sciences and specializes in population genetic surveys, species delimitation and related analyses in insects, including bark beetles. (http://www.biology.ualberta.ca/faculty/felix_sperling/)

Department of Biological Sciences - http://www.biology.ualberta.ca Tria Project website: http://www.thetriaproject.ca

Postdoctoral Fellows Office - http://www.postdoc.ualberta.ca Matt Bryman

Project Manager

THE TRIA PROJECT: Mountain Pine Beetle System Genomics

< http://www.thetriaproject.ca/ >

Phone: 780-492-1990

mbryman@ualberta.ca

UArizona EvolutionaryPhysiology

A postdoctoral position in ecological and evolutionary physiology is available to study the individual-level physiological tradeoffs between flight and fecundity in the hawkmoth Manduca sexta. The study combines field, greenhouse and lab experiments with state of the art flow-through respirometry, carbon stable isotope techniques, flight energetics and micro-surgery.

The postdoc is available for three years with a negotiable start date of April 2011. Starting salary $34,000 USD.

Minimal requirements: PhD in physiology, ecology or evolutionary biology (or related fields), competitive publication record, extensive experience in insect physiology and respirometry, strong statistical ability.

Applications should be submitted through the University Human Resources at the URL: https://www.uacareertrack.com/applicants/jsp/shared/frameset/Frameset.jsp?time=1300730416326and enter job # 46789. Applicants should also send an email directly to goggy@email.arizona.edu

For more information please contact Goggy Davidowitz at: goggy@email.arizona.edu Goggy Davidowitz, Department of Entomology, University of Arizona

Goggy Davidowitz Assistant Professor Department of Entomology University of Arizona

"Davidowitz, Goggy - (goggy)" <goggy@email.arizona.edu>

UCaliforniaRiverside SilkEvolution

UCaliforniaRiverside_SilkEvolution

A postdoctoral opportunity is available to work on the evolution of spider silk. A broad range of projects can be pursued at or across the level of genes, proteins, organisms, and phylogeny. The ideal candidate will have expertise and strong interests in one or more of these areas: molecular evolution, functional genomics, biomechanics, bioinformatics, arachnology. A PhD is required and initial appointment is for one-year. To apply, email (to cheryl.hayashi@ucr.edu) your CV, statement of research interests and experience, representative reprints, and contact information for three referees. Review of applications will begin promptly and continue until the position has been filled.

Sincerely, Cheryl Y. Hayashi Professor of Biology University of California, Riverside

cheryl.hayashi@ucr.edu

UEdinburgh Cooperation and Virulence

Postdoctoral Research Fellow (2yrs funding)

*Ecological and evolutionary dynamics of microbial cooperation and communication * A postdoc position is available in Sam Brown's lab at the University of Edinburgh. The specific project is flexible, but will involve the study of microbial social dynamics on both ecological and evolutionary timescales, with a focus on quorum sensing and/or QS regulated traits.

Current research in the lab combines theoretical, computational and experimental approaches to the study of microbial social evolution, and consequent virulence. Key themes include the interface of microbial sociality with (1) molecular dynamics (Kummerli & Brown 2010), (2) multi-trait interactions (Brown & Taylor 2010), (3) multi-species interactions (Lysenko et al. 2010), (4) mobile genetic elements (Nogueria et al. 2009) and (5) novel therapies (Brown et al. 2009).

Preference will be given to applicants with a background in microbial experimental evolution and/or molecular microbiology. Start date no later than October 2011. Informal enquiries can be made to Sam Brown (sam.brown@ed.ac.uk). Application details are available via http://www.jobs.ed.ac.uk/vacancies/index.cfm?fuseaction=vacancies.detail&vacancy_ref=3014102 Applicants must have, or shortly obtain a PhD.

Sam Brown *new address* Centre for Immunity, Infection and Evolution University of Edinburgh West Mains Road, Edinburgh EH9 3JT http://ciie.bio.ed.ac.uk/ www.zoo.ox.ac.uk/staff/academics/brown_s.htm sam.brown@ed.ac.uk

sampaulbrown@gmail.com

UExeter 2 EvolutionaryRobustness

Two Postdoctoral Researcher Positions on Deciphering and Applying Evolutionary Design Principles Underlying Robustness

These posts, available immediately, will be part of a multidisciplinary project led by Dr. Orkun S. Soyer, Dr. Ozgur Akman and Prof. Declan Bates. The successful applicant will contribute towards research related to the project entitled "Evolving controllers and controlling evolution" and funded by the EPSRC.

In this project, we will combine tools and ideas from the fields of control theory and evolutionary theory to study specific molecular systems in order to derive evolutionary design principles underlying their robustness. In particular, we are interested in understanding which evolutionary conditions can result in the emergence of robustness in these systems and through what kinds of molecular or network-level mechanisms it is underpinned. We will then combine this evolutionary insight with in silico evolution approaches to design robust synthetic systems and engineering applications, in particular in aerospace control engineering.

For further information and application details, please see the online ad at: https://jobs.exeter.ac.uk/hrpr_webrecruitment/wrd/run/ETREC107GF.open?VACANCY_ID=1971873ZNQ&WVID=3817591jNg&LANG=USA
To apply please send your application CV, covering letter and the details of three referees to Dr Orkun S. Soyer at O.S.Soyer@exeter.ac.uk quoting the reference number N3289 in any correspondence.

best regards, orkun soyer.

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

UGeorgia InvasiveSpecies

UNIVERSITY OF GEORGIA DEPARTMENT OF GENETICS

POSTDOCTORAL POSITION IN INVASIVE SPECIES PHYLOGEOGRAPHY

A postdoctoral position is available in my lab. Although I am particularly interested in an individual with skills in phylogeography, I would also consider an individual more broadly interested in the ecological genetics of invasive species (see http://www.genetics.uga.edu/mauriciolab/ and http://www.genetics.uga.edu/pire/ for more details). I am interested in hiring someone with some background in evolutionary or ecological genetics and with good bench skills. The ideal candidate will be organized, pay close attention to detail, and be able to work both independently and in collaboration with others. In particular, the candidate may work closely with Dr. Travis Glenn on next-gen approaches. Independent side projects on the part of the postdoc are encouraged and will be supported intellectually and financially if feasible. A Ph.D. is required.

There also may be an opportunity for this postdoc to gain independent teaching experience (for extra pay) by teaching a small, 1-credit, discussion section for our undergraduate evolutionary biology course each semester.

The start date is late summer/early fall 2011, although there is some flexibility in start dates. The initial appointment is for one year, with an additional year of funding available conditional on satisfactory performance. The annual salary for this position will be commensurate with experience, and includes benefits. The University of Georgia is an Equal Opportunity Employer and I encourage applications from candidates from groups underrepresented in the life sciences.

Please send me an e-mail (mauricio@uga.edu) with the following information: a statement detailing your interest and qualifications for the position, a CV, and the names and contact information for 2 people who could write on your behalf.

Rodney Mauricio Department of Genetics University of Georgia Athens, GA 30602-7223

mauricio@uga.edu

UGuelph Biomonitoring Postdoc GraduateStud

Project Manager, Postdoc and Graduate Student positions available at Biodiversity Institute of Ontario, University of Guelph

Biodiversity Institute of Ontario based at University of Guelph, Canada, is leading a large-scale project in the use of Next Generation Sequencing for biodiversity analysis from various environmental samples. We are currently seeking applications for various positions:

1. Project Manager (based at University of Guelph, Ontario), starting May-June 2011. Qualifications: MSc or PhD in biology (or computer science), minimum

2 years of experience in large-scale project management and budgeting (accounting), articulate and well-organized. Being computer/web savvy is an asset as the project manager will be in charge of updating the project website. We would also consider exceptional candidates who would like to pursue an alternative career path in science management after their PhD/postdoc. Duration: 3 years (initial contract for one year).

2. Postdoctoral Fellow (based at University of Guelph, Ontario, Hajibabaei group), starting July-September 2011. PhD in molecular evolution, phylogenetics, molecular ecology, population genetics, bioinformatics or related fields. Excellent theoretical knowledge and experience in comparative sequence data analysis for biodiversity, evolutionary or ecological analysis, preferably using NGS data. Experience in using Linux and Python (or similar scripting languages) and knowledge of R would be desirable. Duration: 3 years (initial contract for one year).

3. GIS Software Developer (based at Dalhousie University, Halifax, Nova Scotia, Beiko group), starting May-June 2011. BSc or MSc in Computer Science, Bioinformatics or a related field. The scope of the project would also permit an applicant with a PhD to carry out research in the context of a postdoctoral position. Must be proficient in Python and C++, and ideally experienced in OpenGL and graphical software development. Experience with previous development projects is essential. Duration: 3 years (initial contract for one year).

4. Postdoctoral Fellow (based at University of Guelph, Ontario, Hajibabaei group), starting June-Sept, 2011. PhD in biological sciences preferably in molecular ecology, phylogenetics or related fields with expertise in molecular method development/optimization. Experience in soil biodiversity/ecology is highly desirable. Duration: 2 years (initial contract for one year).

5. Graduate Student positions (MSc/PhD, 3 positions) based at University of Guelph, Department of Integrative Biology (2 positions) and Dalhousie University, Department of Biology (1 position). These positions involve the use of NGS data to address evolutionary and ecological questions in arthropod, plant and soil biodiversity. Graduate students will be supervised jointly by members of Biomonitoring 2.0 project and will gain insights in using NGS genomics approaches as well as bioinformatics tools to develop and explore their own hypotheses in ecology and evolutionary biology.

6. MSc Student position at the University of New Brunswick, Canadian Rivers Institute / Aurora Research Institute. This position will examine the use and application of Biomonitoring 2.0 techniques by local communities in Canada's North.

For each position, please submit your CV (including names and contact information of 3 references) and a cover letter to Dr. Mehrdad Hajibabaei (mhajibab@uoguelph.ca). Please indicate the title of the position you are applying for in the subject line of your email. We will start reviewing the applications on April 15, 2011.

Mehrdad Hajibabaei, PhD Assistant Professor Biodiversity Institute of Ontario & Integrative Biology University of Guelph Guelph, ON N1G 2W1 Canada Phone: 519-824-4120 x52487 Fax: 519-824-5703 Email: mhajibab@uoguelph.ca www.ibarcode.org/-hajibabaei www.biodiversity.ca www.dnabarcoding.ca < http://www.dnabarcoding.ca/ >

Mehrdad Hajibabaei <mhajibab@uoguelph.ca>

ULaRochelle BivalveAdaptation

Post-doctoral Fellow

Laboratoire Â« Littoral, Environnement et SociÃ©tÃ©s Â», CNRS â ULR UMR 6250, Ã©quipe AMARE

UniversitÃ© de La Rochelle

Contact : Prof Pascale Garcia (CNRS â ULR UMR 6250, pgarciam@univ-lr.fr)

The genetic basis and history of adaptive differentiation in Macoma balthica, a high gene flow marine bivalve species

Keywords: Marine Genomics - Demographic Patterns - Adaptive differentiation.

The laboratory Â« Littoral, Environment and Societies Â» at the University of La Rochelle seeks a motivated and productive postdoctoral researcher to work on the genetic basis of adaptive differentiation in marine bivalves. LIENSs is a Research Unit (CNRS / University of La Rochelle), which includes expertise in various scientific fields including environmental sciences (biology, ecology, geophysics), humanities (geography), chemistry and biotechnology. Our primary object of study is the littoral. It includes some sixty teachers and researchers, twenty administrative and technical staff, and almost sixty doctoral students under the Research Training. The scientific activities of the unit receive significant support from Europe through programs and research funding ERDF (European Regional Development Fund). The impact of global change on ecosystems is one of the key focus areas of our research. This focus area includes research into the adaptive differentiation of marine animals.

The originality of marine population genetics is to manipulate extreme values of demographic parameters: high fecundity, huge population sizes and long distance dispersal via a planktonic larval stage. Correlatively, exceptionally high genetic diversity and low geographic differentiation are observed in many marine species. Local adaptation should be more costly for marine than for terrestrial species because larval movements exceed in scale the grain of habitat heterogeneity. Paradoxically, marine animals have proven able to pay the cost of local adaptation. We propose two hypotheses to resolve this old paradox of local adaptation in the sea: (i) A long history of non-equilibrium conditions (colonization, range expansion, fragmentation) has a bearing on the existence and maintenance of environmental adaptation. (ii) Marine species are routinely structured into hidden differentiated endogenous backgrounds, so-called genetic barriers, which secondarily came to coincide with environmental transitions.

