EvolDir

July 1, 2012

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

Ankara StudentCongressEvolBiol Sep29-Oct1

We would like to invite you and your students to attend the 1st International Student Congress of Evolutionary Biology in Middle East Technical University, Ankara/Turkey from 29 September - 1 October.

- We decided to organize this congress because of lack of an Evolutionary Biology Congress for students and also increasing attacks of fundamentalist and ignored opponents of the evolution. We want to sharing of information about Evolutionary Biology between the students comes from all over the world. Also want to show, young people adopt the Theory of Evolution.

Make an announcement to large masses is very important for us. If you will inform about our congress to your students also your colleagues, we will be thankful.

Please visit webpage of congress.

http://isceb.org/ Sincerely yours,

Babur Erdem

Middle East Technical University Biology and Genetics Student Club

Babür ERDEM

Middle East Technical University Biology Department
06800 ankaya Ankara/TURKEY

Homepage: http://metu.edu.tr/ ˜ e165381/ GSM: +905062299206

Babür ERDEM <baburerdem@gmail.com>

Avignon France PetitPois Aug28-31 DeadlineJun4

The deadline for abstract submission has been extended to June 4. Deadline for registration: June 22.

The 34th “Petit Pois Deridé“ meeting will take place next August 28-31, 2012, in Avignon, France.

Program, online registration and abstract submission at http://www.ppd2012.fr (you’ll have to create a user account in order to submit abstracts)

Contact: ppd2012@avignon.inra.fr

Hoping to see you soon, The organizers

vincent.calcagno@sophia.inra.fr

Brussels BarcodeOfLife ECBOL3 Sep17-20

Dear colleague,

As you may know already the Third European Consortium for the Barcode of Life conference (ECBOL3) will take place from 17-20 September 2012 in Brussels (Belgium). The conference will be organised by the Royal Museum for Central Africa (RMCA), the Royal Belgian Institute of Natural Sciences (RBINS) and ECBOL.

This reminder is to notify you that the deadline of early-bird registration for the conference (15 July) is approaching fast! We herewith send you a second circular which summarizes the major information on the conference. Please note that we have excellent invited speakers for each of the five major themes of the conference!

Registration for the conference and abstract submission is open. More information on the conference can be found at http://jemu.myspecies.info/ and in the attached second circular. We are currently negotiating special price offers for ECBOL participants with several hotels; please consult the website for any information on this.

We hope to see you in Brussels!

Yours sincerely,

Thierry Backeljau and Marc De Meyer - conference coordinators

ecbol3 <ecbol3@africamuseum.be>

Cambridge HumanAdaptation Sep28-29

Dear colleagues,

You are warmly invited to take part in a conference on “High Altitude and Cold: Adaptation to the Extremes”. This two-day meeting aims to bring together leading experts in physiology, population genetics and anthropology to discuss advances in our current understanding of high altitude and cold adaptation and the origins of populations living in extreme environments.

The conference will be held at Magdalene College, University of Cambridge, UK, on 28th-29th September 2012.

Registration deadline: June 30, 2012.

Further details, including registration, can be found at: http://mega.bioanth.cam.ac.uk/conf/extreme/ With a web-flyer available at: http://mega.bioanth.cam.ac.uk/conf/extreme/poster.pdf Best wishes, Toomas Kivisild Jay Stock Tiago Antao Alexia Cardona Christina Eichstaedt Luca Pagani Emma Pomeroy

tiagoantao@gmail.com

Dublin SMBE2012 Jun23-26 LastDay

Hi,

Tomorrow is the last day of online registration for SMBE 2012 in Dublin, Ireland. The meeting has >250 talks, with more than 80 by invited speakers. There are four plenary lectures and almost 800 posters. The conference has 26 symposia that are centered on specific topics and there is a plenary symposium for early-stage researchers competing for the Walter Fitch Prize, as offered by the Society for Molecular Biology and Evolution.

You can find more details here:

http://www.smbe2012.org/ Please let people know that you think might be interested.

Best,

James.

James McInerney, Department of Biology, NUI Maynooth, Co. Kildare, Ireland. P: +353 1 7083860 F: +353 1 7083845 W: http://bioinf.nuim.ie/james-mcinerney james.o.mcinerney@nuim.ie

Durham Recombination Jul14-16

Reminder– signups for presentations due JUNE 15, and that's also when the hotel block of rooms is released!

—– The 2012 annual meeting of the American Genetic Association will be held from 14-16 July at the Durham Convention Center in Durham, North Carolina, USA. The conference is entitled "Recombination: Molecular Mechanisms & Evolutionary Consequences".

"Recombination" affects myriad areas of biology in general and evolution in particular, ranging from proper segregation of chromosomes to advantages associated with sexual reproduction to patterns of DNA sequence variation within and between species to processes of species formation. Come to this exciting conference and meet our delightful presenters (see below) and participants from diverse areas of biology.

We invite contributed posters in ANY area of biology that even touches on recombination (virtually all do...).

Registration and conference information are online (http://www.theaga.org/2012/)

Deadline for poster presentation signup is *June 15*. Block of rooms at hotel also releases June 15. Conference attendance registration deadline July 1.

If you would like additional information about these exciting events, please email noor@duke.edu . Hope to see you there!

Distinguished lecture: Brian Charlesworth- University of Edinburgh, UK Talk title: "Background selection and patterns of molecular evolution and variation"

Symposium speakers: Adam Auton- Albert Einstein College of Medicine Justin Blumenstiel- University of Kansas Francesca Cole- Sloan Kettering Greg Coperhaver- University of North Carolina Justin Fay- Washington University (St Louis) Bret Payseur- University of Wisconsin Tom Petes- Duke University Jeff Sekelsky- University of North Carolina Nadia Singh- North Carolina State University John Willis- Duke University

Mohamed A. F. Noor noor@duke.edu Earl D. McLean Professor Tel: 919-613-8156 & Associate Chair Biology Department Lab: 919-613-8193 Box 90338 FAX: 919-660-7293 Duke University Durham, NC 27708 USA http://www.biology.duke.edu/noorlab/ noor@duke.edu

Glasgow PopGenetics Dec18-21

Hello:

This is an announcement that the next annual meeting of the Population Genetics Group will be held in Glasgow, from Dec. 18-21, 2012. This year's plenary speakers are Mike Arnold, Chariie Baer and Rod Page.

We hope to open registration in mid-August and early bird registration will close in mid-November. We have started updating the website (www.populationgeneticsgroup.org), where you can find more details on the schedule and events. This year's meeting has received generous sponsorship from the the Glasgow City Marketing Board, the Genetics Society, Nature Reviews Genetics, and the Institute of Biodiversity, Animal Health & Comparative Medicine (IBAHCM) at the University of Glasgow.

You can subscribe to the email list using the following link (https://spreadsheets.google.com/viewform?formkey=3DdEN2Y016ODdPTWRnNXhKSUFmbXY1RkE6MA) Please reply to pgg@populationgeneticsgroup.org if you have queries about the meeting.

We hope to see you in Glasgow in December.

Barbara Mable

Barbara Mable Dr. Barbara Mable Rm 404 Graham Kerr Building Institute of Biodiversity, Animal Health and Comparative Medicine College of Medical, Veterinary & Life Sciences University of Glasgow Glasgow, Scotland G12 8QQ Email: barbara.mable@glasgow.ac.uk Phone: +44 (0)141 330 3532 Fax: +44 (0)141 330 5971

barbara.mable@glasgow.ac.uk

KansasCity Genomics Oct26-28

Save the datesK and plan to attend the 10th Annual Ecological Genomics Symposium on October 26-28, 2012, in Kansas City. We will convene in the Kansas City Marriott Country Club at 6:00 p.m. on Friday, October 26th and conclude on Sunday October 28th at noon. Registration will be opening soon!

This year marks the 10th anniversary of the Ecological Genomics Symposia and we have put together an outstanding and extended lineup of thirteen speakers that will cover the latest research results as well as a retrospective on progress in Ecological Genomics over the last 10 years and challenges and opportunities for the future.

FEATURED SPEAKERS: Jennifer Brisson V University of Nebraska William Cresko V University of Oregon Scott Edward V Harvard University Martin Feder V University of Chicago Loretta Johnson V Kansas State University Jan Kammenga V Wageningen University Thomas Mitchell-Olds V Duke University Jeanne Serb V Iowa State University Emilie Snell-Rood V University of Minnesota John Werren V University of Rochester Christopher Wheat V Stockholm University Tom Whitham V Northern Arizona University Patricia Wittkopp V University of Michigan

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

Please share this announcement with colleagues and students who are interested in learning more about the field of Ecological Genomics. If you have questions, please contact Michael Herman or Loretta Johnson.

Funding for this symposium is provided by Kansas State University.

Ecological Genomics Institute Directors: Dr. Loretta Johnson, johnson@ksu.edu Dr. Michael Herman, mherman@ksu.edu

Kansas State University, Division of Biology 116 Ackert Hall, Manhattan, KS 66506-4901 ecogen.ksu.edu

Michael Herman <mherman@ksu.edu>

Leipzig Retrovirus Aug26-29

I'm writing on behalf of the organizing committee for the 11th International Feline Retrovirus Research Symposium (IFRRS) to be held August 26-29, 2012 in Leipzig (Germany) and would like bring the symposium to the attention of the 'Evolution Directory' readers:

The IFRRS is a bi-annual conference which brings together renowned experts from the international scientific community who study feline retroviruses and related topics and employ feline models of retroviral research. The symposium focuses on the latest advances in genomics, immunology, and infectious disease as well as gene therapy, anti-viral therapy and vaccine development from the perspective of feline health and the potential translational applications to human health. The IFRRS attracts and brings together a large group of researchers from academia, industry, and clinical specialists in veterinary as well as human medicine. As such the symposium provides a forum to share latest cutting-edge research findings and ideas and to foster collaborative efforts to improve feline and human health. Due to several requests we extended the deadlines for early registration and abstract submission for the 11th International Feline Retrovirus Research Symposium (IFRRS) until 15th of June 2012!

The symposium will start with a workshop on bioinformatics/genomic tools and a session on feline genomics/viral evolution. The following days will cover research areas including retroviral pathogenesis, restriction factors, immune response/modulation, vaccines and clinical/therapeutic aspects. The last day will focus on other feline viral infections and emerging diseases in cats. We look forwards to welcome you in Leipzig to share latest cutting-edge research findings on viral diseases of cats and to foster collaborative efforts to improve feline and human health.

All informations for the symposium can be found on our website at www.ifrrs.org.

If you have any questions, please don't hesitate to contact us.

On behalf of the organizing committee

Yours sincerely,

Thomas Vahlenkamp

Prof. Thomas W. Vahlenkamp, DVM, PhD

University of Leipzig Institute of Virology An den Tierkliniken 29 04103 Leipzig (Germany) phone: +49-(0)341/9738-200, -201 fax: +49-(0)341/9738-219

11th International Feline Retrovirus Research Symposium August, 26th- 29th 2012 , Leipzig, Germany www.ifrrs.org < http://www.ifrrs.org/ >

"Vahlenkamp, Prof. Dr. Thomas" <thomas.vahlenkamp@uni-leipzig.de>

Lund SpeciationBehaviour Aug18

Symposium (FroSpects/Lund): "The role of behaviour in non-adaptive and non-ecological speciation" (August 18 2012)

Dear evolutionary biologists,

We would like to remind about the FroSpects-symposium “The Role of Behaviour in non-adaptive and non-ecological specation” that will take place in Lund (Sweden) on August 18 2012. This one-day symposium is open to anybody who wish to attend, and we also welcome contributed talks (15 minutes), in addition to the three plenary speakers:

Rampal S. Etienne (Groningen University, Netherlands) Ruth Shaw (Cornell University, USA) John Wiens (SUNY, Stony Brook, USA)

For more information about the symposium, check this link: http://svenssonresearchlaboratory.blogspot.se/-2011/07/esflund18aug2012.html This speciation-symposium is one of several so-called “Post-conference symposia” that will take place after the ISBE-congress (12-17 August) that preceeds these one-day meetings. You can sign up here (do not forget to tick in the symposium you wish to attend and submit your Abstract if you intend to give a presentation):

https://docs.google.com/-spreadsheet/viewform?formkey=-dFZCR0lMRS1BRmwxZ2dEV0Zfb1ZPZmc6MQ#gid=0 Deadline for registration: June 15 2012. If you have any questions, please contact Maren Wellenreuther (maren.wellenreuther@biol.lu.se).

We wish you to Lund on August 18 2012!

Erik Svensson

Organizing committé:

Anna Runemark Erik Svensson Machteld Verzijden Maren Wellenreuther

Erik Svensson Professor Evolutionary Ecology Unit Department of Biology, Lund University SE-223 62 Lund SWEDEN

Phone: +46 46 222 38 19 Fax: +46 46 222 47 17 E-mail: erik.svensson@zooekol.lu.se

Webpage: http://www.lu.se/o.o.i.s/26007 Lab blog: http://svenssonresearchlaboratory.blogspot.com/ Researcher ID: http://www.researcherid.com/rid/E-8324-2010 Erik Svensson <Erik.Svensson@biol.lu.se>

LundU OxStress 18Aug deadline

ISBE post-conference symposium on “Oxidative stress as evolutionary and behavioral constraints - where are we now?”, Saturday 18 August 2012, Lund, Sweden (http://www.isbe2012lund.org/post-conference-symposia).

ABSTRACT SUBMISSION CLOSES FRIDAY 1 June Abstracts can be submitted online *http://-/tinyurl.com/bvfl8lf* or sent directly to either caroline.isaksson@biol.lu.se or michael.tobler@biol.lu.se.

The aim of the symposium is to examine the evidence for and against the role of oxidative stress as behavioral and evolutionary constraints by bringing together behavioral ecologists working on various mechanistic aspects. We wish to have a broad taxonomic representation, and to have organized group meetings and panel discussions to promote a dialogue between participants from different fields, countries and seniority. The symposium will be divided into three sessions with talks: development and ageing, immune defence and energetics, and reproduction and behavior, which will build the basis for group and panel discussions.

The symposium is free of charge but registration is required for all participants. Registration for participants who do not wish to present is open until 31 July (register online *http://tinyurl.com/-bvfl8lf*). More information and detailed program will be posted at http://www.isbe2012lund.org/post-conference-symposia by mid June.

We hope to see you in Lund!

Michael & Caroline

Dr Michael Tobler | Marie Curie Postdoctoral Fellow Department of Biology | Lund University | Ecology Building | SE-223 62 Lund | Sweden

School of Biological Sciences | The University of Sydney | Heydon-Laurence Building A08 | NSW 2006 Australia

Michael.Tobler@biol.lu.se

LundU SexualSelection Aug18

Dear EvolDir-members,

We would like to inform you about the speakers on the ISBE post conference symposium entitled “Recent developments in sexual selection research: History, trends and new horizons”. This symposium will take place on August 18 in Lund (Sweden), just after the ISBE-meeting (August 12 - 17, 2012) in the Ecology Building at Lund University.

In this symposium, we take a fresh look at the state of sexual selection and discuss possible future directions of this dynamic field of behavioral research. We focus on three areas of advancement within the field: 1) development of sexual selection theory, 2) sexual selection in females and 3) the genetics of sexual selection. A selection of experts will introduce each topic, and the symposium will end with both group and joint discussions. You can read more about the symposium here: http://www.isbe2012lund.org/post-conference-symposia/ Invited speakers:

Prof. Marlene Zuk, University of Minnesota

Introduction: Historical perspective of sexual selection theory

Prof. Hanna Kokko, Australian National University

OSR and Bateman gradient, unite!

Dr. Malin Ah-King, Uppsala University

Beyond the Darwin-Bateman paradigm: reaction norm of sex, flexible mate choice and a new theoretical framework

Dr. Jessica Abbott, Lund University

Sexual antagonism in hermaphrodites: an individual-level genetic tug-of-war

Prof. Tim Clutton-Brock, Cambridge University

Limits to sexual selection

Prof. Anders Berglund, Uppsala University

When do females invest in armaments, ornaments or offspring?

Prof. Nina Wedell, Univ. of Exeter

Sexual antagonism, selfish genes and insecticide resistance in flies

Prof. Hans Ellegren, Uppsala University

Sex-biased gene expression in birds**

Participation in the symposium is free of charge and it is not required that one has participated in the ISBE-conference. However, transport, accommodation and food has to be covered by the participants themselves.

You can sign up to this symposium and other post-conference symposia through this link (deadline June 15, 2012): https://docs.google.com/spreadsheet/viewform?formkey=dFZCR0lMRS1BRmwxZ2dEV0Zfb1ZPZmc6MQ#gid=0 Everyone is most welcome!

Kenyon Mobley and Kristina Karlsson Green on behalf of the organizing committee

Kenyon Mobley, Ph.D Max Planck Institute for Evolutionary Biology Department of Evolutionary Ecology August-Thienemann-Straße 2 24306 Plön, Germany +49 (0)4522-763-347

Max Planck Institute Research Page < http://www.evolbio.mpg.de/english/people/staff/wissPersonal/wissM89/index.html > SYNG BIO: < http://www.syngbio.org/ > a community resource for Syngnathid biologists

kenyon mobley <mobley@evolbio.mpg.de>

Madison EvoSysBio Jul30-Aug1

Dear All,

For those with an interest in interdisciplinary meetings, here is a perfect excuse to visit beautiful Madison, Wisconsin at short notice.