The aim of this project is to take advantage of these recent advances in marine genomics to identify genomic regions influenced by selection. The genetic basis and history of adaptive differentiation in marine conditions will be studied experimentally by population genomics approaches (âgenome scanâ) in a marine bivalve species, Macoma balthica. A high-throughput 454 pyrosequencing has been performed on M. balthica and 14,000 SNPs are yet available.

(i) SNPs with a high differentiation in the sequencing of 454 samples will be selected.

(ii) Using the SNPs selected, a genome scan of differentiation will be performed at different spatial and temporal scales:

Â meso-scale analyses will be carried out among regions to analyze adaptation during range expansion (introduction point vs. peripheral populations at the margin)

Â macro-scale studies will analyze adaptive differentiation during colonization process and adaptive differentiation and introgression between well-recognized differentiated genomes (e.g. sub- or cryptic species).

The position requires an individual with a PhD and experience in population genetics and evolutionary biology. Outstanding molecular, genomics and computational skills are particularly advantageous.

This project is part of a program funded by the ANR (Hi-Flo: Genetic BASIS and history of adaptive differentiation in high gene flow marine species). Funding is available for a 12-month position, for a minimum of 1 year.

Thanks very much for your help Pascale Garcia

Pascale Garcia <pgarciam@univ-lr.fr>

ULeicester ModellingMigration

Two postdoctoral research associate positions (up to 4 yrs funding)

The Impact of Diasporas on the Making of Britain Funded by the Leverhulme Trust

Two postdoc positions are available at the University of Leicester as part of a major multi-disciplinary research programme funded by the Leverhulme Trust: The Impact of Diasporas on the Making of Britain. The research associates will work on one of two interdisciplinary projects: 1) Modeling migration 2) Genetics and early British population history. Both projects are linked with Professor Mark Jobling's lab in the Department of Genetics at the University of Leicester.

Modeling migration

This project will use computer simulations in a geographically-explicit framework to model processes of genetic change in populations in Britain over historical time (i.e. Late Iron Age to the present). A possible approach is the simulation of patterns of genetic diversity (initially focusing on uniparentally inherited Y-chromosomal and mitochondrial DNA [mtDNA] markers) within modern British populations and multiple source populations for putative migrations, using coalescent methods. Different sets of starting conditions, population growth parameters, sex-specific processes, migration rates and modes could be explored, informed by historical, archaeological, onomastic and linguistic data, to address compatibility with defined hypotheses. Approximate Bayesian computation (ABC) simulations could be used to choose the best-fitting models of population history, and to estimate demographic parameters.

Genetics and early British population history

This project will seek novel molecular markers for historical population analysis in regions of the British Isles. Sources such as the 1000 Genomes Project, the

Cancer Genome Project and UK10K can be mined for new Y-SNPs, accumulating whole mtDNA sequence data and genome-wide SNP data can be evaluated, and the informativeness of autosomal and X-chromosomal haplotype blocks containing SNPs and STRs can be investigated. The project will also compile and evaluate extant and emerging population genetic data sets as tools to investigate specific questions relevant to the overall programme. These could include forensic databases and growing British and European datasets held at Leicester. Other rich sources of emerging data will be the People of the British Isles Project (www.peopleofthebritishisles.org), the Genographic Project (www.genographic.nationalgeographic.com), and geographically-linked genome-wide SNP data from the new high-throughput studies aiming to characterise genes involved in common disease.

The website for the programme is www.le.ac.uk/-diasporas. Informal enquiries can be made to Dr Turi King (diasporas@le.ac.uk) Application details are available via the University of Leicester job pages www.le.ac.uk/joinus The references number for both jobs is AHL00103. Closing date for applications is May 3rd, 2011.

tek2@leicester.ac.uk

UManchester ComputationalAnalysis DrugResistance

Post Doctoral Research Associate - Computational analysis of HIV-1 drug resistance Computational and Evolutionary Biology, Faculty of Life Sciences, The Univ. of Manchester

Closing date: 21/04/2011; Reference: LS/11949

Applications are invited for a 12 month postdoctoral position in the research group of Dr David Robertson (http://www.bioinf.manchester.ac.uk/robertson) at the University of Manchester. The objective of the project will be to investigate the evolution and emergence of resistance to drugs that bind the CCR5 receptor used by HIV-1 to enter cells. The overall aim is to improve prediction of HIV-1 drug resistance. The research will be computer-based and is funded by the MRC as part of an academia- industry partner scheme.

You should have (or expect to hold) a relevant PhD. Experience of bioinformatics and/or computational biology research is required and experience in molecular evolution, phylogenetics and/or protein structure analysis an advantage.

Salary: £29,099 p.a.; informal enquiries: Dr David Robertson, email: david.robertson@manchester.ac.uk .

See http://www.manchester.ac.uk/aboutus/jobs/-vacancies/research/ for further details including a link to an application form (search for ref LS/11949).

– David L. Robertson, PhD Michael Smith Blding, Faculty of Life Sciences, Univ. of Manchester. Tel:+44 (0)161 275 5089, http://www.manchester.ac.uk/ceb david.robertson@manchester.ac.uk

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UMass Boston EvolutionaryBiol

Postdoctoral Researcher Professional Staff one year Trust funded Benefitted appointment Start date: August 2011

The Department of Biology seeks applicants interested in obtaining postdoctoral research experience in evolutionary ecology of lizards and/or computational methods in evolutionary biology (particularly phylogenetic methods). The candidate will assist the lab PI (Revell) in new and ongoing research projects in the lab. Depending on his or her prior experience and interests, the researcher may also be asked to help organize and participate in field research expeditions and/or assist in running and maintaining the lab. Duties will depend on the researcher's interests and prior experience and may include programming in R or C languages; conducting and supervising basic molecular and morphological lab work; organizing and leading field expeditions to tropical locales; handling and working with live animals (lizards). Applicants must hold a Ph.D degree or must expect to earn one before August 2011. A detailed description of Dr. Revell's research is available on his lab webpage: http://faculty.umb.edu/liam.revell/ .Interested individuals should send a cover letter, a curriculum vitae, and a two letters of recommendation, along with a maximum two page statement of research experience and interest. The material can be submitted electronically to the liam.revell@umb.edu (preferably as a single PDF file) or by mail Dr. Liam Revell, Biology Department, University of Massachusetts Boston, 100 Morrissey Blvd, Boston MA 02125.

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

– Liam J. Revell University of Massachusetts Boston web: http://faculty.umb.edu/liam.revell/ email: liam.revell@umb.edu blog: http://phytools.blogspot.com Liam.Revell@umb.edu

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UNewHampshire MicrobialEvolutionaryGenomics

Vaughn Cooper's laboratory at the University of New Hampshire (http://cooperlab.wikidot.com) seeks a motivated and productive postdoctoral researcher to work on NSF-funded research to quantify the distribution of effects of adaptive mutations in bacterial populations. Major interests of the laboratory are 1) adaptation in biofilms 2) how adaptive alleles interact with their genomic and external environments 3) bacterial adaptation to novel hosts 4) the ecology and population structure of potentially pathogenic bacteria and 5) how genome organization influences evolutionary rates.

The funded project is studying the distribution of pleiotropic effects among various collections of beneficial alleles, employing experimental evolution, various physiological assays and genome resequencing to link mutations to their functional consequences.As such, the position requires an individual with a PhD and experience in microbiology, evolutionary biology, ecology, physiology, or related fields. Outstanding molecular, quantitative, or computational skills are particularly advantageous.

Additional opportunities exist for individuals interested in developing their skills in teaching, mentorship, and outreach as portions of this research will be conducted in the classrooms of partner secondary schools.

Funding is available for a 12-month position, for a minimum of 1 year, and may be extended upon mutual agreement. Preference will be given to candidates with a high probability of applying for (with the help of the PI) and obtaining independent funding. There will be ample opportunity for the candidate to pursue his or her own research program within the context of the grant proposal, and in collaboration with the PI and other colleagues.

The starting date can be immediate, and the position will remain open until filled. For primary consideration, applicants should apply by May 1, 2011. Informal inquiries are welcomed prior to formal application.

To receive full consideration, please attach the following documents to the online employment site:

1. A curriculum vitae 2. Names of three references willing to provide a letter of recommendation upon request 3. A brief statement of how your research goals relate to those of the lab. 4. A brief statement of interest, ideas, and qualifications for independent fellowship and/or grant applications.

For a more comprehensive job description or to apply, visit https://jobs.usnh.edu Computer access/assistance is available at the Human Resources Office, 2 Leavitt Lane, Durham, NH 03824 or call 603-862-0501 (TTY Users 603-862-3227).

/UNH is an AA/EEOEmployer. UNH is committed to excellence through the diversity of its faculty and staff and encourages women and minorities to apply./

vscooper@gmail.com

UOslo ComputationalBiology

Centre for Ecological and Evolutionary Synthesis (CEES), Department of Biology Renewed announcement - Postdoctoral Research Fellow in computational biology - (2010/2225)

CEES is a well-funded Centre of Excellence for integrative biological research. It provides a stimulating research environment, situated at the Department of Biology, with many young international and Norwegian scientists working on a variety of theoretical and empirical topics within ecology, evolution, population genetics, genomics, phylogenetics, molecular biology, and biostatistical methodology. Research themes of particular importance to the centre are specifically addressed in a sequence of 4 partly overlapping interdisciplinary research colloquia, each lasting 3 years. The announced postdoc position belongs to Colloquium 2. It brings together a highly interdisciplinary team that aims to address key topics in ecology and evolutionary biology that currently suffer from the conceptual and methodological gap that exists between classical ecological and evolutionary research on one side, and molecular genetics, genomics and systems biology on the other side. CEES is chaired by Professor Nils Chr. Stenseth and currently employs 20 faculty members, 40 postdocs/researchers, 35 PhD students and 36 MSc students. Information about the centre can be found at: http://www.cees.uio.no . The fellowship period is 2 years. Starting date: August 1, 2011.

Job description: The postdoctoral fellow will be part of a Colloquium 2 project having as its major goal to provide the foundation for a long-term theoretical-experimental research programme addressing the phenomenon of epigenetic inheritance (transgenerational phenotypic plasticity) in a truly integrative way; bridging the mechanistic, ecological and evolutionary explanatory domains attached to the phenomenon. As epigenetic inheritance is a complex multiscale systemic phenomenon, we intend to start out with building a portfolio of pioneering mathematical models linking proximate and ultimate causation. The postdoctoral fellow is expected to play a key role in the conceptualization as well as analyses of these models in close interaction with an interdisciplinary research team consisting of both theoretical and experimental biologists. The fellowship period is 2 years.

Within the framework of the position, duties may be assigned. There will also be openings for being involved in other Colloquium 2 activities when this is found to benefit the overall scientific output.

Requirements: Applicants must hold a PhD-degree (or equivalent) and have solid experience in computational biology. Experience with modelling of chromatin dynamics and/or signal transduction and/or gene regulation will be a strong advantage. Furthermore, experience from collaboration with experimentally inclined biologists will be considered an asset. We seek a highly motivated and skilled person, who is eager to both gain and share insight while being continuously focused on publishing papers in leading, international journals.

A good command of English is required. http://www.matnat.uio.no/english/research/education/proficiency_in_English.html The main purpose of post-doctoral research fellowships is to qualify researchers for work in top academic positions within their disciplines. No one can be appointed for more than one period at the same institution.

Please also refer to the regulations pertaining to the conditions of employment for postdoctoral fellowship positions: http://www.uio.no/admhb/reglhb/personal/tilsettingvitenskapelig/regulationstermcondition.xml Salary: Postdoctoral Research Fellow (SKO, 1352), pay grade: 57 â 64 (NOK 448 200â510 000 depending on qualifications and seniority).

The application must include: â Application letter including a statement of interest, summarizing the applicant's scientific work and interests and describing how she/he fits the description of the person we seek â CV (summarizing education, positions, pedagogical experience, administrative experience and other qualifying activity), including a list of published and unpublished works â Copies of educational certificates, transcript of records, letters of recommendation â A complete list of publications and up to 5 academic work that applicant wishes to be considered by the evaluation committee â Names and contact details of 2-3 references (name, relation to candidate, e-mail and telephone number)

Foreign applicants are advised to attach an explanation of their University's grading system. Please remember that all documents should be in English or a Scandinavian language.

To apply for the position:

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

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USheffield 2 EvolutionBehaviour

I have a couple of postdoc positions open on human behavioural ecology at the University of Sheffield, and because I am hoping to find candidates with a degree on evolutionary biology and strong background on e.g. quantitative genetics.

Two postdoc positions on human behavioural ecology at the Department of Animal and Plant Sciences, University of Sheffield

We are looking for two post-doctoral research associates to work at the interface between evolutionary biology, epidemiology, demography and anthropology on the genetic, ecological and demographic factors influencing life-history patterns and senescence rate in humans. The overall aim of the project is to understand the evolutionary ecology of human reproductive behavior across the large demographic and social changes occurring during the past 200 years, and how natural selection has affected human populations at different periods. The post-holder will be in charge of managing and analysing a large pedigree database on the demography of historical Finnish families spanning the time since early 1700s until the end of 1900s. More information about the research group is available at http://www.huli.group.shef.ac.uk/. The successful candidate will have a PhD in evolutionary biology or related topic and a good track record of publishing in leading specialist or multidisciplinary journals. Strong statistical skills are essential. The post is fixed-term with a start date of 1st April 2011 (or as soon as possible thereafter) and an end date of 31st March 2013 with a possibility of an extension subject to funding. The work will be performed at the Department of Animal and Plant Sciences, University of Sheffield - one of the largest departments in the UK devoted to the study of whole organism biology. We are ranked joint 3rd in the UK for biology research and 70% of our research activity has been judged to be "world-leading" or internationally excellent (RAE 2008). The position is funded by the European Research Council (ERC). Closing date: 14.3. 2011.

For all on-line application system queries and support, contact: e-Recruitment@sheffield.ac.uk

For informal enquiries about this job and department, contact: Dr Virpi Lummaa v.lummaa@sheffield.ac.uk or +44 (0)114 2220051

– Dr. Virpi Lummaa Department of Animal and Plant Sciences University of Sheffield Western Bank, Sheffield S10 2TN United Kingdom

tel. +44 (0)114 222 0051 fax. +44 (0)114 222 0002 email. v.lummaa@sheffield.ac.uk http://www.huli.group.shef.ac.uk/ http://www.shef.ac.uk/aps/staff/acadstaff/lummaa.html Virpi Lummaa <V.Lummaa@sheffield.ac.uk>

USheffield EvolutionaryGenetics

There is a Postdoctoral Research Associate position available at the University of Sheffield, Department of Animal and Plant Sciences to work with Dr. Rhonda Snook, Prof. Roger Butlin, and Prof. Kevin Gaston on landscape genomics, adaptation and climate change.

The postdoc will be responsible for coordinating the collection of samples of caged populations of Drosophila subobscura across 6 latitudinal sites in Europe, working in close collaboration with Project Partners at each site. Samples will subsequently be analysed for high throughput sequence and expression data. The central aim of the project is to determine the genetic responses to environmental variation. Specifically, we will test the hypothesis that differential gene expression and/or coding sequence evolution is involved in the evolution of local adaptation along an environmental temperature gradient and is associated with genome structure.

This is an exciting prospect for an ambitious and skilful Post-doctoral Research Associate to work at the interface between evolutionary biology and climate change, providing an excellent opportunity to use the latest molecular genetic tools on a project involving collaboration with partners across Europe. The post-holder should have experience in research in evolutionary genetics and handling sequence and/or expression data, along good people skills.

The position is funded by the National Environment Research Council (NERC), UK. The post is a fixed term with a start date of 1st April 2011 (or as soon as possible thereafter) and an end date of 31st March 2013 with a possibility of an extension subject to funding. The work will be performed at the Department of Animal and Plant Sciences, University of Sheffield - one of the largest departments in the UK devoted to the study of whole organism biology. We are ranked joint 3rd in the UK for biology research and 70% of our research activity has been judged to be "world-leading" or internationally excellent (RAE 2008). The University of Sheffield is ranked 7th in the world for research on the Environment and Ecology (THE 2008).

Closing date: 25th March 2011

Applications must be submitted online using the following link:

For all on-line application system queries and support, contact: e-Recruitment@sheffield.ac.uk

For informal enquiries about this job and the department, contact: Dr. Rhonda Snook, r.snook@sheffield.ac.uk

For more information on the Principal Investigators, please see:

http://www.shef.ac.uk/aps/staff/acadstaff/snook.html http://www.shef.ac.uk/aps/staff/acadstaff/butlin.html http://www.shef.ac.uk/aps/staff/acadstaff/gaston.html Dr. Rhonda Snook Senior Lecturer Department of Animal and Plant Sciences University of Sheffield Alfred Denny Building, Western Bank Sheffield S10 2TN UK

telephone: +44 (0) 114 222 0126 fax: +44 (0) 114 222 0002 webpage: http://www.shef.ac.uk/aps/staff/acadstaff/snook.html lab webpage: http://snook-lab.group.shef.ac.uk/index.html r.snook@sheffield.ac.uk

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USouthAustralia UrbanAdaptation

RESEARCH FELLOW, Barbara Hardy Institute, University of South Australia

The Barbara Hardy Institute is currently seeking a Research Fellow to undertake, apply and deliver research in the area of Urban Ecology with the Barbara Hardy Institute at the University of South Australia.

The Urban Ecology group undertakes research into how animals adapt to urban environments, how people connect with and treat wildlife in their back yards, and the threats and opportunities cities create for wildlife. Urban ecological communities change rapidly as the size and style of our green space changes. We can lose species or have plagues appear rapidly. How we can manage wildlife is a major area of research.

This position will be required to actively contribute to the research of the Urban Ecology group by implementing and leading research projects under the direction of Professor Phil Weinstien. The position is a fixed term contract for three years. This position will be required to build and promote the profile and research emanating from the Urban Ecology group by preparing and publishing scientific research in high quality peer reviewed journals and presenting the research outcomes at leading national and international conferences.

The successful candidate will have a PhD in ecology, zoology, botany health science, social science, environment science, conservation biology, or related area and experimental research experience, demonstrated track record and demonstrated experience and knowledge in preparing and applying for grants.

For further information, including a copy of the position description please visit www.unisa.edu.au/hrm/careers For further information, please contact Professor Phil Weinstein, Dean of Graduate Studies on telephone: +61 8 8302 5129 or email: phil.weinstein@unisa.edu.au

Applications close: 9.00am Monday 04 April 2011

Your assistance is appreciated.

With Thanks

Susan Corbisiero Institute Manager | Barbara Hardy Institute University of South Australia | Mawson Lakes Campus

Ph: 08 8302 5347 | M: 0435 969 818

Susan Corbisiero <Susan.Corbisiero@unisa.edu.au>

UStellenbosch InvasivePlants

South Africa- Spread of invasive plants (deadline 10 April 2011)

Post-doctoral Fellow-Stellenbosch CSIR Natural Resources and Environment (NRE) unit conducts world-class, directed interdisciplinary research and technological innovation, with partners and stakeholders in the field of natural resources and the environment to contribute to the social, economic and environmental improvement of South Africa and Africa. The impact of global change on ecosystems is one of the key focus areas of our research. This focus area includes research into the ecology and management of invasive alien plants, and much of this research is carried out on behalf of the Working for Water programme, a government initiative that seeks to reduce these impacts in all areas of South Africa. We are looking to appoint a Post-doctoral Fellow for two years. He/she will work on a project funded by the Working for Water programme, and will be based at the Stellenbosch office.

The work will focus on modelling the future potential spread of invasive alien plants at a landscape scale in South Africa. The incumbent will work as part of a team of invasion ecologists based at the CSIR and at the Centre for Invasion Biology. The team is under the leadership of Dr Brian van Wilgen.

Key responsibilities: ** Review, in consultation with leading experts, the current levels of understanding in this field. ** Develop models to predict the potential extent of invasion and rate of spread of invasive alien plants under South African conditions. ** Test these models on a set of invasive species in case studies.

Qualifications, skills and experience: **A doctorate in the natural sciences. **Experience in plant population dynamics modelling, invasive alien plant ecology or applied mathematics would be advantageous. **Demonstrated ability to publish work in the peer-reviewed literature. **Proven ability to conduct independent research. **Good communication and interpersonal skills. **Ability to work in a cross-disciplinary project team environment. **Highly self-motivated.

Should you meet the above requirements, please go to the URL indicated below in order to apply, select the position reference number 4963 complete the application form and attach your CV. URL: www.csir.co.za/apply.php Closing date: 10 April 2011 PLEASE NOTE THAT FEEDBACK WILL BE GIVEN TO SHORTLISTED CANDIDATES ONLY. Should you experience any problems in submitting your application, please contact the CSIR Recruitment Centre at Recruitmentqueries@csir.co.za. Please do not submit your application to this mailbox.

"Spear, Dian, Dr <dspear@sun.ac.za>" <DSPEAR@sun.ac.za>

UVienna AnimalBiodiversity

At the University of Vienna (15 faculties, 3 centres, about 180 fields of study, approx. 8.600 members of staff, approx. 85.000 students) the position of a University Assistant (post doc) at the Department of Animal Biodiversity is vacant.

Identification number of advertisement: 1979

Molecular data are nowadays an indispensable source of information to answer research questions in ecology and biodiversity. In our department we study patterns of species diversity and species composition at the community level in order to unravel mechanisms that generate and maintain biodiversity. Emphasis is on tropical biota, but temperate-zone communities are also studied (see www.univie.ac.at/animal_biodiversity). We are seeking for a scientist with an organismal perspective and broad command of molecular biology techniques, working at the interface between biodiversity research, ecology, and evolution. The focus should be on insects as target organisms. A fully equipped lab is available, as is support through a technician. The successful candidate is expected to develop an independent, internationally visible research agenda. Teaching obligation is 4 hours per semester week.

Degree of Employment: 40 hours/week

Areas of work: Generating and using of DNA sequence data for research questions in evolution and ecology. Teaching in the field of biology, with emphasis on animal biodiversity, evolution and ecology.

Profile: PhD degree in Biology, preferably with focus on ecology, evolution, or zoology. Postdoc experience from a competitive research laboratory. Experience with applying relevant analytical skills, techniques and methods, including a broad range of molecular biology techniques. Good command of up-to-date statistical and bioinformatics methods to analyse molecular data. Strong interest in the field of biodiversity and evolution. Good command of English language. Interest in academic teaching in BSc and MSc curricula (e.g. molecular methods for biologists, insect biodiversity). High motivation and commitment to work in a team.

Expertise in conservation biology would be welcome.

Applications including a letter of motivation (German or English) should be sent via Job Center to the University of Vienna (http://jobcenter.univie.ac.at) no later than 31.03.2011 and be referenced to the identification number 1979.

For further information please contact Univ.-Prof. Mag. Dr. Konrad Fiedler (konrad.fiedler@univie.ac.at).

The University of Vienna intends to increase the number of women on its faculty, particularly in high-level positions, and therefore specifically invites applications by women. Among equally qualified applicants women will receive preferential consideration.

Identification number of advertisement: 1979

E-Mail: jobcenter@univie.ac.at

brigitte.gottsberger@univie.ac.at

UVirginia GenomicsBioinformatics

Post-doctoral Research Associate

The Department of Biology at the University of Virginia invites applications for a post-doctoral Research Associate position in genomics and/or bioinformatics. The research will focus primarily on the evolutionary interaction between the nuclear and cytoplasmic genomes of the plant, Silene vulgaris, but the candidate will also be encouraged to broaden the use of genomic resources in this system to different projects and collaborations. The position also involves preparing materials for publication, data management and dissemination, website maintenance, and mentoring graduate and undergraduate students.

The completion of Ph.D. degree in Biology or a related discipline by appointment start date is required. Candidates with a background in evolutionary biology or population genetics are preferred, as are those with some experience in bioinformatics, genomics, or next-generation sequencing. Candidates must have effective oral and written communication skills.

To apply, please submit a candidate profile on-line and attach a cover letter, curriculum vitae, and the contact information for three references through Jobs@UVA (https://jobs.virginia.edu); search on posting number 0607328.