>From July 30 to Aug 1, 2012 will be the first meeting on Evolutionary Systems Biology with an associated workshop on modeling languages at the University of Wisconsin-Madison:

http://evolutionarysystemsbiology.org/meeting/2012-Madison/ The purpose of the EvoSysBio meeting is to explore, how to best bring together evolutionary biology and current systems biology and what new insights might result from this. Evolutionary systems biology analyses critically depend on our ability to build and analyze quantitative models of dynamical systems. Many important questions will require such quantitative analyses on scales that demand full automation. Appropriately designed problem specific programming languages are a powerful way for achieving such automation. The purpose of the associated workshop on modeling languages is to collect examples for what analyses might be desirable and how a modeling language might look like that could facilitate this. This is a place where you can say what you want! This discussion will inform future development of evolvix, a new user friendly model description language currently under development in the Evolutionary Systems Biology Group at UW-Madison.

The meeting is free, but registration is required for catering and other reasons. Registration will be open until July 21 and is easy, see link on website.

Posters can be contributed until July 21 and there is still the possibility to compete for a very small number of talks.

We expect many exciting interdisciplinary discussions and look forward to seeing you in Madison!

All the best, Laurence Loewe

– Laurence Loewe Assistant Professor Evolutionary Systems Biology Group Laboratory of Genetics and Wisconsin Institute for Discovery University of Wisconsin-Madison 330 North Orchard Street, Madison, WI 53715, USA http://evolution.ws/people/loewe Tel: +1-608-316-4324

loewe@wisc.edu

Mainz Germany BiodiversityEvolutionaryBiol Sep16-19

Dear Colleagues,

This is to remind you that registration and abstract submission for the

21st International Symposium Biodiversity and Evolutionary Biology of the German Botanical Society

(16th - 19th September at Mainz/Germany; http://www.biodivevol2012.uni-mainz.de/)

will close on Sunday 1st July.

We are looking forward to seeing you in Mainz!

Joachim W. Kadereit

Prof. Joachim W. Kadereit, Ph.D. Institut für Spezielle Botanik und Botanischer Garten Johannes Gutenberg-Universität Mainz

D-55099 Mainz/Germany

Tel.: +49 6131 3923755/3922533 Fax: +49 6131 3923524

“Gehrke, Berit” <gehrke@uni-mainz.de>

Marseilles EvolBiol Sep18-21 AcceptedAbstracts

Dear all the list of the first accepted abstracts for the 16th evolutionary biology meeting at Marseilles is available on the web site: http://sites.univ-provence.fr/evol-cgr/ regards Pierre Pontarotti

Pierre PONTAROTTI <Pierre.Pontarotti@univ-provence.fr>

Niteroi Brazil ComparativeGenomics Oct17-19

Tenth Annual RECOMB Satellite Workshop on Comparative Genomics

October 17-19, 2012, Niterói, Brazil

Website: www.uff.br/recombcg ** Due to several requests, the submission deadline has been extended to June 19th **

The increasing amount of genome-related data is a fruitful source for biological research. By comparing complete or partial genomes it is possible to infer a great amount of new biological information, including gene function, evolutionary relationship between species and ancestral genome organization. Due to the dimension of the available data, efficient computational tools are imperative to accomplish these tasks.

The RECOMB CG satellite workshop brings together leading researchers in the mathematical, computational and life sciences to discuss cutting edge research in comparative genomics, with an emphasis on computational approaches and novel experimental results. The program will include both invited speakers and contributed talks.

Contributions to the workshop are welcomed on any theoretical and/or empirical approach to genome-wide comparison. This includes genome evolution, algorithms for genome rearrangement, comparative tools for assembly, gene identification or annotation, comparison of functional networks, genomic variation in humans and model organisms, cancer genomics, duplication patterns of genes, segments and whole genomes, and comparative epigenetics. We encourage paper submissions that offer new biological findings or otherwise highlight their relevance to biology. Refereed papers will be published as open-access manuscripts in the journal BMC Bioinformatics.

The workshop will be held on the campus of the Universidade Federal Fluminense, in Niterói, Brazil.

CONFIRMED KEYNOTE SPEAKERS

- E. Virginia Armbrust (University of Washington, USA)

- Mariangela Hungria da Cunha (Embrapa, Brazil)

- J. Peter Gogarten (University of Connecticut, USA)

- Dario Grattapaglia (Embrapa, Brazil)

- J. Chris Pires (University of Missouri, USA)

KEY DATES

Paper submission deadline June 19, 2012

Acceptance notification July 10, 2012

Workshop October 17-19, 2012 - Niterói, Brazil

THEME AND SCOPE

The continuing advance of DNA sequencing technology has produced an avalanche of genome sequence and genome structural information across the evolutionary spectrum. Transforming that information into biological knowledge requires creative and innovative new computational and statistical methods for comparative genomics.

The RECOMB Satellite Workshop on Comparative Genomics aims to provide the premier forum for new computational developments applied to all aspects of comparative genomics. We solicit contributions on topics including comparison of genome structure and organization, genome function, and evolution. We particularly encourage contributions that use new computational methods to acquire new insight into biological processes. Advances in computational theory are welcome, though all submissions should include genome-scale analyses informed by comparative data.

All peer-reviewed and accepted RECOMB-CG manuscripts will be published in a supplement to BMC Bioinformatics as open-access, author-subsidized, articles.

Specific topics of interest include but are not limited to:

. Gene and genome duplication . Gene family evolution . Genome structural variation . Algorithms for comparative genomics . Genome rearrangements . Ancestral genome reconstruction . Multiple genome alignment . Genome sequence comparison . Modeling genome evolution . Comparative genomics for genome annotation . Gene tree reconciliation . Species and gene tree inference . Comparative metagenomics . Comparative genomics linked to proteomics, metabolomics, and other ˜omic data . Comparative genomics and gene expression and regulation . Applications of comparative genomic methods

CALL FOR PAPERS

Papers should be submitted via the EasyChair system: https://www.easychair.org/conferences/?conf=recombcg12. Submissions must be received in electronic form by 11:59pm (Samoa time), June 12th, 2012.

Papers submitted for review should represent original, previously unpublished work. At the time the paper is submitted to the conference, and for the entire review period, the paper should not be under review by any other conference or scientific journal.

At least one author per each successful submission is required to register and present the paper at the workshop. The paper will be included in the conference proceedings, which will be published in BMC Bioinformatics as open-access author-subsidized articles.

Authors are encouraged to use the BMC document templates when preparing manuscripts. Templates are available in Microsoft and LaTeX formats. Otherwise, submissions should be typeset as double-spaced A4

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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

Ottawa Evolution2012 Jul6-10 EvolutionEducation

If you are attending Evolution 2012, and are interested in evolution education, please attend the session described below. Your feedback, comments, and suggestions are needed!

Expanding SSE's Education Activities – Sunday, July 8, 8:30 – 10:00 am, Rm. 108

The SSE Education Committee is exploring the possibility of an education section within the society. The proposed section would compliment SSE members' scientific interests and address the practical career needs of members who teach. As a first step, the committee has proposed to hold a one day mini-conference on teaching evolution immediately following the Evolution 2013 main conference. This mini-conference would not replace education activities during the main meeting which include the Education Symposium, an education strand, and and posters. A planning meeting will be held at Evolution 2012 on Sunday morning, July 8. The first hour will be for public comments, ideas, and requests for both the mini-conference and an education section. The second hour will be a planning committee meeting. If you would like to volunteer to serve on the planning committee, please contact: Louise Mead (lsmead@msu.edu) or Kristin Jenkins (kjenkins@nescent.org)

*

Louise S. Mead, PhD Education Director BEACON Center for the Study of Evolution in Action Biomedical and Physical Sciences Building Room 1441 567 Wilson Road Michigan State University East Lansing, MI 48824 (517) 884-2560

Louise Mead <lsmead@msu.edu>

Ottawa Evolution2012 Jul7 Education

SSE Education Symposium at Evolution 2012

Teaching with data: Opportunities to engage students in doing science Saturday July 7, 2012 8:30am-12:00pm

Data lies at the heart of both doing science and understanding scientific knowledge. Yet, we often teach biology in data-poor classrooms. This years education symposium will directly address this challenge with presentations framing what we know about teaching with data and a break-out session with interactive demonstrations of important data-centric teaching and learning resources. Join us to learn about resources for teaching with data or ways to contribute data rich teaching materials.

For more information go to: http://bit.ly/-SSE_EdSymposium2012 Kristin Jenkins, PhD Education and Outreach Program National Evolutionary Synthesis Center 2024 W. Main Street, Suite A200 Durham, NC www.nescent.org Cell 608.622.9394

Kristin Jenkins <kjenkins@nescent.org>

Ottawa iEvoBioChallengeCompetition Deadline

The deadline for submissions to the yearly iEvoBio Challenge is June 25, 2012, and is rapidly approaching! This is our last reminder. This year's theme is "Synthesizing Phylogenies," and further information on criteria for challenge entries, how to submit them, and award amount can be found at http://-ievobio.org/challenge.html . Also, Biomatters Ltd is running the Geneious Challenge alongside iEvoBio's competition. The goal of this challenge is to develop a new and exciting visualization or analysis plugin to Geneious Pro, using the public API. See http://-ievobio.org/geneious_challenge.html for more information. The deadline for this competition is also June 25.

More details about the iEvoBio conference and program are available at http://ievobio.org. You can also find continuous updates on the conference's Twitter feed at http://twitter.com/iEvoBio and Google+ page, or subscribe to the low-traffic iEvoBio announcements mailing list at http://groups.google.com/group/-ievobio-announce . iEvoBio 2012 is sponsored by the US National Evolutionary Synthesis Center (NESCent) and by Biomatters Ltd., in partnership with the Society for the Study of Evolution (SSE) and the Society of Systematic Biologists (SSB).

The iEvoBio 2012 Organizing Committee: Hilmar Lapp, US National Evolutionary Synthesis Center (chair) Robert Beiko, Dalhousie University Nico Cellinese, University of Florida Robert Guralnick, University of Colorado at Boulder Rebecca Kao, Denver Botanic Gardens Ellinor Michel, Natural History Museum, London Nadia Talent, Royal Ontario Museum Andrea Thomer, University of Illinois at Urbana-Champaign

hlapp@nescent.org

StonyBrookU ExptEvol HonorOfDykhuizen Nov3

SAVE THE DATE:

SYMPOSIUM IN HONOR OF DANIEL E. DYKHUIZEN, NOVEMBER 3, 2012

EXPERIMENTAL EVOLUTION AND DNA

A one-day symposium entitled Evolution and DNA will be held at Stony Brook University on November 3, 2012. The symposium will recognize the scientific achievements of Dan Dykhuizen and mark his 70th birthday. The speakers, who have worked with Dan as students and colleagues, will include:

Daniel Hartl, Harvard University, . E. Dykhuizen, Pervasive Weak Selection and Finicky Proteins.

Antony M. Dean, University of Minnesota, : The Making of a Modern Science.

Daniel M. Stoebel, Harvey Mudd College, Role of Mobile Genetic Elements in Adaptive Evolution.

Lin Chao, University of California, San Diego V of Aging, Mortality and Immortality in Bacteria.

Evgeni Sokurenko, University of Washington, Mutations in Bacterial Genomes.

David S. Guttman, University of Toronto, Genomic Dissection of Innate Immunity Elicitors.

Michael Feldgarden, Broad Institute, Microbial Population Genetics: Linking Genomics and Infectious Disease.

Dustin Brisson, University of Pennsylvania; Paul W. Ewald, University of Louisville, Weigang Qiu, City University of New York; and Ing-Nang Wang, University at Albany: -Table Discussion: of Ecology and Evolution to the Study of Infectious Disease.

A dinner honoring Dan will be held on the evening of November 3 after the symposium.

Information for online registration, the schedule, and logistics will follow shortly. For further information, please contact:

Michael A. Bell

Department of Ecology and Evolution Stony Brook University Stony Brook, NY 11794-5245, USA Office Phone: 1-631-632-8574

Department Phone: 1-631-6328600

email: mabell@life.bio.sunysb.edu http://life.bio.sunysb.edu/ee/belllab/ "Michael A. Bell" <mabell@life.bio.sunysb.edu>

ULisbon PrimateEvolution Sep10-12

Apologies for cross postings.

2nd CFP: From grooming to speaking:

recent trends in social primatology and human ethology

Centre for Philosophy of Science, University of Lisbon, Portugal | September 10-12th, 2012.

Conference website

http://cfcul.fc.ul.pt/linhas_investigacao/Philosophy%20of%20Life%20Sciences/int_col/index.htm Plenary talks

Johan Bolhuis, Constança Carvalho & Luis Vicente, Augusta Gaspar, Nathalie Gontier, Mary Lee Jensvold, Simone Pika, Tim Racine, Jeroen Stevens, Jordan Zlatev.

Abstracts of the talks are now available online.

CFP: deadline June 30th

We call for primatologists, ethologists, anthropologists, sociobiologists, evolutionary, cognitive and comparative psychologists, biolinguists, evolutionary linguists, bioethicists, philosophers and historians of science, to provide talks on:

1. Historical reviews on the introduction and use of primate studies to acquire knowledge on the origin and evolution of communication and language

2. Methodologies of primate communication and language research

3. Theories on primate communication and the evolution of language

4. Ethical issues in social primatology and human ethology

Abstracts can be send to Ricardo Santos: rssantos@fc.ul.pt.

The author of the best abstract will be awarded a Springer Book Voucher for the worth of 180 euro. And a selection of talks will be published in an anthology for the Springer Book Series "Interdisciplinary Evolution Research".

Scientific committee

Rod Bennison, Rudie Botha, Massimiliano L. Cappuccio, Daniel Dor, Luc Faucher, Nathalie Gontier (chair), David Leavens, Robert Lickliter, Jorge M.L. Marques da Silva, Mark Nelissen, Eugenia Ramirez Goicoechea, Emanuele Serrelli, Chris Sinha, James Steele, Ian Tattersall, Natalie Uomini, Arie Verhagen, Luis Vicente.

Prof dr Nathalie Gontier Philosopher of evolutionary sciences http://vub.academia.edu/NathalieGontier nathalie.gontier@vub.ac.be

Vigo Spain ComputationalPhylogenomics Sep13-14

Computational and Statistical Phylogenomics meeting Vigo, Spain, September 13-14, 2012

Dear all,

We are organizing an international meeting on Computational and Statistical Phylogenomics in Vigo, NW Spain, this September that might be of your interest:

http://csphylo12.uvigo.es/ There will be invited talks by some of the most relevant scientists in the field, but no contributed talks. Confirmed speakers are: Bastien Boussau (USA), Oliver Eulenstein (USA), Olivier Gascuel (France), Laura Kubatko (USA), Jens Lagergren (Sweden), Nicolas Lartillot (Canada), Luay Nakleh (USA), Alexis Stamatakis (Germany), Marc Suchard (USA), Tandy Warnow (USA) and Ziheng Yang (UK).

We hope this meeting becomes a platform for the exchange of ideas, brainstorming and discussion around phylogenomics. We believe this is a timely meeting given that NGS techniques have opened a new era in phylogenomics, prompting the need for accurate statistical methods that take into account the complexities of this type of data and are implemented in efficient computational tools.

Besides the science, we will organize some social activities, like a visit to a National Park nearby at the astonishing Cies Islands.

For any questions, please contact us at csphylo12@gmail.com.

All the best,

David Posada University of Vigo Spain

dposada@uvigo.es

GradStudentPositions

Europe 13 EvolGenetics

Thirteen very generously funded graduate-level training places are available in the INTERCROSSING network. They are open to young researchers from any country in the world*. INTERCROSSING is an ITN funded by the European Union (see http://tinyurl.com/cnm22d4)

Successful candidates can register for a PhD*

The positions are in Austria, Denmark, France, Germany, the Netherlands, Slovenia, Spain and Britain*.

Each position combines training in Evolutionary Genetics with Statistics and Bioinformatics. As well as carrying out research, the thirteen successful candidates will attend frequent joint training courses around Europe. They will work in partnerships between Universities and Industrial partners to apply the research.

Applications by 5th July should be made at http://intercrossing.wikispaces.com/Apply+here%C2%A0 where much additional information including is available on the research topics etc.

*See the web site for definitions of 'young researchers'. Note places are also open to PhD students who will not graduate before Oct 2012. The residency criteria encourage movement between countries.

Richard Nichols Professor of Genetics http://webspace.qmul.ac.uk/ranichols/research.htm richard.alan.nichols@gmail.com

Finland FarmAnimalEvolution

Open position

A PhD-student position in farm animal genomics is available at the Biotechnology and Food Research Unit of MTT Agrifood Research Finland (http://www.mtt.fi/english) in Jokioinen, Finland from August 2012 till August 2014, with a possibility of extension for two years. The student will join the Animal Genomics Research Team.

The student will work in the sheep genomics SOMICS-project funded by the Academy of Finland. The project aims to investigate genetic, genomic, evolutionary, nutritional and environmental factors affecting the prolificacy trait of domestic sheep breeds, by using state-of-art genomic technologies, such as whole-genome SNP genotyping, transcriptomics and bioinformatics, statistical and population genetics tools. Systems biology methods will be applied. The research will be carried out at the MTT Agrifood Research Finland, in the collaboration with the Chinese Academy of Sciences, the Russian Academy of Agricultural Sciences and the University of Helsinki.

The PhD student will be registered in one of the Finnish universities to carry out PhD studies and to defend his/her thesis. The studies will be conducted under the supervision of MTT senior researchers on animal genomics. The candidate applying this position should have MSc or equivalent level in bioinformatics, molecular and population genetics, animal science, biotechnology, veterinary medicine or other relevant disciplines. The candidate should have good written and oral skills in English.

The salary will be based on the job grade (the present position will be on the levels 10-12) and personal work performance.