Review of applications will begin April 11, 2011; however, the position will remain open until filled. Questions regarding this position should be directed to:

Dr. Douglas Taylor 434-982-5217 drt3b@virginia.edu

Questions regarding the Candidate Profile process or Jobs@UVA should be directed to:

Shawna Edinger 434-982-5615 se5k@virginia.edu

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

"Edinger, Shawna (se5k)" <se5k@eservices.virginia.edu>

UWisconsin Madison EvolutionaryGeneticsGenomics 2

Postdoctoral Position in Evolutionary Genetics/Genomics

A postdoctoral position is available immediately in the Laboratory of Professor Carol Lee in the Center of Rapid Evolution (CORE) at the University of Wisconsin, Madison to work on a project in collaboration with Joana Silva at the Institute for Genome Sciences.

The research focuses on the evolutionary genetics and genomics of invasive populations. We are exploring the systematic and functional composition of microbial communities associated with an invading host, the copepod Eurytemora affinis, and how microbial-host interactions shift following habitat invasions. The project will make extensive use of microbiome and metagenome methodologies to study the microbiota, and of transcriptome sequencing and analyses to characterize metabolic shifts within the copepod host.

Requirements for this position include a Ph.D., a strong background in molecular biology/genomics and strong analytical and quantitative skills. Relevant training and experience include research in transcriptomics, metagenomics, culturing of bacteria from environmental samples, and genomic data analysis.

Applicants should email a cover letter, CV, a brief statement of research interests and experience, and up to three representative publications to: carollee@wisc.edu. Applicants should also arrange for three letters of recommendation to be sent by email. Any questions regarding this position are welcome. Application Deadline: March 30, 2010 (preferably sooner).

The University of Wisconsin, Madison provides an intellectually vibrant research environment, with ~37 biology departments and ~800 biology faculty, including a strong community of evolutionary biologists and geneticists. The University of Wisconsin is an Equal Opportunity/Affirmative Action Employer.

Carol Eunmi Lee, Ph.D. Associate Professor Center of Rapid Evolution (CORE) 430 Lincoln Drive, Birge Hall University of Wisconsin Madison, WI 53706 carollee@wisc.edu

https://mywebspace.wisc.edu/carollee/web/Lee/-Lee.html carollee@wisc.edu

UWisconsin-MadisonUWisconsin-Madison EvolutionaryGeneticsGenomics

Postdoctoral Position in Evolutionary Genetics/Genomics

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The research focuses on the evolutionary genetics and genomics of invasive populations. We are exploring the systematic and functional composition of microbial communities associated with an invading host, the copepod Eurytemora affinis, and how microbial-host interactions shift following habitat invasions. The project will make extensive use of microbiome and metagenome methodologies to study the microbiota, and of transcriptome sequencing and analyses to characterize metabolic shifts within the copepod host.

Requirements for this position include a Ph.D., a strong background in molecular biology/genomics and strong analytical and quantitative skills. Applicants should email a cover letter, CV, a brief statement of research interests and experience, and up to three representative publications to: carollee@wisc.edu.

The University of Wisconsin, Madison provides an intellectually vibrant research environment, with ~37 biology departments and ~800 biology faculty, including a strong community of evolutionary biologists and geneticists. The University of Wisconsin is an Equal Opportunity/Affirmative Action Employer.

Carol Eunmi Lee, Ph.D. Associate Professor Center of Rapid Evolution (CORE) 430 Lincoln Drive, Birge Hall University of Wisconsin Madison, WI 53706 carollee@wisc.edu

https://mywebspace.wisc.edu/carollee/web/Lee/-Lee.html carollee@wisc.edu

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WashingtonU HumanGenomics

A Postdoctoral position in Human Genomics is available in the lab of Don Conrad at Washington University School of Medicine. The lab is engaged in a range of projects centered around population genetics and human reproduction (see www.genetics.wustl.edu/dclab). We are interested in understanding the processes of gametogenesis, fertilization and pregnancy through genetic analysis of reproduction-related traits and functional genomic analysis of reproduction-related cell types, and ultimately translating our findings to improvements in the diagnosis and treatment of reproductive disorders. We have an extremely strong record in the discovery and analysis of genetic variation and can offer mentoring in the design of genomics experiments and the use of computational statistics. Through Washington University and various collaborations we have access to material from thousands of patients seen by reproductive specialists, giving us tremendous scope in the type of problems we can address.

Responsibilities include leading analyses of next-generation sequence and genotype data collected from sources such as blood and sperm from healthy individuals and infertile ones, developing novel analytical methods as needed and distilling research results into tools that can be used by the clinical and basic research communities. The post offers the opportunity for direct collaboration with clinicians in an IVF setting as well as experimentation with new techniques in DNA preparation and sequencing. We are committed to the career development and personal growth of our team.

Required Qualifications

-Highly motivated to do interesting research, transform medicine, and have fun doing it

-Ph.D. in a related molecular bioscience (genomics, proteomics, biochemistry, mol bio, etc.) or related quantitative science (computational biology, biostatistics, comp sci, etc). MDs or MD/PhDs with appropriate training are also welcome to apply.

-Previous success as a research scientist demonstrated by first-author publications.

-Excellent computational skills are required for most projects in the lab. The ideal applicant will know a compiled language (e.g. C, Java), a scripting language (e.g. PERL, Python), and R.

-Effective written and oral communication and proven ability to work in a collaborative environment

Informal inquiries as well as applications (including a CV, copies of relevant publications and contact information for at least two references) should be emailed to D Conrad at <dconrad@genetics.wustl.edu>. Starting date is flexible but the position is open immediately.

About Washington University School of Medicine

Washington University (WashU), situated in St. Louis, MO, USA, provides an elite research environment that includes one of the country's top five medical schools; top ten hospitals; world-renowned researchers; and the legacy of 19 Nobel Laureates. It is home to one of the largest genome sequencing centers in the world which generated more than 20 percent of the sequence for the Human Genome Project. A highly collaborative, interdisciplinary environment makes WashU an ideal place for people looking to do translational work, for instance related to genomic medicine.

Don Conrad

Assistant Professor Department of Genetics Department of Pathology & Immunology Washington University School of Medicine Saint Louis, MO, USA

WayneStateU TriboliumGenomics

Postdoc: Wayne State. Genomic analysis of Tribolium eye development.

The Friedrich lab at Wayne State University, Detroit (https://sites.google.com/site/friedrichlab/), invites applications to fill a 2-year NSF funded postdoc position in functional genomics with possible extension. The project focuses on the analysis of eye development in the red flour beetle Tribolium castaneum in collaboration with Dr. Rui Chen's group in the Department of Molecular and Human Genetics at Baylor College of Medicine (http://-www.bcm.edu/genetics/?pmid=10863). The postdoc will join ongoing efforts to test gene network predictions from differential transcriptome analysis by

RNAi, in situ hybridization and quantitative PCR and develop a comprehensive model of Tribolium eye specification for comparison with Drosophila and vertebrate systems (http://www.nsf.gov/-awardsearch/showAward.do?AwardNumber=-0951886&WT.z_pims_id=501087).

Ph.D. experience in molecular developmental biology is essential. Background or strong interests in bioinformatics, the visual system and evolution will be advantageous. Tribolium has matured into a powerful satellite system for studying insect development and evolution. Development of personal research directions related to the visual system will be strongly encouraged.

To apply, or inquire about further details contact Dr. Markus Friedrich (friedrichwsu@gmail.com).

Applications should be submitted as pdf file by email no later than April 30st and include CV, list of publications, statement of research interests and the names of three referees.

Markus Friedrich Associate Professor Department of Biological Sciences Wayne State University 5047 Gullen Mall Detroit, MI 48202

– Markus Friedrich Associate Professor Department of Biological Sciences Wayne State University 5047 Gullen Mall Detroit, MI 48202

office: 313 577 9612 lab: 313 577 5120 fax: 313 577-6891 http://friedrichlab.googlepages.com/home Markus Friedrich <friedrichwsu@gmail.com>

WestVirginiaU MicrobialEvolution

A postdoctoral position is available immediately in Dr. Olga Zhaxybayeva's lab in the Biology Department of West Virginia University in Morgantown, WV. The successful candidate will perform research in the area of computational genomics, focusing on deciphering processes governing microbial evolution through the analysis of patterns in genomic and metagenomic data sets. More information about the laboratory is available at http://ecg.bio.wvu.edu . Ph.D. in bioinformatics, biology, computer science, statistics or a related field with strong background in molecular evolution; solid computational skills; extensive programming and scripting experience; and evidence of successful team-work abilities are required. Experience working with next-generation sequence data and Unix operating system are desirable.

The successful applicant will be expected to contribute to a variety of ongoing collaborative research projects with teams across the United States and Canada, as well as establish his/her own independent projects, and will be provided with training opportunities of grant writing and student supervision.

Review of applications will begin April 1, 2011 and continue until the position is filled. The initial appointment is for one year with the possibility of renewal for up to two additional years contingent upon performance, need, and funding. Salary will be offered commensurate with experience and skills. Competitive benefits package is included.

Interested applicants should send a single PDF file containing CV, one-page statement of research interests and contact information of three references to ECGLabJobs@gmail.com.

West Virginia University is an Affirmative Action/Equal Opportunity Employer and the recipient of an NSF ADVANCE award for gender equity.

– Olga Zhaxybayeva, Ph.D. Assistant Professor Department of Biology West Virginia University PO Box 6057 Morgantown, WV 26506 USA

Office: (304) 293-5201 ext. 31531 Lab: (304) 293-5201 ext. 31331 Fax: (304) 293-6363 Email: olgazh@mail.wvu.edu Web: http://ecg.bio.wvu.edu/ olgazh@mail.wvu.edu

YaleU MosquitoEvolution

One year postdoc available to study the evolutionary genetics/genomics of the major mosquito vector, Aedes aegypti. Experience in population genetics/genomics including good analytical skills required. Experience with particular organism less important. This is an NIH Training Grant position and thus the applicant must be a US Citizen. Possibility of extension dependent upon successful grant applications. Send CV and letter describing your availability and reasons for interest in this position to: jeffrey.powell@yale.edu Application deadline: April 10.

jeff powell <jeffrey.powell@yale.edu>

WorkshopsCourses

Arolla Switzerland EvolBiol Jun26-Jul2

Dear Colleagues, we still have a few places available at this workshop, please bring it to the attention of potential participants. Tad Kawecki

Evolutionary Biology Workshop in the Alps

26 June- 2 July 2011 Arolla, Switzerland

3 ETSC credit points

Faculty: John Pannell (University of Oxford, UK) Mike Ritchie (University of St. Andrews, UK) Jerome Goudet (University of Lausanne, Switzerland) Tadeusz Kawecki (University of Lausanne, Switzerland)

Target participants: PhD students, advanced master students This workshop, based on a concept developed by Steve Stearns and John Maynard Smith, takes place in a small Alpine village (Arolla), which will allow you to focus while being able to enjoy the landscape and the Alpine flora. The main goals of this course are to develop the following skills: - developing your scientific ideas through discussions in groups - thinking critically and expressing oneself clearly - turning a general idea into a research project - writing a research proposal and defending it It is you, the students, who will be in charge in this course. You will be divided in groups of 4-5 students. In those groups, you will work on your ideas. You, as a group, will decide what the important questions in broadly defined evolutionary biology are, you will choose one, and attempt to develop a proposal for a research project that will address it. The faculty will visit the groups during the discussions to answer your questions, provide coaching and give you feedback on your projects, but they will generally take the back seat. Additionally, the faculty will give informal talks about their research and be available for informal discussion with individual students. At the end you will present your projects to other participants, and we will party.

Costs: CHF 430.- for room and board.

More information under http://biologie.cuso.ch/ecologie-evolution/activities/detail-activity/item/courses/evolutionary-biology-workshop-in-the-alps-1/

To apply, send a single file (pdf or rtf) containing a short motivation letter, a cv and the name of your scientific advisor to tadeusz.kawecki@unil.ch.

Deadline for application: 28 February 2011.

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

tadeusz.kawecki@unil.ch

BamfieldStation EvolutionModels Jul24-Aug12

Dear Evoldir,

Registration is still open for "Models in Evolution," a course that at the Bamfield Marine Sciences Station, on Vancouver Island, British Columbia, Canada (July 25-Aug 12).

The Bamfield Marine Sciences Station is an amazing place for students to learn about the life sciences (stunning scenery, enthusiastic classmates, small classes, many "hands on" opportunities).