Applications, including CV and references should be addressed to director Eeva-Liisa Ryhänen, MTT Biotechnology and Food Research and sent by mail MTT/kirjaamo, Humppilantie 14, 31600 Jokioinen, Finland or email in a single pdf-file to the Registry Office of MTT kirjaamo@mtt.fi no later than the 1st of August 2012, 3PM Finnish time.

Information about the position can be obtained from Professor Juha Kantanen, phone +358 29 531 7309, juha.kantanen@mtt.fi or the Director of Biotechnology and Food Research Unit of MTT, Dr Eeva-Liisa Ryhänen, phone +358 29 531 7692, eeva-liisa.ryhanen@mtt.fi or Docent Jaana Peippo, phone +358 29 531 7604, jaana.peippo@mtt.fi.

terhi.iso-touru@mtt.fi

Grenoble StatPopGenetics

PhD position available in statistical genetics in Grenoble (France)

The lab develops statistical methods for population genetics including Approximate Bayesian Computation, genome scans for selection, inference of population structure and association studies. The lab (http://membres-timc.imag.fr/Michael.Blum/) is in a beautiful alpine environment and offers an excellent research environment.

Applications from highly motivated and outstanding students with a Masters degree (or equivalent) in one of the following disciplines will be considered: bioinformatics, statistics or machine learning, evolutionary genetics, theoretical population genetics. Students from related disciplines, such as physics, computer sciences or mathematics are also welcome to apply. Applicants with a genuine interest for interdisciplinary PhD education will be preferred.

Contact Michael.blum@imag.fr

Blum michael <michael.blum@imag.fr>

ImperialCollege London EvolutionaryParasitology

Two PhD positions are available for research on the ecology and evolution of parasites in my newly created group at the University of Neuchâtel.

The general goal of the group is to integrate evolutionary and ecological thinking into the epidemiology and control of infectious diseases. We develop a theoretical basis of this integration and test empirically the assumptions and predictions of the theory, using malaria, microsporidians and the mosquitoes that transmit them as experimental systems. If you are interested, please see my webpage for a list of publications and more details: http://www3.imperial.ac.uk/-people/j.koella. Successful candidates will have the opportunity to develop their own projects within the frame-work of the group.

Neuchâtel is located in the French part of Switzerland and is an attractive city with a high quality of life. The city is located on the shore of Lake Neuchâtel with the Jura Mountains to the North and a view of the Bernese Alps to the South. For outdoors enthusiasts, this is an excellent area for outdoor activities such as hiking, climbing or skiing.

* *

Job requirements: The positions require independent, highly motivated, enthusiastic, and scientifically curious individuals with a background in ecology, evolutionary biology, immunology or related fields. An MSc (or equivalent) in Biology is required. The positions require some teaching of undergraduate biology labs in French.

Start data: The positions are available on September 1, 2012; starting dates are flexible.

Application requirements: Formal applications should include: a 1-2 page cover letter (in English) indicating research interests, your CV, and two letters of reference. Application deadline is July 15, 2012. Applications and informal enquiries can be submitted by email to: jkoella@gmail.comJacob Koella

Jacob Koella

Current address:

Division of Biology Imperial College London Silwood Park Campus Ascot, Berkshire SL5 7PY United Kingdom

Address from September onwards:

Institut de Biologie Université de Neuchâtel Rue Emile-Argand 11 2000 Neuchâtel Switzerland

Jacob Koella <jkoella@gmail.com>

MaxPlanck Jena 6 EvolutionaryBiol

“Ecological interactions at surfaces and interfaces”

The International Max Planck Research School (IMPRS) “The Exploration of Ecological Interactions with Molecular and Chemical Techniques” in Jena, Germany, invites applications for 6 PhD fellowships beginning in January 2013.

Many key ecological interactions between plants, herbivores, bacteria and fungi occur at different surfaces. These form the boundaries between organisms and their aerial, aquatic, or subterranean environments, as well as the interfaces of organisms interacting with each other. The release or detection of odors and other chemical signals occurs at surfaces; surface biofilms made by bacteria and diatoms create unique environmental niches. Yet very little information is available on compounds and proteins playing a role in the local communication processes at these interfaces. New methods are required to study these interactions at a mechanistic level. Our aim is to develop such methods and apply them to different projects and research questions. Approaches will include mass spectrometry based techniques and different imaging technologies. The development of new bioinformatics tools for data analysis is also needed. A complete list of projects offered is available on our website.

We are looking for enthusiastic PhD students with strong interests in the above described central topic. Applicants should have a firm background in one of the following fields: bioinformatics, analytical chemistry, entomology, neurobiology, molecular biology, biochemistry, plant physiology and genetics. All our projects are highly integrative and require willingness to closely collaborate with researchers of different backgrounds.

The Research School is a joint initiative of the Max Planck Institute for Chemical Ecology, Friedrich Schiller University, Jena, the Leibniz Institute for Natural Product Research and Infection Biology, and the Leibniz Institute of Plant Genetics and Crop Plant Research. We offer state of the art equipment, an excellent research environment, supervision by a thesis committee and a structured training program including scientific courses, training in transferable skills and internal conferences. Successful candidates will receive an IMPRS fellowship. Working language is English.

Application deadline is June 29, 2012.

For detailed information on the IMPRS, projects offered and application requirements, please visit our website http://imprs.ice.mpg.de/ . Dr. Tim Sharbel Apomixis Research Group Leader Dept. of Cytogenetics and Genome Analysis Leibniz Institute of Plant Genetics and Crop Plant Research (IPK) Corrensstraße 3, D-06466 Gatersleben Germany

NOTE NEW WEBPAGE: Apomixis Group Webpage

International Max Planck Research School (IMPRS) faculty member

IPK Webpage www.ipk-gatersleben.de tel: +049 (0)39482 5608 fax: +049 (0)39482 5137

sharbel@ipk-gatersleben.de

MPI EcologicalGenomics Sticklebacks

*PhD student position in Ecological Genomics / Bioinformatics at the Max Planck Institute for Evolutionary Biology

We are inviting applications for a PhD position in the evolutionary ecology department to work on a project dealing with detecting patterns of selection and adaptation across three-spined stickleback genomes using next-generation sequencing data. The position is available starting August/September 2012 and is funded for 3 years.

We are looking for a motivated student with a background in bioinformatics andstrong interests in genome evolution, population genetics and speciation. The successful candidate can choose to work on various aspects of genome evolution across stickleback populations and will be required to analyse genomic data. Computer programming/scripting skills are desirable, and experience dealing with next generation sequencing data or databases is a plus. Additional wet lab work is possible if desired to aid in validating results.

The three-spined stickleback /Gasterosteus aculeatus /has become a model organism for evolutionary ecology because of its repeated independent adaptations to different freshwater environments within the last few thousand years, the associated morphological changes such as loss of bony armour, and a well-annotated reference genome. Our main focus deals with investigating genome architecture across various populations from distinct environments harbouring habitat-specific parasite communities. We have previously shown experimentally that parasites can select for particular resistant alleles in stickleback populations that increase in frequency in a single generation. The analysis of high throughput sequence data will therefore enable us to garner a broader genome-wide understanding of the genetic changes underlying such adaptations and population differentiation in an ecological context.

The research will be carried out in the lab of Prof. Manfred Milinski (http://www.evolbio.mpg.de/english/-abteilungen/evolutionsoekologie/index.html) in close collaboration with PhD students and postdocs as well as with Prof. Thorsten Reusch from the Helmholtz Centre for Marine Sciences (IFM-Geomar), Prof. Erich Bornberg-Bauer (University of Münster) and Prof. Monika Stoll (Leibniz-Institute Münster). As a Max Planck Institute we have labs and technical equipment of the highest standards including facilities for genome analysis. The MPI for Evolutionary Biology offers a stimulating scientific environment dedicated to evolutionary biology. The working language at the institute is English.

Our institute is located in Plön, a Northern German town surrounded by lakes and ideal for outdoor activities. In the vicinity are two major cities (Kiel and Lübeck) as well as the Baltic Sea. Hamburg is reachable by train or car in 90 minutes. The institute maintains links to the Christian Albrechts University of Kiel and the Helmholtz Centre for Marine Sciences (IFM-Geomar).

The Max Planck Society is an equal opportunity employer and encourages female scientists and scientists with disabilities to apply.

We ask applicants to send a PDF of their CV and motivation letter as well as contact information of two references by e-mail to milinski@evolbio.mpg.de We will begin reviewing applications starting July 2^nd until the position is filled.

*Inquiries about additional details are also most welcome (milinski@evolbio.mpg.de).

chain@evolbio.mpg.de

Portugal InvasivePlants

Apologies for re-posting. This year opening accepts candidatures from citizens of ANY European Union State Member.

Daniel

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Coimbra, June 11, 2012

We are looking for candidates that want to apply for an FCT (Portuguese Foundation for Science and Technology) doctoral fellowship to join us at the Centre for Functional Ecology (cfe.uc.pt) of the Department of Life Sciences of the University of Coimbra (Portugal).

The successful candidate will be expected to develop his/her research within the framework of the European project ReproWeed, which will investigate the creation of reproductive barriers between native and non-native ranges of the invasive weed /Centaurea solstitialis/. The research involves laboratory and field-based work and involves the interaction with an international network of collaborators, with the possibility to travel to California, Chile, Argentina, Australia, Turkey and Spain.

The candidate should have a good scientific background, with an interest into reproductive and evolutionary ecology of invasive weeds, and willingness to learn genetic molecular techniques. A good knowledge of the English language, experience with molecular techniques and ecological statistics is highly desirable. Candidates should be citizens of any European Union Member State, or from third states if they are permanent residents of Portugal, and comply with the conditions to be a candidate for the FCT Doctoral Grants: https://www.fct.pt/apoios/bolsas/concursos/individuais.phtml.en The doctoral fellowship includes a monthly payment of 980 euros (tax-free), plus an accident insurance and a monthly contribution to the Portuguese Social Security system (full healthcare and retirement, but no unemployment benefits). The project ReproWeed will cover for all research costs, including travels, attendance to conferences, etc. The scholarship is renewable for up to four years, at the end of which the candidate is expected to defend his or her PhD. dissertation thesis.

A call for fellowship applications will be open until July 3, 2012 but contacts should be made before June 21, at 5pm CET. Interested candidates should send a covering letter describing their research interests and experience, a CV, and the contact information for up to three professional referees to Daniel Montesinos (danimontesinos@gmail.com) or Sílvia Castro (scastro@bot.uc.pt). Informal inquiries are welcome.

More informations about the group:

http://www.mendeley.com/profiles/daniel-montesinos/ http://cfe.uc.pt/scastro http://www.uc.pt/en/fctuc/ID/plantecolevol —- Daniel Montesinos Centro de Ecologia Funcional Universidade de Coimbra Apartado 3046 3001-401 Coimbra, Portugal T: (+351) 239 855 238 (ext. 139) http://cfe.uc.pt/daniel-montesinos http://www.mendeley.com/profiles/daniel-montesinos Daniel Montesinos <danimontesinos@gmail.com>

QMULondon 2 EvolGenetics

Two Post-Graduate Research Fellowships in Plant Genome Analysis

CLC bio and Queen Mary University London now offer two joint 3 year fellowships as part of the INTERCROSSING network under a Marie Curie ITN Program. These provide an exceptional opportunity for young researchers to further their careers in academia and the private sector, and gain a PhD from the University of London.

The two fellows will work together in the development and application of biological data, bioinformatics tools and statistical methods to study epigenetic modifications of polyploid genomes and the evolution of polyploid genomes through the mechanisms of mutation, selection and introgression.

Fellow 1 will be based at CLC Bio, Aarhus, Denmark, with a six month outplacement at Queen Mary University of London. He/she will research and develop bioinformatics methods for the analysis of polyploid genomes, including genome mapping, identification of SNPs, gene losses, and copy number variations. Fellow 1 will collaborate with Fellow 2 in the practical application of these methods.

Fellow 2 will be based at Queen Mary University of

London, with a six month outplacement at CLC Bio, Denmark. He/she will generate whole genome and genome-wide sub-sampled data from diploid and polyploid species of Betula (Birch). He/she will analyze genomic and geographic patterns of introgressive hybridisation and genome evolution in natural populations using bioinformatics methods developed in collaboration with Fellow 1.

The INTERCROSSING network is funded by the European Commission under the Marie Curie Initial Training Network Program, and draws on resources across the European research community to provide training for 13 young researchers. The principal strategic objective of INTERCROSSING is the cultivation of a new type of early stage researcher (ESR) to deal with challenges of exploiting the latest Next Generation Sequencing (NGS) technologies.

Both fellows will be jointly supervised by Dr Roald Forsberg (Director of R&D at CLC Bio; www.clcbio.com) and Dr Richard Buggs (Senior Lecturer and NERC Fellow, Queen Mary University of London; http://www.sbcs.qmul.ac.uk/staff/-richardbuggs.html).The fellowships are open to outstanding candidates of any nationality, who are within 4 years of gaining a degree that would give access to doctoral studies, but do not yet have a PhD. They must have spent less than 12 months in the last 3 years in the country of new employment.

We encourage candidates to make informal enquiries about the project by email to the supervisors (r.buggs@qmul.ac.uk, hr@clcbio.com). To apply, please complete an online application form via the following link: http://intercrossing.wikispaces.com/-Apply+here%C2%A0. Fellow 1 is INTERCROSSING position #4, and Fellow 2 INTERCROSSING position #5.

The formal deadline for applications is: 5th July 2012

– Richard Buggs MA, DPhil NERC Fellow & Senior Lecturer School of Biological and Chemical Sciences Queen Mary, University of London London E1 4NS United Kingdom

email: r.buggs@qmul.ac.uk website: http://-www.sbcs.qmul.ac.uk/staff/richardbuggs.html office: +44(0)207 882 3058 mobile: +44(0)772 992 0401 twitter: @RJABuggs

Richard Buggs <r.buggs@qmul.ac.uk>

TrinityCollege Dublin FossilPrimates

Fully-funded 3 YEAR PhD studentship at Trinity College Dublin, Ireland

Evolutionary ecology and extinct species: how do fossils change our interpretations of present-day biodiversity patterns?

Evolutionary ecology, the study of patterns and processes at the interface of evolutionary biology and ecology, is an exciting and rapidly growing research area. However, most studies ignore one important factor: extinction. The aim of this PhD project is to test and develop methods for adding fossil species into phylogenies and evolutionary ecology analyses, using primates as a study group.

Primates are a fascinating group in which to study the effects of extinct species because there is substantial extinct diversity in the order. There are currently 376 species in two suborders: Strepsirrhini (lemurs, lorises, galagos and aye-ayes: 88 species) and Haplorrhini (tarsiers, New World monkeys, Old World monkeys and apes: 288 species). The earliest primate fossils date from around 55 million years ago during the early Eocene, and come from two major groups; Adapoidea (putative ancestors of Strepsirrhini) and Omomyoidea (putative ancestors of Haplorrhini). These primates were widespread, ranging across North America, Asia, Europe and Africa, and also species rich (nearly 100 species in each group) so apparently represented very successful radiations. However, the majority of these species were extinct by the end of the Eocene. Other fossil primates became extinct more recently, for example, at least one of the 17 species of extinct giant lemurs in Madagascar may have survived into the 17th century. These species are particularly interesting because they range in body mass from approximately 10-160kg, whereas present-day lemurs have a maximum body mass of only around 7kg.

The student will first collate a morphological dataset for extant and extinct primates, using published sources and collecting extra data from museums in the USA and UK. They will then build phylogenies using Bayesian approaches, and finally they will use these phylogenies to tackle interesting evolutionary ecology questions. The exact questions tackled will depend on the interests of the student. However, some potential questions include: (i) Can historical primate extinctions be explained by competition with other species of primate? (ii) Does adding extinct giant lemurs into analyses of primate body size evolution alter our conclusions about rates of evolution in primates, particularly in the Strepsirrhini (lemurs and relatives)? (iii) If all of the presently endangered primates become extinct, what will the consequences be for the morphological and functional diversity of primates? How will this affect the functioning of the ecosystems they inhabit? The results of these a nalyses will have implications for evolutionary ecology methods, evolutionary theory, and conservation planning.

The project will be supervised by Dr. Natalie Cooper at the School of Natural Sciences, Trinity College Dublin. The School is particularly strong in the area of Ecology and Evolution, with a dedicated seminar series and a range of peer-learning initiatives. The expected start date is September 2012. Full funding is provided for a 3 year PhD studentship from Trinity College Dublin. Stipend is euro 16,000 per annum plus fees for 3 years. There are no limitations on student nationality.

Applicants must have (or realistically expect to achieve) a first or upper second class Bachelors, or Masters degree in a relevant subject (Biology, Ecology, Anthropology, Palaeontology, Mathematics, Statistics or similar). The candidate will preferably have a high-level of numerical competency. Much of this work is collaborative and the candidate will be expected to be keen, motivated and willing to work as part of a team. In addition, applicants must be competent in written and spoken English and be prepared to travel to the USA and UK for data collection and collaborator meetings.

Applicants should submit a curriculum vitae detailing their qualifications and experience and containing the names and contact details of at least two referees, together with a covering letter explaining why they wish to pursue this project. Please direct any enquiries about the research to Dr. Natalie Cooper (ncooper@tcd.ie). Applications to be received electronically or as hard copy to Fiona Maloney (FIMOLONY@tcd.ie) on or before 15th July 2012.