The modelling course – one of many courses at BMSC – deals with topics that would be of particular interest to undergraduates or graduate students studying evolutionary ecology. A full course description can be found at

http://www.bms.bc.ca/university/courses2011/-summer11_des.html#models and registration info can be found at

http://www.bms.bc.ca/university.html If you have any questions, don't hesitate to contact me (gwild@uwo.ca).

-Geoff Wild Applied Math University of Western Ontario

gwild@uwo.ca

Berlin Evolutionary Genomics Sep14-22

We are pleased to announce the Otto Warburg International Summer School and Research Symposium on Evolutionary Genomics, to be held in Berlin from September 14th to 22nd, 2011.

http://ows.molgen.mpg.de/ The following speakers have confirmed their attendance at the school:

Hans Ellegren (Uppsala) Nicolas Galtier (Montpellier) Laurence Hurst (Bath) Henrik Kaessmann (Lausanne) Fyodor Kondrashov (Barcelona) Michael Lynch (Indiana) Duncan Odom (Cambridge) H. Allen Orr (Rochester) Dmitri Petrov (Stanford) Stephan Schuster (Philadelphia) Ken Wolfe (Dublin)

The scientific coordinators of the OWS are Martin Vingron, Peter Arndt and Brian Cusack at the Max Planck Institute for Molecular Genetics in Berlin. The aim of this program is to bring together researchers and PhD students from different backgrounds (including molecular biology, bioinformatics, biological physics, mathematics) to discuss recent advances in evolutionary genomics in an interactive environment. The program focuses on high-level teaching and topical research seminars. Participants are expected to give poster presentations or contribute talks.

We invite applications from PhD students and a limited number of PostDocs. Please apply for attendance before June 12, 2011 via our website http://-ows.molgen.mpg.de/ .

The programs (and video streams) of previous Summer Schools can also be found on the school's website.

For questions please contact the school organiser, Kirsten Kelleher (kelleher@molgen.mpg.de)

cusack@molgen.mpg.de

FortCollins Colorado MolEvol Jul24-Aug6 2

Workshop on Molecular Evolution, North America 2011

Fort Collins, Colorado, USA

24 July - 6 August 2011

Application Deadline: 15 May is the preferred application deadline, however, later applications are accepted.

http://www.molecularevolution.org/workshops/WME Michael P. Cummings, Scott A. Handley and Kendra Nightingale, Co-Directors

The Workshop consists of a series of lectures, demonstrations and computer laboratories that cover various aspects of molecular evolution. Faculty are chosen exclusively for their effectiveness in teaching theory and practice in molecular evolution. Included among the faculty are developers and other experts in the use of computer programs and packages such as BEAST, *BEAST, DataMonkey, FigTree, Genealogical Sorting Index, GARLI, HyPhy, LAMARC, MAFFT, MrBayes, and SeaView who provide demonstrations and consultations.

The course is designed for established investigators, postdoctoral scholars, and advanced graduate students with prior experience in molecular evolution and related fields. Scientists with strong interests in molecular evolution, phylogenetics, population genetics, and related fields are encouraged to apply for admission. Scheduled lectures and computer laboratories total ~96 hours of instruction. Admission is limited and highly competitive.

Topics to be covered include:

- Phylogenetic analysis: theoretical, mathematical and statistical bases; sampling properties of sequence data; Bayesian analysis; hypothesis testing - Maximum likelihood and Bayesian theory and practice in phylogenetics and population genetics: coalescent theory; estimation of population genetic parameters - Detecting positive selection: theory and practice; codon models - Dating phylogenies: theory and practice - Coalescent species trees

2011 Fee: 1100 USD does not include other meals or housing. Special discounted housing and meals are available on the campus of Colorado State University.

For more information and online application see the Workshop web site -

http://www.molecularevolution.org/workshops/WME and for housing and payment information see -

https://regstg.com/Registration/RegForm.aspx?rid=3D76c8770d-9b70-44e5-9d1d-804beeceb915&action=add The Workshop on Comparative Genomics is also being offered immediately before the Workshop on Molecular Evolution, see http://www.molecularevolution.org/workshops/WCG
mike@umiacs.umd.edu

FortCollins NGS analysis Jul10-23

Workshop on Comparative Genomics, North America 2011

Fort Collins, Colorado, USA

10 - 23 July 2011

Application Deadline: 15 May is the preferred application deadline, however, later applications are accepted.

http://www.molecularevolution.org/workshops/WCG
Scott A. Handley, Michael Cummings and Kendra Nightingale, Co-Directors

The Workshop on Comparative Genomics consists of a series of lectures, demonstrations and computer laboratories that cover various aspects of comparative genomics focusing on next-generation sequencing data. Faculty are chosen exclusively for their effectiveness in teaching theory and practice in comparative genomics. Included among the faculty are developers and other experts in the use of computer programs and packages such as ABySS, bowtie, velvet, bioperl, Scripture, GMOD, Gbrowse, Galaxy, PyCogent, QIIME who provide demonstrations and consultations. The course is designed for established investigators, postdoctoral scholars, and advanced graduate students. Scientists with strong interests in the uses of short-read sequence data, analytical methods, comparative structure of genomes, metagenomics, genome visualization tools and related areas are encouraged to apply for admission. Lectures and computer laboratories total ~96 hours of scheduled instruction. Admission is limited. No programming experience is required, however, detailed instruction suitable for the novice will be provided during the early days of the Workshop on the use of the command line, editing tools and basic scripting.

Topics to be covered include: - Linux command line usage and scripting for next-generation sequence analysis - Sequencing technologies and study design - Sequence data quality control - Assembly and alignment - Functional annotation - Transcriptomics - Metagenomic analysis - Evolutionary genomics - Population genomics

2011 Fee: 1800 USD does not include other meals or housing. Special discounted housing and meals are available on the campus of Colorado State University.

For more information and online application see the Workshop web site -

http://www.molecularevolution.org/workshops/WCG and for housing and payment information see -

https://regstg.com/Registration/RegForm.aspx?rid=3Dd41e4a6a-bf9f-40f0-8b0a-74fba75088b4&action=add The Workshop on Molecular Evolution is also being offered immediately after the Workshop on Comparative Genomics.

http://www.molecularevolution.org/workshops/WME
mike@umiacs.umd.edu

Gregynog Wales Hybridisation Oct23-26

Frontiers in Speciation Research Workshop: Hybridisation and Speciation

Gregynog Conference Centre, 23-26 October 2011

The European Science Foundation research network, Frontiers in Speciation Research (http://www.iiasa.ac.at/Research/EEP/FroSpects/), invites participants to a workshop on the roles of hybridisation in the process of speciation. This is intended to be a high-level discussion meeting, rather than a training workshop. It will focus around sessions led by invited participants (Alex Buerkle, Jim Mallet, Karin Pfennig, Arne Nolte, Pierre Boursot and Richard Abbott) and the aim is to draft a Perspective article on the topic during the meeting. Attendance will be limited to 40 participants. The meeting will cover two and a half days (arrival Sunday 23 October, departure pm Wednesday 26 October) and it will be held in the beautiful surroundings of the Gregynog Conference Centre in mid-Wales (http://www.wales.ac.uk/en/UniversityConferenceCentre/GregynogHall.aspx).

The meeting is subsidised by the ESF network but participants will need to pay a contribution of 200UK-pounds towards the costs of food and accommodation and cover their own travel expenses. If you would like to be considered for a place at the workshop, please send a brief CV and statement of research interests (maximum one side of A4 each) to Angela Wright (a.p.wright@shef.ac.uk) by 8 April 2011. Please note that the CV and statement may be circulated to other participants at the workshop.

The meeting is organised by Roger Butlin, Mike Ritchie, Jacek Szymura, Ulf Dieckmann and Ake Brannstrom on behalf of FroSpects.

r.k.butlin@sheffield.ac.uk

Gregynog Wales Hybridisation Oct23-26 2

Reminder: closing date 8 April

Frontiers in Speciation Research Workshop: Hybridisation and Speciation

Gregynog Conference Centre, 23-26 October 2011

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r.k.butlin@sheffield.ac.uk

Hinxton HumanGenomeAnalysis Jul23-29

Human Genome Analysis: Genetic Analysis of Multifactorial Diseases 23-29 July 2011

Wellcome Trust Genome Campus, Hinxton, Cambridge
Deadline for applications: 15 April 2011

http://www.wellcome.ac.uk/Education-resources/Courses-and-conferences/Advanced-Courses-and-Scientific-Conferences/Advanced-Courses/-

WTX026851.htm Course summary An intensive, residential, computer-based course aimed at scientists actively involved in genetic analysis of multifactorial traits.

Confirmed 2011 Guest speakers Professor William O. Cookson (Imperial College London, UK) Professor Elizabeth R. Hauser (Duke University Medical Center, USA) Professor Aarno Palotie (Wellcome Trust Sanger Institute, UK) Professor Mingyao Li (University of Pennsylvania School of Medicine, USA) Professor Sebastian Zöllner (University of Michigan, USA)

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 Nacional d'Anàlisi Genòmica (CNAG), Barcelona, Spain)

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 software. 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.

Janet@mednet.ucla.edu

MichiganStateU DataAnalysis Jun6-17

Analyzing Next-Generation Sequencing Data

June 6th - June 17th, 2011 Kellogg Biological Station, Michigan State University

Instructors: Dr. C. Titus Brown, Dr. Ian Dworkin, and Dr. Istvan Albert.

Applications must be received by March 25th for full consideration.

More information and application link here:

http://bioinformatics.msu.edu/ngs-summer-course-2011 Course Description:

This intensive two week summer course will introduce students with a strong biology background to the practice of analyzing short-read sequencing data from Roche 454, Illumina GA2, ABI SOLiD, Pacific Biosciences, and other next-gen platforms. The first week will introduce students to computational thinking and large-scale data analysis on UNIX platforms. The second week will focus on mapping, assembly, and analysis of short-read data for resequencing, ChIP-seq, and RNAseq.

No prior programming experience is required, although familiarity with some programming concepts is helpful, and bravery in the face of the unknown is necessary. 2 years or more of graduate school in a biological science is strongly suggested.

Students will gain practical experience in:

* Python and bash shell scripting * cloud computing/Amazon EC2 * basic software installation on UNIX * installing and running maq, bowtie, and velvet * querying mappings and evaluating assemblies

Materials from last year's course are available at http://ged.msu.edu/angus/ under a Creative Commons/use+reuse license.

Ian Dworkin <idworkin@msu.edu>

MtDesertIsland Evolution and Medicine Aug8-12

A new one-week course will be offered this summer at the Mt. Desert Island Biological Laboratory:

*Evolutionary Foundations for Medicine and Public Health, August 8-12, 2011< http://www.mdibl.org/courses/Evolution_and_Medicine/296/ > *

We are now accepting applications for 40 participants. For an application or more information, please see the MDIBL website< http://www.mdibl.org/courses/Evolution_and_Medicine/296/ >or the course description, below.

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August 8 to August 12, 2011

Mount Desert Island Biological Laboratory Summer Course on

*Evolutionary Foundations for Medicine and Public Health< http://www.mdibl.org/courses/Evolution_and_Medicine/296/ > *

(Special expertise on evolution and reproduction available this year)

* Faculty*

- William Aird â Harvard University - Gillian Bentley â Durham University, UK - Carl Bergstrom â University of Washington - Peter Gluckman â University of Auckland - Peter Ellison â Harvard University - Randolph Nesse â University of Michigan (Course director) - Chris Reiber â SUNY Binghamton - Stephen Stearns â Yale University

Participants This course will be limited to 40 participants. It will be appropriate for those with a background in biology and/or medicine at diverse levels. While special expertise in evolutionary biology is not required, those with background in evolutionary biology will have specialized opportunities. To maximize benefits to this developing field, admission preference will be offered to physicians and professors who teach or anticipate teaching courses on the subject and to members of minority groups who may be eligible for support from the National Evolutionary Synthesis Center. Researchers and students from advanced undergraduates to postdocs will be warmly welcomed if there is space.