Dr Natalie Cooper Assistant Professor Zoology Department School of Natural Sciences Trinity College Dublin 2 College Green, Dublin 2 +353 (0)1 896 1926 (work) +353 (0) 87193 5856 (mobile)

ncooper@tcd.ie

UBourgogne AvianSexualSelection

PhD PROPOSAL

Post-copulatory sexual selection in the houbara bustard

/A three year PhD position is available to work on a collaborative project dealing with the post-copulatory sexual selection in the houbara bustard./

In most animal species, females mate with multiple males giving rise to the potential for sperm competition and cryptic female choice. These post-copulatory components of sexual selection add to those acting on males to attract mates (pre-copulatory sexual selection).

Although the study of post-copulatory sexual selection has flourished in the last decade, there are very few biological systems that are amenable to the experimental study of sperm competition and cryptic choice.

Houbara bustards are endangered bird species living in North Africa (/Chlamydotis undulata/), Middle East and Central Asia (/Chlamydotis macqueeni/). In order to restore and reinforce natural populations of houbara in Middle East, the National Avian Research Center (NARC) has promoted a captive breeding program in Abu Dhabi (EAU) under the leadership of the International Fund for Houbara Conservation. This breeding program is based on the collection of sperm which is subsequently used to artificially inseminate females under standardized conditions (Saint Jalme et al. 1994). This allows investigating several aspects related to sperm competition and cryptic choice, in a species where both pre- and post-copulatory sexual selection is supposed to be a strong selective force. Indeed, males harbor extravagant sexual displays (Chargé et al. 2010, 2011; Preston et al. 2011) and females have been shown to mate with multiple males in the wild, where the proportion of clutches sired by multiple fathers is fairly high (60%) (Lesobre et al. 2010).

In the first stage of the PhD thesis, we expect to better characterize sperm traits that determine the likelihood to successfully fertilize eggs. Then, experimental work could be conducted to explore the following questions:

1)Is there a trade-off between pre- and post-copulatory components of sexual selection?

2)Is fertilization success mostly driven by sperm competition or cryptic choice?

3)Is there a scope for sexual conflict in this system?

In addition to their fundamental interest, the obtained results could also be valuable with respect to the genetic management of the captive breeding. On one hand, inseminating with a mix of semen could facilitate insemination procedure by reducing the time spent to select precise pedigree and by optimizing semen utilization (mixture of small ejaculates that are usually discarded could be easily used). On the other hand, sperm competition might result in severely biased paternity with a potential for strong involuntary selection acting on breeding males.

This is a collaborative project involving the NARC (Yves Hingrat, Loic Lesobre, Tony Chalah) where all the experimental work will be carried out and where the successful applicant will spend most of the time, the French CNRS in Dijon (Gabriele Sorci) and the Museum of Natural History in Paris (Michel Saint Jalme).

Interested applicants should send a CV and the name of three references to Gabriele Sorci (gabriele.sorci@u-bourgogne.fr <mailto:gabriele.sorci@u-bourgogne.fr>) and Michel Saint Jalme (mstjalme@mnhn.fr <mailto:mstjalme@mnhn.fr>).

Salary: 1,250 euros per month. Accommodation and food is provided by the NARC with no fees for the student.

Selected articles published by the group related to the project

Chargé R. et al. 2011. Immune-Mediated Change in the Expression of a Sexual Trait Predicts Offspring Survival in the Wild. PLoS ONE 6: e25305.

Preston B. et al. 2011. Sexually extravagant males age more rapidly. Ecology Letters 14: 1017-1024.

Chargé et al. 2010. Male health status, signalled by courtship display, reveals ejaculate quality and hatching success in a lekking species. Journal of Animal Ecology 79: 843-850.

Lesobre L. et al. 2010. Conservation genetics of Houbara Bustard (Chlamydotis undulata undulata): population structure and its implications for the reinforcement of wild populations. Conservation Genetics 11: 1489-1497.

Lesobre L. et al. 2010. Absence of male reproductive skew, along with high frequency of polyandry and conspecific brood parasitism in the lekking Houbara bustard Chlamydotis undulata undulata. Journal of Avian Biology 41: 117-127.

Saint Jalme M. et al. 1994.Artificial insemination in Houbara bustard (Chlamydotis undulata): influence of the number of spermatozoa and insemination frequency on fertility and ability to hatch. Journal of Reproduction and Fertility 100: 93-103.

Gabriele Sorci <gabriele.sorci@u-bourgogne.fr>

UChester EndangeredSpecies

Endangered species genetics

We are seeking expressions of interest from individuals who wish to apply for a fully funded PhD studentship, investigating the application of molecular tools to the management of breeding programmes for endangered species. The research will focus on African wild dogs and pygmy hippos but there is considerable scope for wider applications.

Applicants will be considered for nomination as a candidate for an International Postgraduate Research Scholarship (IPRS) tenable at the University of Western Australia: http://www.scholarships.uwa.edu.au/future-students/postgrad/international .If successful in any subsequent application for a scholarship, the PhD candidate will be co-supervised jointly by the University of Western Australia and the University of Chester (UK), with the student spending time at both institutions. Please note that there will be a further application process to undertake at a later point.

Given the precarious status of many in-situ large mammal populations, the need to establish long-term, viable breeding programmes in zoos, will become increasingly important. The goal of these breeding programmes is to maintain genetic diversity and reduce inbreeding over multiple generations. To help achieve this, studbooks are in place that provide breeding recommendations to ensure unrelated animals are paired together. However, to do this effectively, the genetic relatedness of the founders needs to be known. In reality this data is not available and so the default position is that all founders are assumed to be unrelated.

This PhD project will assess the founder relatedness in the African wild dog and the pygmy hippo studbooks to test the validity of the assumption of zero relatedness amongst founders. The genetic relatedness of the contemporary population will also be established and, importantly, genetically under-represented individuals will be identified for gene banking. This is an exciting opportunity to make a significant impact on conservation of endangered species.

Successful candidates should have a strong background in genetics, or evolutionary biology. Experience with a wide range of molecular techniques is essential and a strong interest in conservation is desirable. It also a key requirement that the candidate has at last one scientific publication to ensure competitiveness for a scholarship.

Interested candidates should contact Dr. Paul O'Donoghue (p.odonoghue@chester.ac.uk) or Dr Monique Paris (mparis@ibream.org) for further information.

Expressions of interest are invited until July 7th 2012 and should be sent to Dr Paul O'Donoghue (p.donoghue@chester.ac.uk).

Kind Regards

Natalie

Natalie Hough <n.hough@chester.ac.uk>

UIceland AmphipodEvolGenomics

Ph.D. position in evolutionary biology - evolutionary genomics of a groundwater amphipod.

A three year PhD position is available at the Department of Life and Environmental Scicences at University of Iceland, Reykjavik, supervised by Snæbjörn Pálsson, Associate professor, in collaboration with Christophe J. Douady, Professor at Claude Bernard University in Lyon, France.

The project is on population and evolutionary genomics of Crangonyx islandicus, a recently discovered subterranean amphipod endemic to Iceland. Novel high throughput sequencing methods will be applied. Firstly to evaluate the genetic patterns, partition and diversity with respect to habitats. Secondly to compare the transcriptome of the C. islandicus with Crangonyx pseudogracilis, living in surface freshwater. If unknown species in Icelandic groundwater will be found, their phylogeny and phylogeography will be explored.

Recent work in Snæbjörn Pálssons lab has shown that C. islandicus is composed of two or more cryptic species. Based on geographical patterns of genetic variation we showed that the species has diverged within Iceland for the last five million years, and has thus survived repeated glaciations of Ice age in groundwater. Analysis of the diversity points to refugias in fissures along the tectonic plate boundary in Iceland.

Applicants should have a masters degree, preferrably with experience in bioinformatics, genomics and/or population genetics. Good computer skills are helpful. The position is financed by the University of Iceland Research Fund. The candidate will be selected based on his or her education, research interest, former work and two letters of recommendation.

The application, with recommendation letter, should be sent to Snæbjörn Pálsson (snaebj@hi.is), before the July 15th 2012. Further information is provided by Snæbjörn, and can be obtained at http://www.hi.is/~snaebj . Snæbjörn Pálsson <snaebj@hi.is>

UJyvaskyla Finland ParasiteCoInfections

A PhD-student position is available in a project funded by the Academy of Finland at University of Jyväskylä (Department of Biological and Environmental Science), Finland

EVOLUTIONARY ECOLOGY OF CO-INFECTIONS IN PARASITES WITH COMPLEX LIFE CYCLES

Wild hosts are typically infected with a range of parasite species and genotypes of one species at the same time. This has significant implications for parasite-parasite interactions (one factor underlying parasite virulence) and for host's ability to defend itself against infections. These associations may also be subjected to considerable variation depending on the stage of a parasite life cycle. This is particularly true for parasites with complex life cycles that include several consecutive hosts with different conditions for co-infections in each. However, very little is currently known about these interactions in natural host-parasite systems.

This project will explore responses of parasites and their hosts to multiple parasite species and genotype infections, primarily using trematodes of the genus Diplostomum. The aims of the project are to determine (1) the role of antagonistic and facilitative parasite interactions in shaping co-infection dynamics, (2) the role of different types of host responses in determining the outcome of multiple infections, and (3) the influence of spatiotemporal dynamics of host-parasite interactions on patterns of parasite community assembly. Considerable latitude in specific research questions will be given to the student based on his/her personals interests.

Recent related papers:

Karvonen, A., Rellstab, C., Louhi, K.-R., Jokela, J. (2012). Synchronous attack is advantageous - mixed genotype infections lead to higher infection success in trematode parasites. Proceedings of the Royal Society B 279, 171-176.

Rellstab, C., Louhi, K.-R., Karvonen, A., Jokela, J. (2011). Analysis of trematode parasite communities in fish eye lenses by pyrosequencing of naturally pooled DNA. Infection, Genetics and Evolution 11, 1276-1286.

Karvonen, A., Seppälä, O., Valtonen, E.T. (2009). Host immunisation shapes interspecific associations in trematode parasites. Journal of Animal Ecology 78, 945-952.

Seppälä, O., Karvonen, A., Valtonen, E.T., Jokela, J. (2009). Interactions among co-infecting parasite species: a mechanism maintaining genetic variation in parasites? Proceedings of the Royal Society B 276, 691-697.

I invite highly motivated students with a background in evolutionary ecology / parasitology to apply. Starting date: 1st January 2013.

If interested, please submit your CV, contact information for two references, and a brief summary of research experience and interests as one PDF file to Dr. Anssi Karvonen (anssi.t.karvonen@jyu.fi<mailto:anssi.t.karvonen@jyu.fi>). Top candidates will be interviewed. For further information about the project, duration and salary email anssi.t.karvonen@jyu.fi<mailto:anssi.t.karvonen@jyu.fi> and visit http://users.jyu.fi/ ˜ anskarv/ Application deadline is 29th July 2012.

Dr. Anssi Karvonen

anssi.t.karvonen@jyu.fi

Karvonen Anssi <anssi.t.karvonen@jyu.fi>

ULeicester HumanGeneticsGIS

Funded PhD position in Geographic Information Science (GISc) as a tool for the analysis of human genetic and genomic data

University of Leicester, UK

Supervisors: Prof Mark A Jobling (Genetics), Dr Nick Tate (Geography)

Background: Genetic data on human populations are expanding exponentially through the activities of medical genetic consortia, individual research groups, and thousands of private individuals purchasing genomic predictive health testing and genetic genealogy services. All these data share a geographical (spatial) element: sampling locations, birthplaces of DNA donors, or ancestral locations based on grandparental birthplaces. There are other relevant geographically restricted variables, too: in complex disease epidemiology, these are interacting environmental factors, while for genetic ancestry, they are factors affecting population structure, such as indicators of past migrations in surnames, place-names, or archaeological evidence. So far, these geographical relationships have been assessed by a mix of ad hoc methods, with limited power to understand correlations and their explanations. There is a need to study geographical patterns of genetic diversity in a more sophisticated way, and an ideal and unexploited tool exists to do this: Geographic Information Systems (GIS), the scientific marriage of cartography, statistical analysis, and database technology.

Aims: The project lies at the interface between Genetics and Geographical Information Science (GISc) and will provide you with a unique opportunity to be trained in and work across these two disciplines. It aims to: (i) Explore and develop the use of GIS to represent and analyse existing genetic datasets, including data based on binary SNPs (single nucleotide polymorphisms) and multiallelic short tandem repeats; (ii) Develop methods to co-analyse existing and forthcoming genetic and non-genetic data taking into account different levels of spatial granularity and scale; (iii) Address a specific genetical and geographic research question that will be defined within the first year. The novel nature of the project makes it inappropriate to specify the research question beforehand, but an example might be an analysis of the distribution of rare variants that may contribute to disease phenotype heritability, within the context of other data relevant to both disease aetiology and population structure.

Methodology: Genetic datasets that can be considered include: available Y-chromosomal data; available whole-genome SNP data from the Wellcome Trust Case Control Consortium; forthcoming TwinsUK whole genome SNP data; whole-genome SNP data from the 'People of the British Isles' project. Possible spatial analytical tools and techniques from GISc for use with these datasets include Kernel Density Estimation and Geographically Weighted Regression.

Supervision and support: You will be cosupervised by Prof Mark Jobling (Genetics) and Dr Nick Tate (Geography), who have worked together on the HALOGEN project (History, Archaeology, Linguistics, Onomastics, GENetics: throwing light on the past through cross-disciplinary databasing http://www2.le.ac.uk/offices/itservices/resources/cs/pso/project-websites/halogen). You will gain dynamic interdisciplinary support through membership of the Impact of Diasporas (http://www2.le.ac.uk/projects/impact-of-diasporas) group, which includes historians, linguists, archaeologists, geneticists and mathematical modellers. Training will take place in both Genetics and Geography Departments. Please contact either Mark (maj4@le.ac.uk) or Nick (njt9@le.ac.uk) for further details.

Funding: Applicants should have or expect to obtain a first-class or upper second-class degree in Geography (ideally with experience of GIS) or Genetics. This studentship is fully funded at UK/EU rates by the University of Leicester. International students are welcome to apply but would need to pay the difference between the UK/EU rate and the international fee rate and must provide evidence of additional funding.

References:

Bowden GR, et al. (2008) Excavating past population structures by surname-based sampling: the genetic legacy of the Vikings in northwest England. Mol Biol Evol, 25:301-309. Paper from the Jobling group using geographically restricted surnames to select males for population genetic sampling.

Balaresque P, et al. (2010). A predominantly Neolithic origin for European paternal lineages. PLoS Biol, 8:e1000285. Paper from the Jobling group containing examples of spatial approaches to archaeological and genetic data.

Longley PA, Cheshire JA, Mateos P (2011). Creating a regional geography of Britain through the spatial analysis of surnames. Geoforum, 42:506-516. An example of the quantitative analysis of spatial distributions of surnames.

To Apply:

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UMontpellier CancerEvolution

PhD Thesis - Theoretical Approaches to Cancer Evolution

I am considering applications for a three-year PhD contract, to be available starting October 1st, 2012 at the University of Montpellier II, France.

The work will be performed in the research group headed by Dr. Michael Hochberg (http://www.eec.univ-montp2.fr/people/mike-hochberg/) and in association with Dr. Daniel Fisher (IGMM, Montpellier), Dr. Jean Clairambault and Prof. Benoit Perthame (INRIA, Paris).

Central objective: To increase our knowledge of cancer progression and therapeutic outcomes in specific systems, using evolutionary principles. What is the level of predictability of cancer dynamics at population and individual organism levels, given knowledge of population ecology, and the genetic, molecular and demographic characteristics of cells and their microenvironments? By applying evolutionary thinking to cancer, we aim to make discoveries that yield valuable insights on the selection pressures that shaped cancer origins and progression, as well as relevant information to improve cancer therapies. We believe that answers to many questions about cancer will result from interdisciplinary approaches, and that our studies will have an immediate impact on the scientific community. Although the idea of cancer as an evolutionary problem is not new, historically, little attention has been focused on applications of evolutionary biology to understand and control neoplastic progression and to prevent therapeutic failures. An accurate evolutionary approach should unite and explain, rather than replace, the insights from mechanistic non-evolutionary studies.

Specific goal: Cyclin-dependent kinases (CDK) are a new class of therapeutic targets for cancer cells, since they are required for cell proliferation and are efficiently inhibited by specific pharmacological agents. However, as with all chemotherapeutic agents, the development of clinical resistance is likely. The student will investigate using a systems biology approach the evolution of resistance to CDK inhibitors. The goal is the development of therapeutic strategies that minimize both tumour progression and chemoresistance. In order to understand how resistance arises, we will first develop a mathematical model of the effects of CDK inhibitors on fundamental cell parameters important in cancer: cell proliferation, growth rates, cell cycle exit (quiescence or senescence), migration, and cell death. Then, we will generate CDK-inhibitor resistant cells by in vitro evolution, using prolonged treatments with escalating doses of CDK inhibitors. Achievement of this project will provide key insights into how cell demography and signalling change through evolution under different therapy scenarios.

Requirements: Masters 2 thesis in applied mathematics (or postgraduate mathematical training), and demonstrated course work in evolutionary biology or training in evolutionary biology with mathematical emphasis.

Interested candidates need to apply by 15 June 2012 by sending (1) a letter of motivation, (2) a CV, and (3) the names, institutions and email addresses of two references to Dr. Michael Hochberg at mhochber@univ-montp2.fr

Michael Hochberg <mhochber@univ-montp2.fr>

UNeuchatel EvolutionaryEcolBioinformatics

2 PhD positions in Evolutionary Ecology / Bioinformatics: The Genomics of Plant Adaptation to Climatic Conditions

What is the genetic basis of local adaptation to heterogeneity in environmental conditions? - This is the main question addressed by a project on the genetics/genomics of adaptation in Arabidopsis lyrata. Two three-year graduate/PhD positions are available to join this project, supervised by Yvonne Willi at the Institute of Biology, University of Neuchatel, Switzerland.