Course description This intensive one-week course will introduce strategies for applying core principles of evolutionary biology to problems in medicine and public health by focusing on selected examples. The relevant principles include life history theory, evolutionary genetics, host pathogen co-evolution, the regulation of defenses, developmental plasticity, and trade-offs shaping reproductive strategies. They will be applied to clinically relevant topics including aging, antibiotic resistance, clinical management of fever, endothelial disease, prenatal experience and metabolic syndrome, and reproductive cancers. This yearâs course will have extensive special expertise available on topics related to reproduction. Mornings will be devoted to lectures and structured discussions. In the early afternoons, participants will work in small groups with faculty and others who share specialized interests. Most groups will investigate a specific disorder, for instance, metabolic syndrome, multiple sclerosis, or breast cancer. Each group will develop a possible research project, for presentation on Friday. Individuals are also free to create their own projects. Late afternoons (except Monday) are not prescheduled, allowing participants to pursue individual interests or organize their own additional discussions and projects.

CME credit CME credit will be available. This activity has been planned and implemented in accordance with the essential areas and policies of the Accreditation Council for Continuing Medical Education through the joint sponsorship of Colby College and the Mount Desert Island Biological Laboratory. Colby College is accredited by the ACCME to sponsor continuing medical education for physicians.

As an institution accredited for CME, Colby College designates this educational activity for a maximum of 29 AMA PRA Category 1 Creditsâ. Physicians should only claim credit commensurate with the extent of their participation in the activity.