The causes and mechanisms of adaptation to environmental change are relevant to many fields of biology, and we will tackle them from multiple angles: assembling environmental data, studying phenotypic differences in morphological and physiological characters within and across (>50) populations, and linking them to SNP frequency shifts.

The project is split into two parts: One student will focus on within-population processes (heterogeneity in soil-water availability, selection, gene flow), and the other will compare populations (large scale climatic variation, phenotypic differences, and associated SNP variation). The work will include analysis of partial-genome-scan data, so a strong background in quantitative thinking, statistical analysis, and bioinformatics programming (in R or Unix) is required.

The Institute of Biology at Neuchatel consists of a dozen groups working in diverse fields of ecology, evolution, physiology, and molecular and cell biology. The University in collaboration with the CUSO offers outstanding PhD programs in Evolutionary Biology and Genomics. For more information, contact Yvonne Willi (yvonne.willi@unine.ch) or see http://www2.unine.ch/-biol/ and http://biologie.cuso.ch/accueil/

Applicants must have a university degree in the natural sciences (ideally in evolutionary biology, genetics, or bioinformatics) that allows entrance to a PhD program, and very good organizational, analytical, and scientific writing skills. Motivated applicants should submit 1) a one-page letter that summarizes interests and relevant experience, 2) a CV, 3) copies of undergraduate and masters/diploma transcripts, and 4) contact information of two references - all as a single PDF - to: yvonne.willi@unine.ch. Applications are welcome until the positions are filled. Earliest evaluation of applications is on July 15, 2012.

WILLI Yvonne <yvonne.willi@unine.ch>

UNeuchatel OxidativeStress

PhD Position in evolutionary ecology, University of NeuchÃtel.

A fully-funded 3-year PhD position is available at the University of NeuchÃtel, Switzerland, to work on the causes and consequences of oxidative stress in avian semen. The position and research project are funded by the Swiss National Science Foundation.

Oxidative stress is pervasive and represents a major selective pressure throughout the animal kingdom. In particular, vertebrate spermatozoa are very susceptible to oxidative stress, which may affect sperm performance and male fertility. Oxidative processes are thus hypothesised to have a profound impact on the development of male reproductive strategies and antioxidant allocation strategies in species where males face sperm competition, the circumstance where sperm of two or more males compete to fertilise the same batch of eggs. This project will test whether antioxidant allocation strategies underlie the development of male reproductive tactics in relation to social status as predicted by sperm competition models. This goal will be achieved using a combination of field observations, field experiments and aviary experiments on house sparrows Passer domesticus.

The ideal candidate is highly motivated and creative with a keen interest in evolutionary questions. He/she shows a capacity to work both independently and as a team member and has excellent writing and communication skills in English. She/he has a background in evolutionary biology, behavioural ecology and/or ecophysiology. Previous experience with bird handling, lab work, experimental design and/or statistics is not essential but desirable. A MSc (or equivalent) in Biology is required.

The successful applicant will be based at the Institute of Biology, University of NeuchÃtel. This post offers opportunities to collaborate and interact with researchers working in related and complementary fields (http://www2.unine.ch/biol/page-7860_en.html). Our research groups are international and our working language is English. Knowledge of French is useful, but not essential. NeuchÃtel is an attractive city, situated by a beautiful lake at the foot of the Jura mountains and facing the Berner Oberland mountains. The city provides plenty of opportunities for cultural activities and sports and offers a high quality of life. Its excellent public transports make it easy to leave the city and head to the mountains for outdoor activities such as hiking, climbing or skiing.

Starting date: October 1, 2012.

Application requirements: Applications should include 1) a 1-2 page cover letter outlining motivations, research interests and relevant experience, 2) a CV with list of publications (if any), 3) copies of academic qualiï, 4) the contact details of two academic referees, and 5) a 1-page description of your MSc project. Send the above as a single pdf-ïto fabrice.helfenstein@unine.ch Applications received before July 31, 2012, will be given full consideration.

For further information, please do not hesitate to contact Fabrice Helfenstein, Assistant Professor SNF Please note that Fabrice Helfenstein, Assistant Professor SNF, Institute of Biology, University of NeuchÃtel, Emile-Argand 11, CH-2000 NeuchÃtel, Switzerland. Phone: +41 (0)79 427 44 24. Email: fabrice.helfenstein@unine.ch Webpage: http://www.iee.unibe.ch/content/staff/helfenst/index_eng.html Please note that I am currently based at the University of Berne, but, from september 1, 2012, will be based at the University of NeuchÃtel.

Fabrice Helfenstein

Junior Lecturer (Oberassistent) Evolutionary Ecology Group Institute of Ecology & Evolution Bern University Baltzerstr. 6 CH-3012 Bern Switzerland

Tel. +41 (0)31 631 30 19; +41 (0)79 427 44 24 Fax +41 (0)31 631 30 08 http://evolution.unibe.ch/content/index_eng.html http://www.iee.unibe.ch/content/staff/helfenst/index_eng.html Fabrice Helfenstein <fabrice.helfenstein@free.fr>

UOslo 2 EvolutionaryBiol

TWO 4-YEAR PhD POSITIONS (SKO 1017) is available at the Centre for Ecological and Evolutionary Synthesis (CEES), Department of Biology, Faculty of Mathematics and Natural Sciences, University of Oslo.

Candidates with background in evolutionary ecology, molecular biology, genomics, organismal biology, theoretical biology or statistics are encouraged to apply.

The positions are available for a period of four years with 25% compulsory work.

The CEES The projects will be carried out at the Centre for Ecological and Evolutionary Synthesis (CEES), Department of Biology, University of Oslo. The CEES is a centre of excellence for integrative biological research and is well-funded. 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 statistical methodology. The centre has funding to engage in cutting-edge research, it features a modern and well-equipped molecular lab facilitated for high-throughput sequencing, as well as a broad spectrum of field facilities. We are focusing both on the development of new theoretical/statistical methods/models and on diverse ecological and evolutionary questions in empirical systems ranging from microorganisms and plants to aquatic and terrestrial vertebrates. The CEES provides an international, young and inspiring research environment. The centre is chaired by Professor Nils Chr. Stenseth and currently employs 16 faculty members, 49 postdocs/researchers, 32 PhD students and 30 MSc students, and at any time more than 20 visiting researchers. Information about the centre can be found at: www.cees.uio.no . Read more about CEES CEES research in general: www.mn.uio.no/cees/english/research/ Infrastructure and field facilities: www.mn.uio.no/cees/english/research/about/infrastructure/ CEES members: www.mn.uio.no/cees/english/people/ Project Outline The candidates are requested to attach a Project Outline for their PhD-project along with their application. Please consult our webpages (see links above and below) for this, and do not hesitate to contact any of the CEES core members or the centre leader Nils Chr. Stenseth. When evaluating the applications, emphasis will be given to the project outline and the applicant's academic and personal prerequisites to carry out the project.

CEES research areas specifically relevant, though not exclusively so, for developing these PhD projects:

- Potential topic I "Response of Rodent Populations to plague Outbreaks": www.mn.uio.no/cees/english/-about/vacancies/potential-phd-project-plague.html
- Potential topic II "Red Queen hypothesis": www.mn.uio.no/cees/english/about/vacancies/-potential-phd-project-red-queen.html

- Potential topic III "Comparative Fish Genomics and Evolution": www.mn.uio.no/cees/english/about/-vacancies/potential-phd-project-comparative-fish-genomics-and-evolution.html

- Potential topic IV "Clock Gene": www.mn.uio.no/-cees/english/about/vacancies/potential-phd-project-clock-gene.html - Potential topic V "Epigenetics": www.mn.uio.no/cees/english/about/vacancies/-potential-phd-project-epigenetics.html The PhD candidates will each have at least two supervisors and will be trained as part of a collaborative, interdisciplinary research team. A detailed plan for the dissertation work will be developed in collaboration with the supervisors within the first term of the program. Application for the PhD positions requires a Master's degree or equivalent experience. The purpose of the fellowship is research training leading to the successful completion of a PhD degree.

Admission to the PhD Program The purpose for the fellowship is research training leading to a successful completion of a PhD degree. The fellowship requires admission to the research training program at the Faculty of Mathematics and Natural Sciences. Appointment to a research fellowship is conditional upon admission to the Faculty's research training program. An approved

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UPorto GenomeEvolution

PhD Students Proposals Selection of candidates for a PhD grant proposal to submit to the Portuguese Foundation for Science and Technology

We accept applicants for a PhD grant proposal to be submitted to the Portuguese Foundation for the Science and Technology under the following topics:

1. "A genome-wide sequencing study to characterize genes responsible for the development, sensory and adaptation in Vertebrates". Major phenotypic changes in vertebrates (from mammals to fish), occurred by the evolution of various gene products over the last half billion years. Understanding the genetic basis of the diversification of development and sensory genes in vertebrates can provide fundamental biological insight about species evolution, ecological fitness, and genetic diseases.

2. "A molecular genomic approach to unravel the evolution of natural toxins". Gene families, which encode toxins, are found in many marine animals (from deadly poisoning jellyfishes to sea snakes), yet there is limited understanding of their evolution at the nucleotide level and the evolutionary significance of their protein mutations. Understanding the evolution of ecological specialization is important for making inferences about the origins of natural toxins biodiversity.

3. "Genomics and global phylogeny of cyanobacteria species". It is much debated whether microorganisms are easily dispersed globally or whether they, like many macro-organisms, have historical biogeographies. Recent findings using faster evolving genetic markers in protozoa species revealed considerable genetic structure and suggested that protest biodiversity may be significantly higher than previously thought.

Other hot research topics in genomics, molecular evolution and bioinformatics can be considered deepening on the student motivation and ongoing research projects in our lab.

The granted candidates will have a monthly salary of 980 euros and will develop their work at CIIMAR, University of Porto, Portugal (http://www.ciimar.up.pt/). The candidates should have a B.S. or Graduation in Biology, Biochemistry or other related fields with a competitive score (16 or more out of 20 plus a Master degree with 16 or more out of 20) and should have a strong interest in developing research in Molecular Evolution, Genomics and Bioinformatics. Students with published papers in ISI journals will be given priority.

The candidates should include: - Detailed curriculum vitae; - Scanned copy of the Graduation title and Master title if applicable).

Candidates need to be European (EU) citizens or having residence in Portugal.

The applications titled “PhD candidate” should be submitted till 19 June 2012 by email to Dr Agostinho Antunes (aantunes@ciimar.up.pt)

Reference recent papers from our group:

http://www.ncbi.nlm.nih.gov/pubmed/18989457
http://www.ncbi.nlm.nih.gov/pubmed/18424146
http://www.ncbi.nlm.nih.gov/pubmed/16400146
http://www.ncbi.nlm.nih.gov/pubmed/17975172
http://www.ncbi.nlm.nih.gov/pubmed/18318906
http://www.ncbi.nlm.nih.gov/pubmed/12140239
http://www.ncbi.nlm.nih.gov/pubmed/22103247
http://www.ncbi.nlm.nih.gov/pubmed/21288162
http://www.ncbi.nlm.nih.gov/pubmed/22237837
http://www.ncbi.nlm.nih.gov/pubmed/21414966
http://www.ncbi.nlm.nih.gov/pubmed/22046320
http://www.ncbi.nlm.nih.gov/pubmed/21731689
http://www.ncbi.nlm.nih.gov/pubmed/22193333
http://www.ncbi.nlm.nih.gov/pubmed/22319140
Agostinho Antunes <aantunes@ciimar.up.pt>

UppsalaU EvolEcolGenetics

PhD position in evolutionary ecology and genetics

A four-year PhD position in evolutionary ecology and genetics is available at the Evolutionary Biology Center, Uppsala University, Sweden,starting in summer/autumn 2012.

Lineage divergence is a fundamental evolutionary process that can lead to the generation of reproductively isolated species. In this project you will study the evolution of reproductive isolation in a naturally hybridizing species pair of /Silene/. We have identified various reproductive barriers between the two species in previous studies, including habitat adaptation and conspecific pollen precedence. In this project, genomic regions controlling reproductive barriers will be identified in order to study their evolution. The exact work-plan of the thesis will be settled together with the doctoral student.

The PhD student will be based the group of Sophie Karrenberg at the Evolutionary Biology Center, Uppsala University (http://www.ebc.uu.se/forskning/-IEG/Plant/People/Karrenberg_Sophie/) and will be supervised by Sophie Karrenberg (main supervisor) and Alex Widmer, ETH Zurich (co-supervisor).

We seek a highly motivated student (MSc degree or equivalent required) with thorough education and/or strong interest in evolutionary genetics/genomics, ecology, and statistics. Previous experience with next-generation sequencing, bioinformatics, ecological experiments and statistical programming is advantageous. Candidates must be fluent in English (orally and written). We are looking for individuals who excel at working independently and, at the same, time have the interpersonal and communication skills to succeed at working in a team.

The successful candidate will receive her/his postgraduate training within the postgraduate school at the Evolutionary Biology Centre (http://www.ebc.uu.se/-?languageId=1) that is one of world’s leading research institutions in evolutionary biology. The postgraduate training comprises four years of full time studies. The successful candidate will receive a postgraduate fellowship the first year (15500SEK/month) and a postgraduate position year 2-4 (22400-25100 SEK/month). The position can be combined with up to 20% of teaching assistantship, which will then prolong the position accordingly.

Please feel free to contact Sophie Karrenberg (sophie.karrenberg@ebc.uu.se[1], +46 18 471 2863) for more information but please do not send any attachments (note: not available June 24-July 7). Union representatives are Anders Grundström, Saco-rådet, tel. +46 18 471 53 80 och Carin Söderhäll, TCO/ST, tel. +46 18 471 19 96, Stefan Djurström, Seko, tel. +46 18 471 33 15.

How to apply: Please prepare a letter of intent including descriptions of 1) your motivation for PhD studies in general and for this position in particular, 2) your education, especially in evolutionary biology, genetics/genomics/bioinformatics, ecology, and statistics, 3) your research interests. The application should further include a CV, an authorized copy of your MSc degree, and the names and contact information (address, email address, and phone number) of at least two reference persons. Relevant publications (including BSc/MSc thesis) should be enclosed.

YOU ARE WELCOME to submit your application electronically (reference code UFV-PA 2012/739), NO LATER THAN AUGUST 1, 2012, through application form accessible from the following webpage:

http://www.uu.se/jobb/phd-students/-annonsvisning?languageId=1&tarContentId=193566
Sophie Karrenberg Associate Professor

Uppsala University Evolutionary Biology Center Dept. of Ecology and Genetics Plant Ecology and Evolution

Norbyvägen 18 D 752 36 UPPSALA Sweden

+46-(0)18-471 2863

sophie.karrenberg@ebc.uu.se

UppsalaU EvolTrophicInteractions

PhD student position at Uppsala University - evolutionary traits in trophic interactions

Department of Ecology and Genetics, Evolutionary Biology Centre, Uppsala University.

This PhD position is aimed at improving our understanding of the spatial aspects of food web interactions in aquatic ecosystems. Top predators have the ability as mobile consumers to integrate spatially separated food webs and movement across habitats of these predators is key to understand how spatially separated food webs can be coupled. The student will test the importance of ecological factors and evolutionary traits constraining movements and foraging abilities of predators. We use mainly Eurasian perch (Perca fluviatilis) as our model species and the student will conduct a mixture of small scale aquarium studies, mesocosm experiments and field studies.

The candidate will receive her/his postgraduate training within the postgraduate school at the Evolutionary Biology Centre (http://www.ebc.uu.se/?languageId=-1). The school offers a creative and stimulating environment and is very rich in seminars, courses and possibilities to interact with other scholars and students (http://www.ebc.uu.se/education/?languageId=1).

For further information regarding the position, please contact Peter Eklöv (email: peter.eklov@ebc.uu.se, or phone: +46 18 471 2720).

You are welcome to submit your application no later than August 1, 2012, UFV-PA 2012/1553. For more information and how to apply please use the following link.

PhD-student position in limnology: (http://www.uu.se/jobb/phd-students/-annonsvisning?tarContentId=192815)

Peter Eklöv, Professor Limnology/Department of Ecology and Genetics Evolutionary Biology Centre, Uppsala University Norbyvägen 18 d, SE-752 36 Uppsala, Sweden Phone: +46-18-471 2720, mobile: +46-70-260 6856 e-mail: Peter.Eklov@ebc.uu.se http://www.ebc.uu.se/Research/IEG/limno/Staff/-Peter+Eklöv/ Peter Eklöv <peter.eklov@ebc.uu.se>

UUppsala MolEvol

PhD-student position in Molecular Evolution with specialization in metagenomics: http://www.uu.se/-jobb/phd-students/annonsvisning?tarContentId=-3D190218&languageId=1 PhD-student position in Molecular Evolution with specialization in genomics and bioinformatics: http://www.uu.se/-jobb/phd-students/annonsvisning?tarContentId=-3D190194&languageId=1 Text of the ads pasted below:

PhD-student position in Molecular Evolution with specialization in metagenomics

at the Department of Cell and Molecular Biology Apply no later than 2012-06-29

Starting date: September 1, 2012.

We study the molecular evolution of genomes from infectious disease causing bacteria as well as symbiotic and free-living bacteria using bioinformatic analyses of next-generation sequencing data (NGS). The knowledge is important to understand the early evolution of life as well as the mechanisms and selective forces that drive adaptations to different environments. Metagenomics is a new area of research in which all DNA present in a particular environment is sequenced and analyzed. With the aid of metagenomics it is possible to identify and study previously unknown microorganisms that have not been cultivated in the laboratory. Another new exciting technology is single cell genomics, which enables the genomes of single cells to be sequenced. By combining metagenomics and single cell genomics, it is possible to perform an in-depth investigation of the microflora, in a way that was not possible with conventional technologies.

The overall aim of this project is to study how bacterial populations evolve using metagenomics and single cell genomics. Samples will be taken from many different environments, such as lakes, fossils, earth, humans and insets. The work will be conducted in silico and consists of bioinformatics, comparative genomics and phylogenetics. Using single cell genomics, the PhD student will reconstruct the genome from individual cells in the environment. Metagenomic reads will be recruited to the reconstructed genomes, with the aim of inferring the natural sequence variation, and more specifically to compare mutation versus recombination frequencies for different species and environments to better understand the evolutionary forces that drive changes and adaptive processes in nature.

The candidate should have a Master of Science degree in Biology or similar qualifications with specialization in bioinformatics, molecular sequence analysis, microbiology or comparative genomics. Knowledge in bioinformatics analyses of sequence data is desirable, as is prior research experience and high grades. The candidate should be able to work well as part of a team but also independently, and be proficient in both written and spoken English. In filling this position the university aims to recruit persons who, in the combined evaluation of competence, skills and documented qualifications, are judged most suitable to carry out and develop the work-in-hand and to contribute to the positive development of the department. Departmental work, mostly teaching, will constitute at most 20% of the position. Information about research education can be found at the web site of the Faculty of Science and Technology, http://www.teknat.uu.se/cms/. Applicants must be eligible for PhD studies at Uppsala University.

The application should include a letter describing research interests and relevant experiences (maximum one page), CV, copies of grades, exams, master project thesis (or parts thereof) and additional documents. Please provide contact information reference persons and recommendation letters from prior research supervisors.

More information about the position can be obtained from professor Siv Andersson, e-mail: siv.andersson@ebc.uu.se, Phone, +4618-471 64 52 and +4618-471 43 79. Union representatives are Anders Grundström, Saco-rådet, Phone, +4618-471 53 80 och Carin Söderhäll, TCO/ST, Phone, +4618-471 19 96, Stefan Djurström, Seko, Phone, +4618-471 33 15.

You are welcome to submit your application no later than June 29, 2012, UFV-PA 2012/1386. Use the link below to access the application form.

PhD-student position in Molecular Evolution with specialization in genomics and bioinformatics

at the Department of Cell and Molecular Biology. Apply no later than 2012-06-29, UFV-PA 2012/1384

Starting date: September 1, 2012.

We study the molecular evolution of bacterial genomes using bioinformatic analyses of next-generation sequencing data (NGS). The knowledge is important to understand the early evolution of life as well as the mechanisms and selective forces that drive adaptations to different

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UValencia EvolutionaryBiology

Master on 'Integrative Evolutionary Biology'

The 'Cavanilles Institute of Biodiversity and Evolutionary Biology' (ICBiBE, University of Valencia, Spain), offers an official 'Master in Integrative Evolutionary Biology'. This master provides advanced training in Evolutionary Biology, and does so from an integrative perspective. Its main focus is on the ecological and genetic evolutionary analysis of traits and complex systems, and is mainly directed to students who wish to initiate a PhD/Career in Evolutionary Biology. ICBiBE is a modern, leading research institute in Evolutionary Biology and is part of Valencia's International Campus of Excellence. This master also hosts lecturers and professors from several other research institutes within the International Campus of Excellence: IBMCP (Institute of Biomolecular and Cellular Plant Research), COMAV (Institute for the Conservation and Improvement of Valencian Agrodiversity), ai2 (Institute of Automatics and Industrial Informatics), and CIDE (Centre for the Study of Desertification). Subscriptions to this master are now open. More detailed information and subscription at: http://www.uv.es/biodiver/v/docencia/index.htm Dr. Pau Carazo Edward Grey Institute, Dept. of Zoology, University of Oxford, Oxford OX1 3PS email: pau.carazo@uv.es email: pau.carazoferrandis@zoo.ox.ac.uk Phone: (+44) (0)1865 271 258 webpage: http://paucarazo.com Pau Carazo <pau.carazo@uv.es>

UVienna TheoPopGenetics

EU initial training network INTERCROSSING: PhD

Position in Theoretical Population Genetics at the University of Vienna

The mathematics and biosciences group (MaBS, homepage www.mabs.at) led by Joachim Hermisson at the University of Vienna is looking for a strong and highly motivated candidate for a PhD position in evolutionary modeling and statistical data analysis.

Project: * Genetics of Hybrid Zones and Introgression *

Hybrid zones are a fascinating study object from a population genetics perspective since they provide us prime examples of "evolution in action". As the two "species" that meet at a hybrid zone are not yet fully separated, several questions arise: Is a narrow hybrid zone is a natural first step towards full speciation? If so, how do the barriers to gene-flow build up along the chromosome? And how long does this take? Is there a lasting potential for adaptive gene-flow through these barriers – and could adaptive gene-flow inhibit speciation? Finally, can we detect "footprints" of these processes in DNA sequence variation?

In this project, we address these questions with a combination of analytical and statistical modeling, and application of these models to next-generation DNA polymorphism data. The core work of the Vienna PhD student will be the development of models and methods. The project is a collaboration with the Natural History Museum London. At the NHM, data from about 400 populations from a bluebell hybrid zone across Spain has been collected. The analysis of these data will be a joint endeavor. To this end, a six-month placement of the PhD student in London is part of the project.

INTERCROSSING: We are an EU funded excellence program for early career training and research. Further information can be found here:

http://intercrossing.wikispaces.com/-What+is+INTERCROSSING%3F Research environment: Vienna is not only one of the world's most liveable cities, but also offers an excellent research environment and is currently developing into one of the main centers in evolutionary research in Europe. The position will be located at the Max F. Perutz Laboratories, part of the Vienna Biocenter Campus, which houses a vibrant community of researchers from several institutes. As a member of the MaBS group, the student will also interact with Magnus Nordborg and members of his group, and will be part of a larger community of evolutionary biologists and population geneticists through the activities of the Vienna Graduate School for Population Genetics (http://www.popgen-vienna.at) and EvolVienna (www.evolVienna.at).

Conditions: The position is for three years, salary is according to the (very generous) EU rates. The starting date is October 2012 (with some flexibility).

Application: We are looking for a candidate with a strong background in quantitative methods (analytical or computational modeling or data analysis) and interest in evolutionary research. Applicants should have a Master / Diploma degree in natural science (e.g. biology or physics), mathematics, or bioinformatics. Programming skills are highly appreciated. The working language in the group is English. German skills are not essential.

All formal applications run through the INTERCROSSING Webpage. The application deadline is July 5th 2012. The application form is here:

http://intercrossing.wikispaces.com/-Apply+here%C2%A0 For informal inquiries and further information, interested candidates are encouraged to contact Joachim Hermisson (joachim.hermisson[AT]univie.ac.at) before submitting a formal application. In this case, please send a brief statement of interest and CV.

– Joachim Hermisson Professor for Mathematics and Biosciences University of Vienna Department for Mathematics Nordbergstr. 15, 1090 Vienna, Austria and Max F.Perutz Laboratories Dr.-Bohrgasse 9, 1030 Vienna, Austria phone: +43 (0) 1 4277 50648 email: joachim.hermisson@univie.ac.at www.mabs.at Joachim Hermisson <joachim.hermisson@univie.ac.at>

UZurich Evolution

The University of Zurich in Switzerland has recently decided to fund a research priority program on "Evolution in Action: From Genomes to Ecosystems". For the initial four year period (2013-2016) at least 11 PhD studentship will be available in the following 6 collaborative research projects:

*Project 1: Conservation Genomics: from Functional Variation to Population Dynamics

PIs: Lukas Keller and Andreas Wagner, Institute of Evolutionary Biology and Environmental Studies

*Project 2: Evolution in Action: Environment, Agriculture, and Human & Wildlife Disease

PIs: Kentaro Shimizu, Institute of Evolutionary Biology and Environmental Studies, Frank Ruehli (Centre for Evolutionary Medicine), Michael Kruetzen (Anthropological Institute and Museum), Beat Keller (Institute of Plant Biology), Thomas Wicker (Institute of Plant Biology), Ralph Schlapbach (Functional Genomics Center Zurich), Andreas Wagner (Institute of Evolutionary Biology and Environmental Studies), Wolf Blanckenhorn (Institute of Evolutionary Biology and Environmental Studies), Barbara Tschirren (Institute of Evolutionary Biology and Environmental Studies), Barbara Koenig (Institute of Evolutionary Biology and Environmental Studies)

*Project 3: Investigating the Importance of Epigenetics in Adaptation and Coevolution

PIs: Ueli Grossniklaus (Institute of Plant Biology), Florian Schiestl (Institute of Systematic Botany), Owen Petchey (Institute of Evolutionary Biology and Environmental Studies), and Bernhard Schmid (Institute of Evolutionary Biology and Environmental Studies)

*Project 4: Microevolution of Signaling Pathways relevant for Human Disease

PIs: Alex Hajnal, Konrad Basler, Ernst Hafen, and Michael Hengartner (all Institute of Molecular Life Sciences)

*Project 5: The Evolution of Language: an Integrative Approach

PIs: Marta Manser (Institute of Evolutionary Biology and Environmental Studies), Carel van Schaik (Anthropological Institute and Museum), Balthasar Bickel (Department of General Linguistics)

*Project 6: Genomic Correlates of Microbial Coevolution

PIs: Christian von Mering (Institute of Molecular Life Sciences), Jakob Pernthaler, and Leo Eberl (both Institute of Plant Biology)

Although some of these positions will be advertised separately, a good way to apply for them is through the PhD Program in Evolutionary Biology at the University of Zurich (http://www.evobio.uzh.ch/index.html). Applications should be submitted through the Life Science Zurich Graduate School (http://www.lifesciencegraduateschool.ch/). Note that the next deadline is approaching very fast (July 1st, 2012). Independent, creative and highly motivated students with an interest in evolutionary biology are highly encouraged to apply.

lukas.keller@ieu.uzh.ch

Jobs

BarnardCollege EvolutionaryMicrobiology

Adjunct Professor in Microbiology

The Department of Biology at Barnard College, Columbia University, seeks an Adjunct Assistant Professor to teach a lecture course in microbiology, beginning late August 2012. 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 on 15 June 2012. 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 1007 Altschul Barnard College, Columbia University 3009 Broadway New York, NY 10027 212-854-5405

He who laughs most, learns best. - John Cleese

Hilary Callahan <hcallaha@barnard.edu>

EastCarolinaU LabTech EvolGen

Lab Technician - Molecular evolutionary genetics Department of Biology East Carolina University Greenville, NC

We seek a highly motivated lab technician to join the lab of Dr. Ashley N. Egan at East Carolina University, an active lab investigatingpopulation genetics, evolutionary genomics, and phylogenetics of legume andinvasive species. For an outline of current and prospective projects in the lab, please go to http://www.ecu.edu/cs-cas/biology/egan_ashley.cfm . Applicants must have experience with PCR and DNA sequencing and/or microsatellite genotyping. Responsibilities include DNA extractions, sequencing and genotyping of plant samples, database entry and archiving and other duties as required.

Minimum Qualifications: Bachelor's or Master's Degree in an appropriate field such as Biological Sciences, Molecular Biology, or Genetics, PLUS demonstrated research experience that included performing DNA extractions and PCR, and facility with standard computer software programs. Experience with microsatellite genotyping and/or DNA sequencing is required. Applicants should be US citizens. Preference will be given to applicants with a Master's degree or demonstrated experience in the field. This is a full time 1-yr position with possibility of renewal. Applications are being accepted immediately and will be reviewed until the position is filled.

Qualified candidates should submit (via email) a letter of application describing qualifications for the position and reason for interest, CV, and letters from three references detailing the applicant's level of experience with DNA sequencing and/or genotyping, and overall capabilities working in a laboratory setting to egana@ecu.edu

Ashley N. Egan, Ph.D. Assistant Professor, Department of Biology North Carolina Center for Biodiversity Howell Science Complex - Mailstop 551 East Carolina University Greenville, NC 27858-4353 Office: N303a/N304 Lab: N304/N305 Phone (252) 328-4244 fax (252) 328-4178

EGANA@ecu.edu

EAWAG Switzerland FishConservation

Research Group Leader, Ecology and Conservation of River Fish

Eawag, the Swiss Federal Institute of Aquatic Science and Technology, is a Swiss-based and internationally networked aquatic research institute within the domain of theSwiss Federal Institute of Science and Technology. It is committed to the ecologically, economically and socially responsible management of water resources and aquatic ecosystems.

The Fish Ecology & Evolution Department of Eawag, located in Lucerne has a vacancy for a Group Leader in Ecology and Conservation of River Fish

We are looking for applications from individuals with an excellent research record in fish ecology, an earned doctorate in a relevant field (e.g., ecology or conservation biology), and an interest in integrating applied research in fish conservation and habitat restoration with the initiation of a strong research program on river fish ecology in Switzerland. Such a program would draw from evolutionary, ecosystem and community ecology perspectives and will benefit from the large diversity of riverine habitats in Switzerland and also from the huge investment of public funding into the restoration of river habitat over the coming decades. Research that combines field work, data analysis and theory is very much needed to inform and strengthen the scientific basis for decision making in conservation, restoration and management of endangered fish populations and their habitats.

The Center for Ecology, Evolution & Biogeochemistry (CEEB; http://www.eawag.ch/forschung/-cc/ceeb/index_EN) and the Department of Fish Ecology and Evolution (http://www.eawag.ch/forschung/-fishec/index_EN) at Eawag provide excellent opportunities for collaborative research. The Department is also closely affiliated with the Institute of Ecology & Evolution at the University of Bern through the joint appointment of Prof. Ole Seehausen. The successful candidate should take advantage of this collaborative environment and of Eawag's world-class infrastructure and facilities to develop a strong research program, acquire third party funding to support it, recruit PhD and Masters students, and contribute to Eawag's mandate in teaching and expert consulting. The CEEB is an English language working environment and excellent communication skills in English and skills in team work are essential; an ability to communicate in German is important for interaction with stakeholders.

Applications must be submitted by 30.06.2012 and should include an application letter describing your interests and their relevance to this position, a CV and list of publications, and the names and contact information for three references. Applications from women are especially welcome. Applications from mid-career and established researchers are encouraged; the level of the appointment will be commensurate with experience. Eawag is committed to promote equal opportunities for men and woman and to support the compatibility of family and work. The earliest starting date for the position is anticipated to be 01.01.2013.

For further information, please contact Prof. Ole Seehausen (ole.seehausen@eawag.ch).

We look forward to receive your application. The quickest way is to apply online. Please click on http://-internet1.refline.ch/673277/0113/++publications++/-1/index.html .This will take you directly to the application form.

Ole Seehausen

"Seehausen, Ole" <Ole.Seehausen@eawag.ch>

IGFL ULyon ComputationalGenomics

Institut de Gnomique Fonctionnelle de Lyon, France

Joint research unit UMR5242 (ENS de Lyon, CNRS, Universit Lyon 1, INRA)

IGFL call for team leaders Computational genomics / Systems biology

The Institut de Gnomique Fonctionnelle de Lyon (IGFL) is a joint research unit run by ENS de Lyon, CNRS, INRA and Universit Lyon 1. In line with its scientific expansion, the Institute is relocating, in summer 2012, to occupy a newly commissioned 3200 sq. m. building, within a multidisciplinary campus. The new location will host approximately 200 scientists and staff, including 14 experimental teams (wet labs), 5 having been recently recruited through a recurring international call for team leaders (see http://igfl.ens-lyon.fr/).

The IGFL is seeking to recruit outstanding candidates to establish computational biology / systems biology teams whose independent research axes are in line with the IGFLs overarching objectives.

Candidates will demonstrate a proven track record in their field, and their ability to integrate within the Institute environment. They are expected to develop an innovative research project in an area such as evolutionary genomics, modeling of developmental or physiological pathways, or functional genome analysis. 35 sq. m. in silico office space will be provided (up to 8 persons per team).

Applications (in English) should include a curriculum vitae, a short description of achievements and records of self-financing, a proposed research program of 10 pages maximum and contact details for 3 professional references. Please send the application as a single PDF named LASTNAME_IGFL.pdf to direction.igfl@ens-lyon.fr. Enquiries should also be directed to this address. An external panel of experts will review applications. The call will remain open until the two positions are filled.

The call will remain open until the two positions are filled, however, applications received before the 14th of July 2012 will be given priority in the selection process.

fred <frederic.brunet@ens-lyon.fr>

ImperialCollegeLondon 3 Evolution

3 Academic Positions in Ecology and Evolution (Lecturer/Assistant Professor or Reader/Associate Professor or Chair/Full Professor)

IMPERIAL COLLEGE LONDON

Division of Ecology and Evolution, Faculty of Natural Sciences

Lecturer salary: GBP 43,350 - GBP 48,400 per annum

Reader minimum starting salary: GBP 53,450 per annum

Chair minimum starting salary: GBP 68,170 per annum

Silwood Park Campus

The Division of Ecology and Evolution is looking to make three academic appointments in the broad areas of Ecology & Evolution. The posts will be based at the Silwood Park Campus. We anticipate that most appointments will be at Lecturer level. However, there is potential for appointments to be made at more senior academic levels, and welcome applications from more senior researchers. The goal is to improve fundamental scientific understanding of biological and ecological processes and systems. The research will focus on solving ecological, evolutionary and environmental challenges and could fit into a range of disciplines, from ecology, evolution, genomics, conservation science or environmental biology, and focus on microbes, plants, animals or whole ecosystems.