Tentative Schedule

Monday

Tuesday

Wednesday

Thursday

Friday

8-9

Maladaptation and natural selection

Nesse &

Faculty

Reproduction and its disorders
~~~

Ellison

Plasticity & development

Gluckman

Mismatch

Gluckman

Reproductive Cancers

Stearns &

Bentley

9-10

Overview of core evolutionary principles

Faculty

Menopause

Reiber

Regulation of defenses

Nesse

Evolution and the endothelium

Aird

Hygiene and autoimmune diseases

Stearns

10-10:30

Break

Break

Break

Break

Break

10:30-12

Life history theory and aging

Stearns

Consequences of early menarche

Bentley

Seminar on Methodology

Faculty

Teaching/learning strategies

Reiber/Faculty

Antibiotic resistance

Bergstrom

Noon

Lunch

Lunch

Lunch

Lunch

Lunch

1-3

Introductions and organization of Workgroups

Workgroups on topics of personal interest

Workgroups on topics of personal interest

— / —

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

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NESCent DurhamNC NextGenSequencing Aug15-29

Title: Next-gen sequencing: data acquisition, comparative genomics, design and analysis for population genetics, systematics and development Instructors: William Cresko, Brian O'Connor, Mónica Cecilia Muñoz-Torres, Alexie Papanicolaou, Konrad Paszkiewicz, Jennifer Taylor, Francesc López, Jeffrey Townsend Dates: August 15 - 29, 2011 Application deadline: May 15, 2011 Website: academy.nescent.org Where: National Evolutionary Synthesis Center (NESCent), Durham, NC

As part of the new NESCent Academy initiative, NESCent is pleased to open applications for 'Next-gen sequencing: data acquisition, comparative genomics, design and analysis for population genetics, systematics and development'. This course will provide computational training required for those working with Next-generation sequencing data and is aimed in particular at graduate students, research fellows and faculty crossing the field into genomics. The course will be embedded within an array of biological questions but it will be focused around specific technical questions such as: * sequencing strategies, including libraries and RAD-TAG * generation of gene-models from related reference genomes or from NGS transcriptomes * variant calling and alternative splicing detection * analyzing differential expression * generation and use of genome-wide SNP markers * analysis of metagenomic data * phylogeny reconstruction from NGS An added advantage of attending will be networking and the creation of a community of researchers familiar with an interoperable set of tools, providing continued support and the potential for collaboration into the future.

–

Karen Cranston Training Coordinator and Informatics Project Manager nescent.org

Karen Cranston <karen.cranston@nescent.org>

NESCent EvolutionaryQuantitativeGenetics

Title: Evolutionary Quantitative Genetics Primary instructors: Stevan Arnold and Joe Felsenstein Dates: August 8-13, 2011 Application deadline: May 15, 2011 Website: academy.nescent.org Where: National Evolutionary Synthesis Center, Durham, NC

As part of the new NESCent Academy initiative, we are pleased to open applications for Evolutionary Quantitative Genetics. In this workshop we will review the basics of theory in the field of evolutionary quantitative genetics and its connections to evolution that is observed at various time scales. Quantitative genetic theory for natural populations was developed considerably in the period 1970-90 and up to the present time. It has been applied to a wide range of phenomena including the evolution of differences between the sexes, sexual preferences, life history traits, plasticity of traits, as well as the evolution of body size and other morphological measurements. Textbooks have not kept pace with these developments, and currently few universities offer courses in this subject aimed at evolutionary biologists. There is a need for evolutionary biologists to understand this field because of the ability to collect large amounts of data by computer, the development of statistical methods for changes of traits on evolutionary trees and for changes in a single species through time, and the realization that quantitative characters will not soon be fully explained by genomics. This workshop aims to fill this need by reviewing basic aspects of theory and illustrating how that theory can be tested with data. Participants will learn to use R, an open-source statistical programming language, to build and test evolutionary models. The intended participants for this workshop are graduate students, postdocs, and junior faculty members in evolutionary biology.

The course is co-sponsored by the American Society of Naturalists.

–

Karen Cranston Training Coordinator and Informatics Project Manager nescent.org

Karen Cranston <karen.cranston@nescent.org>

NESCent PracticalComputing

Course title: Practical Computing for Biologists Instructors: Steven Haddock and Casey Dunn Dates: June 6-15, 2011 Application deadline: April 15, 2011 Website: academy.nescent.org Where: North Carolina State University, Raleigh, NC

As part of the new NESCent Academy initiative, NESCent is pleased to open applications for Practical Computing for Biologists. This course covers some of the simple but powerful skills that all scientists should know in a world of increasingly complex analyses. This is not a typical bioinformatics course, although the lessons are applicable to molecular data. The skills are applicable to any subdiscipline where gathering and analyzing moderate to large data sets are involved. The specific sections include working with text files, command-line operations, scripting and Python programming, creating scientific graphics, working with servers (remote login, software installation), and a bit about the web and data-acquisition hardware.

This course is timely because biologists and other researchers are expected to analyze larger and more complex data sets, but using inadequate tools like spreadsheets. Although the examples will be shown making use of Mac OSX and its Unix underpinnings, all of the tools discussed are cross-platform and freely available. Participants will be able to take the techniques and skills they learn back to their labs to continue making their own research easier and more effective. The target audience for the course is anyone with data: grad students, post-docs, technicians, and faculty.

Practical Computing for Biologists is based on the book of the same name by Steven Haddock and Casey Dunn. The course is co-sponsored by the NESCent and the Department of Genetics / Initiative in Biological Complexity at North Carolina State University.

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Karen Cranston Training Coordinator and Informatics Project Manager nescent.org

Karen Cranston <karen.cranston@nescent.org>

Phyloseminar ComparativeMethods Mar16

Please come to a free online seminar next week:

Brian O'Meara speaks Wednesday, March 16th at 11am PST on "Making comparative methods as easy as ABC"

Abstract: For decades, biologists have addressed evolutionary and ecological questions using measurements of species traits, phylogenies, and an assortment of comparative methods. Unfortunately, while there is a large assortment of these methods, they are still fairly limited and development of new methods is slow. It took seven years between the introduction of using a simple Brownian motion model for looking at trait evolution (Felsenstein, 1985) and the use of this same model for looking at rates of trait evolution (Garland, 1992), and an additional 14 years to more powerful tests using a small modification of the basic model (O'Meara et al., 2006). Still other promising methods are described and even tested but remain unavailable to empiricists because they are not put into software. As a result, the questions empiricists can ask about the world are limited by the research productivity of the few dozen scientists who develop and implement new methods in phylogenetics. We describe a new approach based on Approximate Bayesian Computation and implemented in R that will allow researchers to easily develop their own models for trait evolution without requiring them to have specialized mathematical or computational knowledge.

Japan 03:00 (03:00 AM) on Thursday, March 17 New Zealand 07:00 (07:00 AM) on Thursday, March 17 West Coast USA 11:00 (11:00 AM) on Wednesday, March 16 East Coast USA 14:00 (02:00 PM) on Wednesday, March 16 England 18:00 (06:00 PM) on Wednesday, March 16 France 19:00 (07:00 PM) on Wednesday, March 16

For more information on how to attend this and other seminars, visit phyloseminar.org.

ematsen@gmail.com

Phyloseminar ComparativeMethods Mar30 Rescheduled

Due to a family emergency, Brian's talk has been pushed forward two weeks. Thank you for your understanding.

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Brian O'Meara speaks Wednesday, March 30th at 11am PST on "Making comparative methods as easy as ABC"

Abstract: For decades, biologists have addressed evolutionary and ecological questions using measurements of species traits, phylogenies, and an assortment of comparative methods. Unfortunately, while there is a large assortment of these methods, they are still fairly limited and development of new methods is slow. It took seven years between the introduction of using a simple Brownian motion model for looking at trait evolution (Felsenstein, 1985) and the use of this same model for looking at rates of trait evolution (Garland, 1992), and an additional 14 years to more powerful tests using a small modification of the basic model (O'Meara et al., 2006). Still other promising methods are described and even tested but remain unavailable to empiricists because they are not put into software. As a result, the questions empiricists can ask about the world are limited by the research productivity of the few dozen scientists who develop and implement new methods in phylogenetics. We describe a new approach based on Approximate Bayesian Computation and implemented in R that will allow researchers to easily develop their own models for trait evolution without requiring them to have specialized mathematical or computational knowledge.

Japan 03:00 (03:00 AM) on Thursday, March 31 New Zealand 07:00 (07:00 AM) on Thursday, March 31 West Coast USA 11:00 (11:00 AM) on Wednesday, March 30 East Coast USA 14:00 (02:00 PM) on Wednesday, March 30 England 19:00 (07:00 PM) on Wednesday, March 30 France 20:00 (08:00 PM) on Wednesday, March 30

For more information on how to attend this and other seminars, visit http://phyloseminar.org . Erick Matsen <matsen@fhcrc.org>

Portal Arizona AntEvolution Aug4-14

ANT COURSE 2011 http://www.antweb.org Southwestern Research Station (SWRS), Portal, AZ, USA August 4-14, 2011

DEADLINE FOR APPLICATION: April 1, 2011 Application form: https://-spreadsheets.google.com/viewform?formkey=-3DdGNTcVh1ZzVGNjd1aVU5cnV1dWZNbVE6MA COURSE OBJECTIVES. - ANT COURSE is designed for systematists, ecologists, behaviorists, conservation biologists, and other biologists whose research responsibilities require a greater understanding of ant taxonomy and field research techniques. Emphasis is on the identification of the ant genera and species occurring in North America. Lectures will include background information on the ecology, life histories and evolution of ants. Field trips are structured to teach collecting and sampling techniques, and associated lab work provides instruction on specimen preparation, sorting and labeling. Information on equipment/supply vendors, literature, and myrmecological contacts are also presented.

COURSE SIGNIFICANCE. - Ant Course is a unique opportunity to acquire training that is unavailable elsewhere. This course will provide students with 1) the confidence and skills to identify the ant genera of North America; 2) an understanding of modern specimen processing and curation techniques; 3) an appreciation for the biological diversity of ants, and 4) experience keying to the species level.

SPONSORS. - California Academy of Sciences and Museum of Comparative Zoology.

BACKGROUND INFORMATION. - ANT COURSE will be taught from August 4 - 14, 2011 at the Southwestern Research Station (SWRS) in Portal Arizona (http://research.amnh.org/swrs/). The Station is centered amid the richest ant fauna in North America. This is an ongoing course, offered annually.

PARTICIPANT ACCEPTANCE CRITERIA. - ANT COURSE is open to all interested individuals. Priority will be given to those students for whom the course will have a significant impact on their research with ants. An entomological background is not required. We aim to include students with a diverse interest in biology, including ant systematics, ecology, behavioral biology, genetics, and conservation. The high instructor to student ratio will allow students to receive individual attention. ANT COURSE is presented in English and limited to 30 participants

COSTS. - Tuition for the 10-day COURSE is $475 for current students and $675 for non-students. In addition, the Southwestern Research Station (SWRS) fee for this period, covering dormitory room and board, is $625. Transportation costs between home and Tucson (air) or SWRS (auto) are to be borne by all participants.

FELLOWSHIPS. - Four fellowships are available for 2011. Two fellowships cover tuition fees and two fellowships cover station fees. Foreign students may apply for additional fellowships to assist in travel. Those interested in attending the course should seek all possible avenues to secure funding for the course. You should only apply for the Ant Course fellowship if you cannot find other support and it is essential for your participation in the course. Beware that if you apply for an ant course fellowship it implies that fellowship funding is essential to your participation in the course. Thus, if you are not selected for a fellowship, you might not be accepted into the course. Please notify the course if your funding request status changes before the application due date.

COURSE APPLICATION. - Application and course information at http://www.antweb.org. The first step is to fill out a form at: https:/-/spreadsheets.google.com/viewform?formkey=-3DdGNTcVh1ZzVGNjd1aVU5cnV1dWZNbVE6MA In addition, you must also submit a CV, personal statement, and letter of reference to AntCourse@gmail.com.

By April 5, you will be notified that your application is complete. If you do not receive a confirmation that your application has been received by April 5, please contact Brian Fisher at AntCourse@gmail.com. You will be notified of your acceptance to the Course around APRIL 15-20.

ANT COURSE is limited to 30 participants. Selection of participants will be carried out by committee, based on your reasons for wishing to take the course at this time. Priority will be given to those students for whom the course will have a significant impact on their research with ants. Because the Course will be offered yearly, and because many well-qualified candidates cannot be accepted because of limited capacity, we urge applicants not selected for this session to apply again the following year.

2011 Possible INSTRUCTORS - Final list announced

Spring 2011: Brian Fisher (Coordinator), Dept. of Entomology, California Academy of

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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

Portugal MolecularEvolution Apr11-15

*** REMINDER ***

Deadline for applications March 29th

Dear All The Bioinformatics Training Course course MEPA11 is OPEN for applications

IMPORTANT DATES for MEPA11 Deadline for applications: March 29th 2011 Notification of acceptance dates: EARLY: March 15th 2011 (on special request, see Application) NORMAL: March 30th 2011 Course date: April 11th - 15th 2011

MEPA11 Molecular Evolution, Phylogenetics and Adaptation with Hernan Dopazo and François Serra

More than 30 years ago, Theodosius Dobzhansky claimed: "Nothing in Biology makes sense except in the light of evolution" Currently, the simplest Bioinformatics analysis uses species comparisons in order to hypothesise the function of a novel biological sequence. Moreover, in most Molecular Biology labs, evolutionary and phylogenetic concepts are constantly being used with more or less formality: homology, similarity, evolutionary rates, long branch attraction, rooted and unrooted trees, monophyletic group, molecular clock, adaptation, lineage effects, neutralism, cladograms, phylograms, etc. The course covers these and other major concepts in Evolutionary Biology and Phylogenetics. Attendees will acquire specific skills in using the methodology in Comparative and Evolutionary Biology problems. The course is designed to be a mixture of theoretical and practical sessions developed in 5 days, where both classic and recently introduced methods for phylogenetic reconstruction will be covered. As outcome of the more recent developments, the course dedicates a day to the analysis of adaptation at a molecular level. The software resources that will be used in the practical sessions include: Phyml, Phylip, MEGA, TreePuzzle, MrBayes, PAML, Modeltest-Protest, and the Phylemon web server.

More details and application instructions at:

http://gtpb.igc.gulbenkian.pt/bicourses/MEPA11

Information on all GTPB courses at http://gtpb.igc.gulbenkian.pt Other courses also open for applications: IB11 Introductory Bioinformatics MAPS11 Model-based Inference in Population Structure BPB11 Bioinformatics using Python for Biologists KDMC11 Knowledge Discovery and Management in Chemoinformatics

About to open: RNA11 RNA Bioinformatics NGSDM11 Next Generation Sequencing Data Management

– Pedro Fernandes GTPB Coordinator

Pedro Fernandes <pfern@igc.gulbenkian.pt>

Portugal PopulationStructure Apr4-7

*** ANNOUNCEMENT ***

Deadline for applications March 26th

Dear All The Bioinformatics Training Course course MAPS11 is OPEN for applications

IMPORTANT DATES for this Course Deadline for applications: March 26th 2011 Notification of acceptance dates: EARLY: March 14th 2011 (on special request, see Application) NORMAL: March 28th 2011 Course date: April 4th to April 7th 2011

MAPS11 Model-based Inference of Population Structure with Mark Beaumont, LounÃs Chikhi and Barbara Parreira

Course description

Course description

Population genetic data are increasingly used in several areas ranging from ecology to anthropology and archaeology. In all these areas, the aim is to infer some aspects of the demographic history of populations based on present-day genetic data. A variety of Monte Carlo techniques have been developed to achieve this. Recent years have seen the development of simulation tools that allow users to simulate genetic data under complex scenarios. At the same time approximate Bayesian computation (ABC) has become a popular approach for inferring population genetic parameters such as migration rates, the size of founding populations, or the time at which populations split from a common ancestor. In this course we will provide an overview of the Monte Carlo techniques that have been used in population genetics.

In this 4-day course we will introduce the main concepts that underlie many of the models that are frequently used in population genetics. We will use classical clustering method such as implemented in the STRUCTURE software and will introduce a variety of Monte Carlo techniques that have been used for inference in population genetics including methods of inference based on ABC. We will discuss genealogical (coalescent-based) methods and also those based on forward-in-time simulations. We will discuss some of the tools that are available and discuss issues such as model validation, model choice, and summary statistics.

More details and application instructions at:

http://gtpb.igc.gulbenkian.pt/bicourses/MAPS11
Information on all GTPB courses at http://gtpb.igc.gulbenkian.pt Other courses also open for applications: IB11 Introductory Bioinformatics MEPA11 Molecular Evolution, Phylogenetics and Adaptation BPB11 Bioinformatics using Python for Biologists KDMC11 Knowledge Discovery and Management in Chemoinformatics

About to open: RNA11 RNA Bioinformatics NGSDM11 Next Generation Sequencing Data Management

– Pedro Fernandes GTPB Coordinator

Pedro Fernandes <pfern@igc.gulbenkian.pt> Pedro Fernandes <pfern@igc.gulbenkian.pt>

Roscoff France MarineEvolutionaryGenomics May15-28

Summer course on marine genomics at the Marine Biological Station of Roscoff (F)