The Division will seek to appoint the best candidates with expertise in relevant areas of Ecology and Evolution. The potential for productive research collaboration with existing staff within the Division and wider Department of Life Sciences will also be carefully assessed. You will contribute to the mission of the Division of Ecology and Evolution, the Department of Life Sciences and further develop and promote the College's work in Ecology, Evolution, Environmental Biology or Conservation Science.

One of the positions will be expected to develop links with the Department of Physics and the Grantham Institute, and will form part of the European-sponsored Knowledge and Innovation Community (KIC) in Climate.

Reporting to the Head of the Division of Ecology and Evolution, you will be expected to identify opportunities in Ecology and Evolution and contribute to teaching and administration within the Division and Department. You will be required to raise financial support, manage your own innovative research programme of international quality in areas of Ecology, Evolution, Environmental Biology or Conservation Science, that would expand on and complement existing activities within the Department of Life Sciences.

You will be expected to contribute to the assurance and enhancement of the quality of teaching, learning and research within the Department, in line with the Colleges standards and will participate in the development of a coherent College postgraduate programme in Environment and Environmental Change. You will be required to disseminate the results of your research internationally via publications in top quality journals and presentations at major scientific meetings. You will also be required to provide encouragement and guidance to junior research staff to do the same.

You will have a good honours degree and a doctorate (or equivalent) in a relevant subject area. You will have an international reputation for research and innovation in Ecology, Evolution, Environmental Biology or Conservation Science underpinned by a record of first-class journal publication. You must have the demonstrated ability to raise external funds from Research Councils, Government, EU and/or industry, in order to establish an independent research program, with the advice and support of the Division.

You must have excellent interpersonal, verbal and written communication skill with an ability to convey ideas and concepts clearly and effectively to a range of audiences through a variety of methods and media. You must have the ability to lead a research team, manage the finance and your staff. You must also have the ability to communicate and inspire students as you will be expected to contribute to our undergraduate and postgraduate teaching programmes. You should have a strong research record for your career stage in a recognised field of Ecology, Evolution, Environmental Biology or Conservation Science. You must also have a proven track record in conducting high quality independent research, evidenced by high quality publications in peer reviewed journals.

For appointment to Reader, in addition to the above, candidates must also have an exceptionally strong research record in Ecology and Evolution or a closely related discipline, and a proven track record of securing research funding. In addition, candidates appointment to Reader will be expected to have extensive experience in postgraduate teaching and undergraduate teaching across a range of subjects within (or close to) the fields of Ecology, Evolution, Environmental Biology or Conservation Science, together with a track record of successful postgraduate student supervision and postdoctoral mentoring.

For appointment to the position of Chair, in addition to the additional

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Kiel MarineGenomics

Tenure track research scientist: Marine Genomics / Bioinformatics

The Helmholtz-Centre of Ocean Research (GEOMAR) is one of the leading institutes in marine research in Germany. With 750 employees and a yearly budget of 65 Mio euro its major goal is fundamental and applied research in all areas of marine sciences. For more information please visit www.geomar.de. The GEOMAR, division of Marine Ecology is offering a position for a

Research scientist -Marine genomics and bioinformatics - tenure track in the research unit Evolutionary Ecology of Marine Fishes

Job Description

We are seeking a highly motivated and enthusiastic candidate who is expected to pursue his / her own research lines within the broad field of Marine Genomics. Collaborations with diverse empirical projects within the group are highly desirable. Research on genomic and transcriptomic questions in the Evolutionary Ecology group currently include:

- immune system evolution in invertebrates and teleosts

adaptation and speciation genetics in sea turtles and teleost fishes

experimental host-parasite co-evolution with bacteria, fish and viruses

genomic and transcriptomic adaptation to ocean acidification

The GEOMAR has full access to the Center of Molecular Life Sciences Kiel with their state-of-the art sequencing facilities. Access to appropriate high-performance computing facilities is also available. The GEOMAR has culturing facilities to conduct experiments, as well as well-equipped immunological, cell biological and molecular genetic laboratories. We are also embedded into the Kiel excellence cluster The Future Ocean with the specific research topic The Evolving Ocean. GEOMAR is also member of the Max-Planck Research School (IMPRS) -Evolutionary Biology'. Close collaboration with the newly established professorship for theoretical biology/bioinformatics at University of Kiel is expected. Candidates with a different background (for example terrestrial model species) are also encouraged to apply, provided they commit to entering the marine world with their model systems. The acquisition of additional third-party funding to expand the research line by the successful applicant is expected.

Qualification

We request a doctorate in natural sciences. Fluency in scripting languages and in analyzing next-generation sequencing data is prerequisite. Experience in the research area is best documented by publications in international scientific journals.

This is a full-time position, the earliest starting data is anticipated 1 October 2012, The position is initially available for 3 years. Upon review, it can be made permanent (“tenure track”). The salary depends on qualification and is up to the class 14 TVÖD of the German salary rate for public employees.

Working language in the group is English. The GEOMAR is an equal opportunity employer and encourages female scientists and scientists with disabilities to apply. Provided equal qualification, they will be preferentially considered.

For further information on this post contact Prof. Thorsten Reusch (treusch@geomar.de).

Please send your applications for this position, including a full cv, a brief description of your research interests and perspective, and two names of possible references, no later than 1 July 2012 by e-mail in a single pdf-file to the personnel office (attn Katharina Mahn, kmahn@geomar.de).

treusch@geomar.de

MemorialU PlantEvolutionaryBiol

The Department of Biology seeks a tenure track PLANT EVOLUTIONARY BIOLOGIST position (VPA-BIOL-2012-001) at the Assistant Professor level with expertise in Biodiversity or Systematics. The successful applicant will be expected to develop an internationally recognized research program, and teach at both undergraduate and graduate levels, including botany and advanced courses in their areas of expertise. Curation of the department's herbarium in lieu of a full teaching load is an option.

Applicant must possess a Ph.D., and have a strong academic and research background. An application package should include a cover letter with the names and addresses (including email) of three referees, a curriculum vitae, research and teaching statements, and list of needed equipment/facilities. The application package should be sent electronically to Ms. Christine Everson (everson@mun.ca) at the Department of Biology, Memorial University. The deadline for receipt of applications is July 3, 2012. This position is subject to budgetary approval.

The Department of Biology (http://www.mun.ca/-biology) at Memorial University, Atlantic Canada's largest research and teaching university, is continuing with its multi-year faculty renewal program. The Department supports one of the largest undergraduate and graduate programs (˜ 130 M.Sc. and Ph.D. students) within the University. Members of the Biology Department have access to many outstanding departmental and university research and teaching facilities, such as the University's Botanical Garden, a DNA sequencing facility, and the Ocean Sciences Centre in St. John's; the Bonne Bay Marine Station in Gros Morne National Park; and the Harlow Campus outside London (England). The Department has strong partnerships with external agencies including Parks Canada, Fisheries and Oceans Canada, Canadian Wildlife Service, Canadian Forest Service, Agriculture & Agri-Food Canada, and Provincial Departments of Natural Resources and Environment & Conservation.

Memorial University is committed to employment equity and encourages applications from qualified women and men, visible minorities, aboriginal people and persons with disabilities. All qualified candidates are encouraged to apply; however, Canadian citizens and permanent residents will be given priority.

Craig Purchase <cfpurchase@mun.ca>

MNHN Paris SystematicBotany

Dear Colleagues,

The Muséum National d'Histoire Naturelle in Paris is seeking applicants for two positions in Systematic Botany (one at the rank of Professor, the other for a Maitre de Conference (=Assistant Professor) position)

Please refer to the MNHN web-pages for further informations about these positions as well as for job openings in other fields:

http://www.mnhn.fr/museum/foffice/national/-national/Services/rub-stages/som-stages/fiche-stage.xsp?ARTICLE_ARTICLE_ID=25640&idx=-1&nav=liste If the link above does not work, please go to www.mnhn.fr and click on "Enseignants-chercheurs" under "Recrutement" on the main page.

Please be aware that in order for an application to qualify for these positions, you need to have successfully passed through the French "qualifications" process last year.

Truly yours,

Thomas Haevermans.

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Dr. Thomas Haevermans - Curator of Monocotyledones Coordinator of the Botany Research Team Muséum national d'histoire naturelle - Herbier National Département Systématique et Evolution UMR 7205 Origine Structure et Evolution de la Biodiversité CP39 - 57, rue Cuvier, 75231 Paris cedex 05 - France Tél.:+33.1.40.79.33.66/Fax.:+33.1.40.79.33.42 haever@mnhn.fr

Herbarium renovation website: http://www.mnhn.fr/-reno-herbier Visit or loan requests: http://-colhelper.mnhn.fr/ Collection database: http://-www.mnhn.fr/base/sonnerat.html haever@mnhn.fr

QueensU EvolutionaryBiologist

Faculty Opening for an Integrative Cell Biologist

We are searching for a biologist who studies cellular processes of eukaryotes in the context of organismal or evolutionary biology. Some examples of research areas are: developmental cell biology, the cellular control of phenotypic plasticity, the cellular basis of environmental sensitivity, epigenetics and the cell biology of symbioses and parasitism. This is a tenure-track position available at the level of Assistant Professor (pending budget approval).

We are looking for an individual who values interdisciplinary research and welcomes interactions with colleagues from different biological fields. Applicants should have a Ph.D. and post-doctoral experience. The primary criterion for hiring will be excellence in research and teaching or teaching potential. The successful candidate will be expected to develop a strong, externally funded program of research and graduate training, and also contribute to undergraduate teaching in cell biology, genetics or physiology. Review of applications will begin 16 July 2012 and will continue until the position is filled; expected date of appointment is 1 July 2013.

The University invites applications from all qualified individuals, however Canada citizens and Permanent Residents will be given priority. Queens is committed to employment equity and diversity in the workplace and welcomes applications from women, visible minorities, aboriginal people, persons with disabilities and persons of any sexual orientation or gender identity. The academic staff at Queen's University are governed by a Collective Agreement < http://www.queensu.ca/provost/faculty/facultyrelations/qufa/collectiveagreement.html > between the Queen's University Faculty Association (QUFA) and the University.

Applicants must submit:

* a curriculum vitae * a statement of research interests * a statement of teaching interests * administrative cover page found here <http://www.queensu.ca/bi- ology/facultyadverts/Application.pdf>, identifying 3 scientists that we can contact for references. (Please note that this cover page pdf is best filled out using Adobe Acrobat, or the free Adobe ReaderXsome features of this pdf are not operational in other pdf readers, like Preview and Skim)

Applications can be submitted via:

* EMAIL to biohead@queensu.ca * FAX to 613 533 6617 * MAIL to Dr. R.M. Robertson, Head, Dept. of Biology, Queens University, Kingston, ON K7L 3N6, Canada.

Adam Chippindale <adam.chippindale@queensu.ca>

Smithsonian MuseumSpecialist

Museum Specialist

SALARY RANGE: $51,630.00 to $67,114.00 / Per Year

OPEN PERIOD: Friday, June 15, 2012 to Friday, July 13, 2012

SERIES & GRADE: GS-1016-09

POSITION INFORMATION: Full-Time, Permanent V Federal

PROMOTIONAL POTENTIAL: GS-1016-11

DUTY LOCATIONS: 2 vacancy(s) in Washington, DC

WHO MAY BE CONSIDERED: This position is open to all U.S. Citizens or U.S. Nationals. USAJOBS announcement number: 12R-JW-297637A-DEU-NMNH. Note: Federal employees with permanent status or individuals eligible for special appointing authorities should apply to Job Announcement #12R-JW-297637-MPA-NMNH.

The Smithsonian Institution seeks two mammalogists for full-time employment as Museum Specialists in the Division of Mammals at the National Museum of Natural History. The positions will be based at the Natural History Museum in Washington DC but work will also be conducted in the field, during which time the Incumbent will be required to live and work outdoors or based out of a research station for up to several weeks at a time. Duties include all tasks associated with the management of a mammal collection to include: processing loans; assisting visitors; cataloguing and installing new collections; confirming species identifications; upgrading collections storage; participating in pest management; and the preparation of specimens.

Active participation in the field of mammalogy is essential to the position, and in addition to the above duties the Incumbent will be asked to help plan and organize scientific collecting trips and to be a part of the effort to disseminate results. Incumbent may be asked to train students and interns in relevant collections and field techniques either informally, or in the context of a field training course. Overall, the Incumbent will be expected to fulfill the role of a mammalogist with a strong allegiance to collections and an expressed desire to advance mammal research. The mammal collection of the National Museum of Natural History is the largest in the World, and the Incumbent should bring to the Institution a strong commitment to its scientific mission.

Questions can be directed to Darrin Lunde (lunded@si.edu), Charley Potter (potterc@si.edu), and Kristofer Helgen (helgenk@si.edu)

How to Apply: Visit http://www.usajobs.gov/GetJob/ViewDetails/319173000 OR http://www.usajobs.gov/GetJob/ViewDetails/319167300 The Smithsonian Institution is an Equal Opportunity Employer

"Helgen, Kristofer" <HELGENK@si.edu>

StonyBrookU LecturerEvolutionaryBiol

Lecturer position in ecology and evolutionary biology (1 year temporary position)

Stony Brook University, Department of Ecology and Evolution

Deadline for applications: July 3, 2012

Start Date: August 15, 2012

* *

*We are seeking to hire a one year Lecturer to teach four courses in 2012/13: *co-teach an introductory biology lecture course, teach an upper division lecture courses in ecology, an upper division course in evolution, and a fourth course (preferably lab/lecture course in plant systematics/diversity); the teaching load will be 1.5 courses in Fall 2012 and 2 course in Spring 2013. This person will also coordinate graduate teaching assistants assigned each course. There will also be the opportunity to conduct research during the academic year and summer. An opportunity will be available to teach additional courses during the summer, with additional summer compensation.

Special Notes: *This is a non-tenure track, 10 month appointment.* FLSA Exempt position, not eligible for the overtime provisions of the FLSA. Internal and external search to occur simultaneously. *Anticipated Start Date:* August 15, 2012.

The selected candidate must successfully clear a background investigation.

Application Procedure: Those interested in this position should submit a State employment application < http://naples.cc.sunysb.edu/Admin/HRSForms.nsf/aac30a50eebe3a8185256a6f004b0a84/5e8ed1b0c905971c8525775e00476b3e/$FILE/HRSF0113.pdf >, cover letter and resume/CV, and two letters of reference to:

Donna DiGiovanni Department of Ecology and Evolution Life Sciences Building, Room 650 Stony Brook University Stony Brook, NY 11794-5245 ****

Applications for this position must be received, as specified in the Application Procedure Section, no later than 5:00 PM Eastern Time on 07/02/2012, unless specifically noted otherwise in the Special Notes Section.****

Stony Brook University, home to many highly ranked graduate research programs, is located 60 miles from New York City on Long Island's scenic North Shore. Our 1,100-acre campus is home to 24,000 undergraduate, graduate, and doctoral students and more than 13,500 faculty and staff. The University is a member of the prestigious Association of American Universities and co-manager of nearby Brookhaven National Laboratory, a multidisciplinary research laboratory supporting world class scientific programs utilizing state-of-the-art facilities. Stony Brook University Medical Center is Suffolk County's only academic medical center and tertiary care provider. Many opportunities exist for collaborative research, and in some cases, joint appointments with BNL or with Medical School departments. ****

** **

Descriptive Title: Lecturer (10 Month Appointment) ****

* REF#:* F-7313-12-06 ****

Budget Title: same as above ****

* Faculty Position* ****

Department: Ecology and Evolution ****

* Campus:* Stony Brook West Campus/HSC ****

* Salary:* Commensurate with experience****

Required Qualifications: Ph.D. or ABD (advanced to candidacy) in Ecology and Evolutionary Biology, Biological Sciences or a closely related discipline. Experience teaching courses in Ecology, Evolution, Plant Systematics and Diversity, and/or introductory Biology as course instructor. *Preferred Qualifications:* Ph.D. and experience in teaching large lecture courses. Experience in teaching laboratory courses. Outstanding teaching evaluations from students and/or supervisors.

STONY BROOK UNIVERSITY IS AN AFFIRMATIVE ACTION/EQUAL OPPORTUNITY EMPLOYER AND EDUCATOR. IF YOU NEED A

DISABILITY-RELATED ACCOMMODATION, PLEASE CALL THE UNIVERSITY HUMAN RESOURCE SERVICES DEPARTMENT AT (631) 632-6161 OR THE UNIVERSITY HOSPITAL HUMAN RESOURCES DEPARTMENT AT (631) 444-4700. IN ACCORDANCE WITH THE TITLE II CRIME AWARENESS AND SECURITY ACT, A COPY OF OUR CRIME STATISTICS IS AVAILABLE UPON REQUEST BY CALLING (631) 632-7786. IT CAN ALSO BE VIEWED ON-LINE AT THE UNIVERSITY POLICE WEBSITE AT http://www.stonybrook.edu/police lmdavalos@gmail.com

UAlaska Bioinformatics

The University of Alaska seeks a Bioinformatics/Genome Scientist with expertise in analysis of next-generation sequencing (NGS) and genomic-scale datasets for the Life Science Informatics program at the Institute of Arctic Biology, University of Alaska Fairbanks. Life Science Informatics (https://biotech.inbre.alaska.edu) provides high-performance computing services, optimization of technical software, custom data analysis pipelining, database development and management, and user training workshops to facilitate the growth and maintenance of a diverse user group in the University of Alaska life sciences and biomedical research community.

The position is jointly supported by campus-wide research groups, including the Institute of Arctic Biology (http://www.iab.uaf.edu), Arctic Region Supercomputing Center (http://www.arsc.edu), IDeA Network of Biomedical Research Excellence (INBRE), College of Natural Science and Mathematics, and grants to individual researchers and off-campus collaborators. Areas of special interest to the Life Science Informatics group include integrative evolutionary and functional studies of genotype and phenotype, population genomics, epidemiology and statistical and quantitative genetics.