>From May 15th - May 28th, 2011 the 7th Summer Course on Marine Evolutionary & Ecological Genomics will take place at the Station Biologique de Roscoff, France.

The course consists of lectures, tutorials and computer based exercises in the following subjects. Phylogeny & tree of life- sequence analyses, phylogenetic techniques (clustering, Bayesian statistics), molecular clock, case studies Phylogeography - molecular evolution through networks, phylogeographical techniques, coalescence, population dynamics, case studies Population genetics - structure, connectivity and gene flow, assignment, effective size and population dynamics, case studies Genomics - next generation sequencing, database searching, basic skills in data handling and bioinformatics Functional genomics - genome structure, molecular evolution at the functional level Comparative genomics - whole genome comparisons, concatenated phylogeny, genome organization, annotating genomic information, co-evolution Environmental genomics - methods for detecting diversity; detecting adaptive variation; NGS: why and how; case studies. Applications in aquaculture, blue biotech, conservation, fisheries, metagenomics, nutrigenomics and the like will be discussed.

Target group PhD students (at least in their second year) and post docs with a solid knowledge in phylogenetics and/or population genetics. Students with an applied background (e.g. aquaculture, blue biotech, fisheries, nutrigenomics) are encouraged to apply.

Application and contact To apply please fill in the application form and send to Jonas Collén (collen@sb-roscoff.fr) together with a 2-page CV before April 10th 2011.

16 participants will be selected on the following criteria:

1. Relevance of the course for their PhD or post-doc project 2. Background and experience of applicant 3. We will aim at mixing people with different research backgrounds; probably not more than one person per institute will be considered. We will also aim at an equal gender distribution.

The selected persons will be notified at the end of April and have to confirm within 7 days. We will have a waiting list in case of non- confirmations and cancellations.

Confirmed teachers Sandie Baldauf, U. Uppsala, SE Jonas Collén, U Paris 6, FR Simon Creer, U Bangor, UK Yves Desdevises, CNRS Banyuls, FR J Jakob Hemmer-Hansen, DTU-Aqua, DK Galice Hoarau, U Bodø, NO Jeanine Olsen, U Groningen, NL Frédéric Partensky, SB-Roscoff, FR Heroen Verbruggen, U Gent, BE Filip Volckaert, KULeuven, BE Mathias Wegner, ETH Zurich, SW

Organizing committee Claudie Perron, SB-Roscoff, FR Jeanine Olsen, Univ Groningen, NL Jonas Collén, SB-Roscoff, FR Filip Volckaert, KULeuven, BE

For information and application forms: Jonas Collén Station Biologique de Roscoff BP 74, F-29680

ROSCOFF CEDEX France Phone: +(33)2 98 29 23 23 Fax: +(33)2 98 29 23 24 Email: collen@sb-roscoff.fr [URL: will be launched on 15 March 2011]

Filip Volckaert <Filip.Volckaert@bio.kuleuven.be>

Roscoff France MarineEvolutionaryGenomics May15-28 2

Summer course on marine genomics at the Marine Biological Station of Roscoff (F)

>From May 15th - May 28th, 2011 the 7th Summer Course on Marine Evolutionary & Ecological Genomics will take place at the Station Biologique de Roscoff, France.

Second announcement

Aims: To introduce genetic and genomic approaches for the analysis of biological diversity, evolution and adaptation at the species and population level in the ocean.

The course consists of lectures, tutorials and computer based exercises in the following subjects. Phylogeny & tree of life- sequence analyses, phylogenetic techniques (clustering, Bayesian statistics), molecular clock, case studies Phylogeography - molecular evolution through networks, phylogeographical techniques, coalescence, population dynamics, case studies Population genetics - structure, connectivity and gene flow, assignment, effective size and population dynamics, case studies Genomics - next generation sequencing, database searching, basic skills in data handling and bioinformatics Functional genomics - genome structure, molecular evolution at the functional level Comparative genomics - whole genome comparisons, concatenated phylogeny, genome organization, annotating genomic information, co-evolution Environmental genomics - methods for detecting diversity; detecting adaptive variation; NGS: why and how; case studies. Applications in aquaculture, blue biotech, conservation, fisheries, nutrigenomics and the like will be discussed.

Target group PhD students (at least in their second year) and post docs with a solid knowledge in phylogenetics and/or population genetics. Students with an applied background (e.g. aquaculture, blue biotech, fisheries, nutrigenomics) are encouraged to apply.

Application and contact To apply please fill in the application form and send to Jonas Collén (collen@sb-roscoff.fr) together with a 2-page CV before April 10th 2011.

16 participants will be selected on the following criteria:

1. Relevance of the course for their PhD or post-doc project 2. Background and experience of applicant 3. 4. We aim at mixing people with different research backgrounds; probably not more than one person per institute will be considered. We will also aim at an equal gender distribution.

The selected persons will be notified at the end of April and have to confirm within 7 days. We will have a waiting list in case of non-confirmations and cancellations.

Teachers Sandie Baldauf, U. Uppsala, SE Jonas Collén, U Paris 6, FR Simon Creer, U Bangor, UK Yves Desdevises, U ParisVI, FR Jakob Hemmer-Hansen, DTU-Aqua, DK Galice Hoarau, U Nordland, NO Jeanine Olsen, U Groningen, NL Frédéric Partensky, SB-Roscoff, FR Heroen Verbruggen, U Gent, BE Filip Volckaert, KULeuven, BE Mathias Wegner, AWI-Sylt, GE

Organizing committee Claudie Peron, SB-Roscoff, FR Jeanine Olsen, Univ Groningen, NL Jonas Collén, SB-Roscoff, FR Filip Volckaert, KULeuven, BE

For information and application forms: Jonas Collén Station Biologique de Roscoff BP 74, F-29680 ROSCOFF CEDEX France Phone: +(33)2 98 29 23 23 Fax: +(33)2 98 29 23 24 Email: collen@sb-roscoff.fr

Filip Volckaert <Filip.Volckaert@bio.kuleuven.be>

Rostock Germany EvolutionaryDemography

The International Max Planck Research School for Demography announces a new course:

Introduction to Evolutionary Demography (IMPRSD 189)

Start: 4 July 2011 End: 9 July 2011 Location: Max Planck Institute for Demographic Research (MPIDR), Rostock, Germany

Instructors:

* Daniel Levitis, MPIDR * Hal Caswell, Woods Hole Oceanographic Institution * David Thomson, University of Hong Kong * Annette Baudisch, MPIDR * Alexander Scheuerlein, MPIDR * Oskar Burger, MPIDR * Maren Rebke, MPIDR

Course description:

Understanding survival, reproduction and other life-history events is central to the study of both demography and evolutionary biology, and each field has developed methods and concepts to observe patterns and elucidate principles. The growing field of evolutionary demography treats demographic variables (patterns of survival, reproduction, and development) as properties of organisms that reflect evolutionary processes, just as morphology, behavior, and physiology do. It draws on both disciplines to search for evolutionary explanations of demographic patterns in terms of adaptation, genetics, phylogeny, and the environment. Further, it applies demographic methods and reasoning to answering evolutionary questions. Demography and evolutionary biology are conceptually unified and inextricably linked, so the questions we want to answer can best be tackled by traversing traditional disciplinary boundaries. This course is intended to introduce early career researchers from both fie lds to the concepts, methods, challenges and questions of evolutionary demography.

Course structure:

We will begin with an introduction to classical evolutionary demography and the motivations for combing evolution and demography, incorporating enough basic evolutionary theory and demographic theory to get everyone on the same page. We will then focus on current topics in evolutionary demography, including:

* Aging across the Tree of Life: Measures and Patterns * Sex-specific differences in mortality patterns: Evolution in action * Modes of adaptive explanation of demographic patterns: a survey * The pace and shape of aging * The evolution of mortality of the young * Age specific reproduction in the wild * Life-history allometry and Charnovian invariants

Finally, pairs of students will be asked to spend the afternoons of the 7th and 8th preparing short presentations, to be presented on July 9th. Each pair will discuss the evolutionary basis of a different demographic trait or phenomenon, what is known about it and how it can be investigated.

Organization:

For July 4-8, each morning will consist of two lectures (one hour each) and each afternoon will have a one hour lab. Then the afternoon of July 9th will be occupied with short presentations by pairs of students.

Prerequisites:

Students should be familiar either with the basics of demographic life- table methods, or with evolutionary theory. Familiarity with Stata or R software will be very helpful.

Examination:

Students will be evaluated on participation in class and on short presentations.

Financial support:

There is no tuition fee for this course. Students are expected to pay their own transportation and living costs. However, a limited number of scholarships are available on a competitive basis for outstanding candidates.

Recruitment of students:

* Applicants should either be enrolled in a PhD program or have received their PhD. * A maximum of 16 students will be admitted. * The selection will be made by the MPIDR based on the applicantsâ scientific qualifications.

How to apply:

Applications should be sent by email to the MPIDR. Please begin your email message with a statement saying that you apply for course IMPRSD 189 - Introduction to Evolutionary Demography.

* You also need to include the following three documents, either in the text of the email or as attached documents. (1) A two-page curriculum vitae, including a list of your scholarly publications. (2) A one-page letter from your supervisor at your home institution supporting your application. (3) A one-page statement of your research and how it relates to course IMPRSD 189. Please indicate whether you would like to be considered for financial support. * Send your email to Heiner Maier (office@imprs-demogr.mpg.de). * Application deadline is 31 March 2011. * Applicants will be informed whether they will be admitted by 15 April 2011.

Readings:

The course will make use of readings from:

* Baudisch, A. 2011. The pace and shape of ageing. Methods in Ecology and Evolution. DOI: 10.1111/j.2041-210X.2010.00087.x * Caswell, H. 2001. Chapter 11, Matrix population models. Sinauer. * Jones, O. R., Gaillard, J. M., Tuljapurkar, S., Alho, J. S., Armitage, K. B., Becker, P. H., Bize, P., Brommer, J., Charmantier, A. &

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UCopenhagen HumanPopGenet Jun20-25

PhD Course in Human Population Genetic Analyses (5 ECTS)

June 20 -25, 2011, Dept. of Biology, University of Copenhagen

Instructors:

Andrew G. Clark, Mark Beaumont, Anders Albrechtsen, Rasmus Nielsen, Line Skotte, and Ida Moltke.

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, haplotype structure, IBD mapping, admixture mapping, genotyping data, re-sequencing data, phasing and imputation, HapMap data, 1000 genomes project, online resources.

The fee for the course is 1800 dkr (approx. US $550) for participants who are not enrolled in a recognized PhD or Masters program. It is free for PhD and Master's students. The fee does not include food and accommodation.

For sign up and questions, please email: cphsummercourse@gmail.com

Rasmus Nielsen <rasmus_nielsen@berkeley.edu>

UMichigan EvolutionaryEpidemiology Jul25-29

Evolutionary Epidemiology and Public Health

The University of Michigan School of Public Health Graduate Summer Session 2011

July 25-29, 2011

Betsy Foxman and Randolph Nesse

Course Description: New applications of evolutionary theory to medicine are growing and helping to explain apparent paradoxes, such as rapidly increasing rates of breast cancer, increased asthma vulnerability in certain populations and the metabolic syndrome (For details see The Evolution Network at http://evolutionandmedicine.org). Epidemiologists have begun to apply these principles and ask new questions, such as do genes that vary by latitude explain hypertension, and how might public health interventions for infectious disease be 'evolution-proofed' This course will explore how epidemiologists and other public health workers can make use of these advances in their own work. Applying evolutionary theory can sharpen research questions, raise new possible explanations for observed phenomena and identify new types of exposure and outcome measures.

Pre-requisites: No prior training in evolutionary biology is assumed.

For more information and registration: http://www.sph.umich.edu/epid/GSS/ nesse@umich.edu

Valencia MEPPA 2011 May30-Jun3 2

SECOND ANNOUNCE

DEADLINE FOR APPLICATIONS: April 29th, 2011

Dear mailing list member,

Registration is now open for:

MEPPA11 - Molecular Evolution, Phylogenetics, Phylogenomics, and Adaptation

Please visit the Course website for details:

http://bioinfo.cipf.es/courses/mol_evol_phylo_6ed/ This course is likely to be very competitive for seats. Our maximum capacity is 25 seats. Early application is recommended!

Instructors: Hernan Dopazo, Toni Gabaldon, François Serra, Jaime Huerta- Cepas, and Salvador Capella

Invited Instructors: David Posada, University of Vigo (Spain) and Rafael Zardoya, MNCN-CSIC (Madrid, Spain)

Duration: 5 days. May 30 to June 03, 2011

Course Fee: Eur 380, include meals. A limited number of grants will be available.

Place: Centro de Investigacion Principe Felipe. Valencia. Spain. http://www.cipf.es/ Course description:

Currently, the simplest Bioinformatics analysis uses species comparisons in order to hypothesise the function of a novel biological sequence. Moreover, in most Molecular Biology labs, evolutionary and phylogenetic concepts are constantly being used with more or less formality: homology, similarity, evolutionary rates, long branch attraction, rooted and unrooted trees, monophyletic group, molecular clock, adaptation, lineage effects, neutralism, cladograms, phylograms, etc. The course aims to provide the necessary background to understand the basic concepts from comparative and evolutionary biology that are frequently used in molecular biology and bioinformatics analyses. The course consists in five full-day sessions with an adequate balance between theory and computer practice, oriented to solve frequent problems and hypothesis testing. The program covers the basic and advanced analysis of Phylogenetic reconstruction, Phylogenomic analysis of genomes and Maximum likelihood tests for molecular adaptation. The software resources that will be used in the practical sessions include: Phyml, Phylip, MEGA, TreePuzzle, MrBayes, PAML, Modeltest-Protest, Jmodeltest and the Phylemon 2.0 web server. (phylemon.bioinfo.cipf.es)

Please feel free to pass this information to colleagues in your community.

Co-ordinators: Hernan Dopazo and François Serra

Hernan Dopazo <hdopazo@cipf.es>

Hernán J. Dopazo, PhD Head of the Evolutionary Genomics Unit Bioinformatics & Genomics Department Centro de Investigación Príncipe Felipe c/ ep Avda. Autopista del Saler 16 (Junto al Oceanográfico) 46012, Valencia, España Tfn: (34) 96 328 96 80 ext: 1008 Fax: (34) 96 328 97 01 hdopazo@cipf.es http://hdopazo.bioinfo.cipf.es/ Hernan Dopazo <hdopazo@cipf.es>

WoodsHole MolEvolution Jul24-Aug3

Subject: Woods Hole Workshop in Molecular Evolution

Workshop in Molecular Evolution

Marine Biological Laboratory, Woods Hole, Massachusetts

July 24th - August 3rd 2011

Application Deadline: April 15, 2011

CONTACT: Admissions Coordinator, admissions@mbl.edu, 508-289-7401 http://www.mbl.edu/education/courses/special_topics/mole.html Course Directors: David Hillis, UT Austin; Mitchell Sogin, MBL, Woods Hole

The Workshop on Molecular Evolution presents a series of lectures, discussions, and bioinformatic exercises that span contemporary topics in molecular evolution. Since its inception in 1988, the workshop has encouraged the exchange of ideas between leading theoreticians, software developers and workshop participants. Lectures and discussions are augmented by computer laboratories focused on providing a sophisticated understanding of software including AWTY, BEAST, Clustal W/X, FASTA, FigTree, GARLI, MIGRATE, LAMARC, MAFFT, MrBayes, PAML, PAUP*, PHYLIP, and SeaView. Topics in the 2011 course include the theoretical, mathematical, and statistical bases of phylogenetic analysis; coalescence theory, maximum likelihood, and Bayesian estimators of population genetic parameters; comparative genomics and systems biology; and approaches to integrating molecular evolution with biochemistry, cell biology, developmental biology, biogeography, ecology, and conservation biology. The workshop serves graduate students, postdoctoral students, and established faculty from around the world.

Faculty for 2011 include:

Peter Beerli, Florida State University Joseph Bielawski, Dalhousie University Casey Dunn, Brown University Scott Edwards, Harvard University Joseph Felsenstein, University of Washington David Hillis, University of Texas Mark Holder, The University of Kansas Laura Kubatko, Ohio State University Paul Lewis, University of Connecticut Axel Meyer, University of Konstanz, Germany William Pearson, University of Virginia Antonis Rokas, Vanderbilt University Marc Suchard, UCLA David Swofford, Duke University Anne Yoder, Duke University Shozo Yokoyama, Emory University Derrick Zwickl, University of Kansas

David Hillis <dhillis@mail.utexas.edu>

Instructions

Instructions: To be added to the EvolDir mailing list please send an email message to Golding@McMaster.CA. At this time provide a binary six letter code that determines which messages will be mailed to you. These are listed in the same order as presented here — Conferences; Graduate Student Positions; Jobs; Other; Post-doctoral positions; WorkshopsCourses. For example to receive the listings that concern conferences and post-doctoral positions this would be 100010. Messages are categorized on the basis of their subject headings. If this subject heading is not successfully parsed, the message will be sent to me at Golding@McMaster.CA. In addition, if it originates from 'blackballed' addresses it will be sent to me at Golding@McMaster.CA. These messages will only be read and dealt with when I have time. The code 000000 has all channels turned off and hence gets only a once monthly notifcation of the availability of a monthly review pdf file.

To be removed from the EvolDir mailing list please send an email message to Golding@McMaster.CA. Note that 'on vacation', etc, style messages are automatically filtered and should not be transmitted to the list (I hope), but should you wish to avoid the e-mail's your code can be temporarily changed to 000000.

To send messages to the EvolDir direct them to the email evoldir@evol.biology.McMaster.CA. Do not include encoded attachments and do not send it as Word files, as HTML files, as LaTeX files, Excel files, etc. . . . plain old ASCII will work great and can be read by everyone. Add a subject header that contains the correct category "Conference:, Graduate position:, Job:, Other:, Postdoc:, Workshop:" and then the message stands a better chance of being correctly parsed. Note that the colon is mandatory.

The message will be stored until the middle of the night (local time). At a predetermined time, the collected messages will be captured and then processed by programs and filters. If the message is caught by one of the filters (e.g. a subject header is not correctly formated) the message will be send to me at Golding@McMaster.CA and processed later. In either case, please do not expect an instant response.

Afterword

This program is an attempt to automatically process a broad variety of e-mail messages. Most preformating is collapsed to save space. At the current time, many features may be incorrectly handled and some email messages may be positively mauled. Although this is being produced by LaTeX do not try to embed LaTeX or TeX in your message (or other formats) since my program will strip these from the message.