The position will be responsible for research service to the University of Alaska bioinformatics community, possibly including such things as collaborations, programming, coauthoring proposals and papers, advising graduate students, individual research, and the development and teaching of workshops. We seek applicants with demonstrated experience developing automated, custom workflows for the analysis of state-of-the-art molecular biology data (e.g., NGS, high-throughput qPCR, etc.) and an interest in integrating these services through a shared, state-of-the-art computational resource serving >150 users. Experience with computer hardware (including networks, clusters, and servers) and an understanding of programming and scripting are required. Capability in Red Hat or any other mainstream Linux distribution is required. Familiarity with Perl, SQL and PHP, and their application in any field of bioinformatics (e.g., BioPerl, BioPHP) are pluses.

The position is a two-year term appointment at the level of Research Associate (Academic) with full benefits and the possibility of renewal or the possibility of leading towards tenure track faculty.

If interested in this postion, please apply at www.uakjobs.com, posting 0064169 or go to quicklink:

www.uakjobs.com/applicants/Central?quickFindw350 This position is open until filled, with application reviews beginning on 15 July 2012.

The University of Alaska is an equal employment opportunity/affirmative action employer and educational institution. Women and minorities are encouraged to apply.

Inquiries about the details of the position may be directed to:

Kevin G. McCracken email: kmccrack@iab.alaska.edu

In brief this is essentially 9 (academic) + 2 (summer) month non-tenure track faculty appointment with a base salary of $75,000 per year paid over 11 months. If the candidate has or receives grant funding that pays salary, there is the potential to renegotiate the monthly salary. There is no start-up, but Life Science Informatics has a base operating budget that includes dedicated programming, system admin, and graduate RA support. The benefits package also includes a moving allowance.

Kevin G. McCracken Institute of Arctic Biology & Department of Biology and Wildlife University of Alaska Fairbanks Fairbanks, Alaska 99775 office (907) 474-6419 Rm. 242 WRRB fax (907) 474-6967 email: kmccrack@iab.alaska.edu www.iab.uaf.edu/~kevin_mccracken/ kmccrack@iab.alaska.edu

UBirmingham DaphniaGenomics

UNIVERSITY OF BIRMINGHAM SCHOOL OF BIOSCIENCES

Experimental Officer (Research Specialist) in Genomics Fixed term for 12 months in the first instance, potential for extension

Salary is from Â£27,578 to Â£38,140

An Experimental Officer (Research Specialist) position is available for experts in Genomics / High-Throughput Biology, who will oversee the day-to-day operations of the Environmental Genomics Lab, and assist in conducting state-of-the-art research involving automation at the University of Birmingham, School of Biosciences. We are seeking prospective candidates that have demonstrated skills in molecular biology or biochemistry, in robotics, data management and analysis.

The successful candidate will work within a vibrant, interdisciplinary, research team that uses high-throughput genomics technologies and the ecological model species Daphnia to study environmental effects on genomic structures and gene functions, and to understand how natural populations adapt to cope with environmental challenges, including chemical contaminants and climate change. Specifically, the Experimental Officer will develop and adapt new techniques in genomics to promote this line of research, allowing the routine processing of thousands of samples for sequencing and gene expression profiling. This job also involves collaborating with investigators, writing laboratory protocols, supervising laboratory personnel, contributing to research publication and grant writing efforts, training students and postdocs in molecular biology, genomics, and in operating robots. Strong organizational, record keeping, oral and written communication skills - coupled with the ability to work independently and cooperatively - are required. Overall, the hired applicant will benefit from the academic life of the School and will gain experience at mentoring early career scientists in the lab.

Applicants should hold a PhD in genomics, molecular biology, biochemistry, systems engineering or related disciplines; have in-depth laboratory experience in performing experiments involving next-generation sequencing, qPCR and microarrays, managing and analyzing genomics data.

Post is available from October 2012

Informal inquiries about these posts can be addressed to Professor John Colbourne by email at: jcolbour@indiana.edu, or Professor Mark Viant (tel: +44 (0)121 414 2219, email: M.Viant@bham.ac.uk).

To download the details and submit an electronic application online visit: www.hr.bham.ac.uk/jobs Closing date: 25 June 2012 or until filled Reference: 47468

Valuing excellence; sustaining investment

"Colbourne, John" <jcolbour@indiana.edu>

UBirmingham DaphniaTechnician

UNIVERSITY OF BIRMINGHAM School of Biosciences

Research Technician (Daphnia Culture) Fixed term for 12 months with potential extension Salary from £20,596 to £25,615 a year

An Animal Technician position is available to oversee the day-to-day operations of a newly established Daphnia Research Laboratory as part of the Environmental Genomics initiative at the University of Birmingham, School of Biosciences, and beginning ca. September 2012. We are seeking prospective candidates that have demonstrated skills in the husbandry of aquatic animals, record management and experimental biology.

The successful candidate will work within a vibrant, interdisciplinary, research team that uses high-throughput genomics technologies and the ecological model species Daphnia to study environmental effects on genomic structures and gene functions, and to understand how natural populations adapt to cope with environmental challenges, including chemical contaminants and climate change. Specifically, the Animal Technician will have experience of animal husbandry techniques and be prepared to learn additional skills. This includes the care and welfare of experimental and natural strains of Daphnia, and the careful maintenance of their genetic identity, health and records within an electronic database. A successful candidate will demonstrate a genuine interest in animals, animal husbandry, experimental biology, and have excellent team working skills. Overall, the hired applicant will benefit from the academic life of the School and will gain valuable experience by conducting laboratory experiments.

Applicants should hold a BSc degree in biology or related disciplines; have strong organizational, record keeping, oral and written communication skills.

Informal inquiries about this post can be addressed to Professor John Colbourne by email at: jcolbour@indiana.edu, or Professor Mark Viant (tel: +44 (0)121 414 2219, email: M.Viant@bham.ac.uk).

Post is available from October 2012

Closing date: 25 June 2012 or until filled Reference:

47471

To obtain further details and submit an electronic application online visit: http://www.hr.bham.ac.uk/jobs Valuing excellence; sustaining investment

“Colbourne, John” <jcolbour@indiana.edu>

UCambridge Chair Genetics

The Professorship of Genetics

University of Cambridge

The Board of Electors to the Professorship of Genetics invite applications for this Professorship from persons whose work falls within the broadly defined field of Genetics, to take up appointment on 1 October 2012 or as soon as possible thereafter. The successful candidate would normally be expected to become the next Head of the Department for a minimum period of five years.

Further information is available at: www.admin.cam.ac.uk/offices/academic/secretary/professorships/ or contact the Academic Secretary, University Offices, The Old Schools, Cambridge, CB2 1TT, (email: ibise@admin.cam.ac.uk) to whom a letter of application should be sent, together with details of current and future research plans, a curriculum vitae, a publications list and form CHRIS/6 (parts 1 and 3 only) with details of two referees, so as to reach him no later than 6 August 2012.

Informal enquiries may be made to Dr. Cahir O’Kane, Head of the Department of Genetics, in the first instance by email (head@gen.cam.ac.uk).

fmj1001@hermes.cam.ac.uk

UFlorida 2 EvolutionaryBiol

TWO Full-time Lecturers in Biology

The Department of Biology at the University of Florida is seeking TWO broadly trained, full-time lecturers (9 month appointment, year-to-year contract, non-tenure accruing) in Biology to begin as soon as August, 2012. Minimum qualifications include a Ph.D. in Biology or related field with an emphasis in either plant or vertebrate biology; evidence of strong teaching at the college/university level is highly desirable. The successful candidates will be expected to teach lower and upper division courses in areas such as Genetics, Evolution, and plant or animal Biodiversity/Form and Function. At least one successful candidate will have expertise in Plant Biology; both candidates can expect to be involved in the development of online courses. Lecturers will be appointed for 9-months, with opportunities for additional teaching in summer; health insurance and retirement benefits will be offered in accordance with university policies. The Department of Biology has a strong commitment to excellence in teaching, fosters collaborative, interdisciplinary research and teaching, and has been establishing community resources for the team teaching of Introductory Biology. For more information on the Department and links to relevant courses go to www.biology.ufl.edu; questions can be sent to kmpatterson@ufl.edu. Applicants should submit a cover letter, curriculum vitae, statement of teaching experience and philosophy, unofficial academic transcripts and the names and email addresses of 3 references to http://jobs.ufl.edu/postings/30681 before July 20, 2012. The University of Florida is an Equal Opportunity Institution. Minorities, women and those from underserved groups are encouraged to apply.

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

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

UPortsmouth 2 Evolution

Two lecturer (=assistant professor) positions in evolution, ecology, and/or conservation ecology are being advertised at the School of Biological Sciences, University of Portsmouth, UK (http://www.port.ac.uk/departments/academic/biology/ (http://www.port.ac.uk)). We are particularly interested in people working on the evolutionary ecology of species interactions, but related areas will be considered. Additional details and instructions for applying are at: http://www.port.ac.uk/vacancies/academic/vacancytitle,157625,en.html and http://www.port.ac.uk/vacancies/academic/-

vacancytitle,157624,en.html . Note that one position requires expertise in plant biology, whereas the second position is open with respect to organisms studied.

Portsmouth is a compact, small city on the south coast of England, with relatively warm, sunny weather (by UK standards). Nearby living situations range from seaside urban to rural, with London and main airports readily accessible by (reasonably) fast trains. Portsmouth lies at the mouth of the Solent/Spithead waterway, which is famous for sailing and ferry connections to the scenic Isle of Wight (which is commutably close).

Note that the positions close very soon; application materials must be submitted electronically by 6 July, 12 noon British Summer Time. (No letters of reference are needed until after the first cut.)

Informal inquiries can be directed to Prof Scott Armbruster (scott.armbruster@port.ac.uk) or Prof Matt Guille, Head of School (matt.guille@port.ac.uk).

Scott Armbruster <Scott.Armbruster@port.ac.uk>

UQuebecMontreal BehaviourEvolution

TENURE TRACK FACULTY POSITION AND CANADA RESEARCH CHAIR (TIER 2) - BEHAVIOURAL ECOLOGY

The department of biological sciences at l'Université du Québec à Montréal is seeking a behavioural ecologist to fill a tenure-track position. The candidate will join a department which is already strong in social foraging, social learning, animal personality, evolutionary genetics, wildlife management, insect ecology, community ecology and evolutionary modelling (see http://www.bio.uqam.ca/themes-de-recherches/-ecologie-animale-evolution-et-comportement.html for details). The department includes research groups in behavioural ecology, forest ecology and aquatic ecology. The candidate will have post-doctoral experience, having received a doctorate in the last 10 years. The candidate will be expected to develop an independent research programme which will reinforce or complement the above fields of study. The candidate will apply for a CRC Research Chair (Tier 2) in April 2013 (for more details about CRC see http://-www.chairs-chaires.gc.ca/home-accueil-eng.aspx). If necessary, the candidate will be given some time to learn to communicate in French. Competence in oral and written French are prerequisites to tenure.

Candidates should submit a detailed curriculum vitae, signed and dated plus reprints and three letters of reference (submitted directly by the referees) BEFORE AUGUST 20, 2012 AT 5PM to:

Mme Catherine Mounier, directrice, Département des sciences biologiques, Université du Québec à Montréal, C.P. 8888, Succursale Centre-Ville, Montréal, Québec, H3C 3P8. Tel: (514) 987-3000 poste 8912â; Fax: (514) 987-4647 ; email : Mounier.catherine@uqam.ca . Internet: http://www.rhu.uqam.ca/visiteurs/?p=-postesProf

Denis Réale <reale.denis@uqam.ca>

Vicksburg DNALabTech

DNA Lab Technician Salary: $25,000-$45,000 Hours: 40 hrs./week; occasional overtime with pay or compensatory time off Start Date: June 18 -July 16 2012 Travel: Rare Requirements: MS degree in Genetics, Molecular Biology, Zoology, Microbiology or related field, or BS degree and 1-years experience as technician in DNA laboratory.

Opportunities exist for positions as lab technicians with the Conservation & Ecological Genetics Team (CEGT) within the Environmental Laboratory, US Army Engineer Research and Development Center in Vicksburg, MS (http://el.erdc.usace.army.mil/index.cfm). The EGGT pursues a wide variety of DNA-based research, including population, conservation, and ecological genetics in plants and animals. Applicants should be familiar with 1) DNA extraction from animals, plants, or prokaryotes, 2) PCR, 3) DNA Sequencing, and 4) plasmid-based cloning of DNA fragments. These positions are not currently federal government hires, but will be filled through various contracting mechanisms. Position guaranteed through September 2013, after which it will either continue or be eliminated depending on program funding. Overseas moving expenses will not be provided; other moving expenses may be covered, but are not guaranteed. If interested, please send your CV/resume to Dr. Richard Lance (richard.f.lance@us.army.mil).

Vicksburg sits on bluffs above the Mississippi River and features many areas of historic significance, including the Vicksburg National Military Park. There are 50,000 residents in the area and the cost of living is very reasonable. The state capitol, Jackson, is an hour drive to the east.

"Edwards, Christine ERDC-EL-MS" <Christine.E.Edwards@usace.army.mil>

YaleU Bioinformatics

The Yale Genomic Resource Facility is looking for a highly motivated Bioinformatics Scientist with a strong functional genomics and computational background and keen interest in collaborating with other investigators at Yale. The position is primarily located in New Haven, Connecticut but will also spend time in West Haven, Connecticut at the Center for Genome Analysis.

A primary responsibility of the Bioinformatics Scientist will be to provide genomic analyses support to the Yale investigators; direct the development of innovative bioinformatics approaches for the analysis of sequence data, develop new search ideas in sequence assembly, genome annotation, SNP, haplotype and transcriptome analysis. Furthermore, the Informatics Scientist will also interact with the Yale High-Performance Computing group to design and build the necessary IT infrastructure for data analysis and storage and to develop mechanisms to ensure the delivery of sequencing data to users.

The ideal candidates will have Ph.D. degree in Bioinformatics or a related scientific field and must have extensive computational and high throughput DNA sequence analysis experience. Candidates should possess programming skills in Perl, C or Java, competency with relational databases, database design/architecture, statistical software packages, knowledge of online genomics databases, and excellent interpersonal and communication skills. Review of the applications will begin on July 1, 2012 and continue until the position is filled. Please submit curriculum vitae, a description of research interests and three letters of reference to:

Shrikant Mane, Ph.D. Shrikant.mane@yale.edu Director, Yale Genomic Resource Yale University School of Medicine Department of Genetics PO Box 208005 New Haven, Ct., 06520-8005

Yale University is an Equal Opportunity/Affirmative Action employer. Women and minorities are encouraged to apply.

"Santana, Sonia" <sonia.santana@yale.edu>

Other

Ancestral Area Reconstruction

Dear EvolDir Members:

would you please suggesting me some software to perform an Ancestral Area Reconstruction using avian CR mtDNA dataset ?

I would like to know the most user friendly and ad hoc programs

Thank you,

Filippo

Filippo Barbanera

Researcher Department of Biology Protistology-Zoology Unit Via A. Volta, 6 I - 56126 Pisa (PI) Italy

Web site: www.biologia.unipi.it Skype: barba_skype room: + 39 050 2211386 lab. : + 39 050 2211343 fax: + 39 050 2211393

Filippo Barbanera <fbarbanera@biologia.unipi.it>

Ancestral Reconstruction Area answers

I want thank you all persons who kindly sent their suggestions. Here below a summary of the indications I have got. They are listed anonymously.

If someone want receiving the email address for a given report, please, write me at

fbarbanera@biologia.unipi.it

—–

1. I have used three different approaches to estimate ancestral area reconstruction. One is S-Diva (statistical dispersal vicariance) of Yu et al. (2010) (http://mnh.scu.edu.cn/S-diva/blog/index.html), which I believe has been superseded by RASP. I used the online version of S-DIVA and it was quite easy to run. You can check my paper Morales-Hojas et al. (2011) Mol. Phyl. Evol. 60. This method allows for phylogenetic uncertainty and can be run with trees from the posterior trees from a MrBayes analysis, and it gives you the probabilities for each ancestral area. The output gives you a tree with the probabilities in each node. I have also used Mesquite to estimate ancestral area with Likelihood. Mesquite is easy to use once you get the hang of it, and the method it uses gives you the probabilities of each state in the node of the phylogeny. And finally you have SIMMAP (http://www.simmap.com/). It estimates the posterior probabilities of character states for each internal node. It has the advantage that it uses a Bayesian approach and allows for uncertainty (you can run it with your posterior trees from MrBayes), but the output is not very user friendly. Nevertheless is not difficult to run and it is quite robust.

2. A good program to do that is MESQUITE. The program can perform this through ML o parsimony analysis. I hope that this information is usefull for you

3. Not sure if you could call these friendly but we have used 3area and Lagrange. Good luck,

4. http://code.google.com/p/lagrange/ 5. One quick suggestion would be the software PhyloMapper: http://www.evotutor.org/PhyloMapper/ —–

Filippo Barbanera

Researcher Department of Biology Protistology-Zoology Unit Via A. Volta, 6 I - 56126 Pisa (PI) Italy

Web site: www.biologia.unipi.it Skype: barba_skype room: + 39 050 2211386 lab. : + 39 050 2211343 fax: + 39 050 2211393

Filippo Barbanera <fbarbanera@biologia.unipi.it>

DAMBE workshop Jul6-11

Dear Colleagues,

I will offer a DAMBE Phylogenetics Workshop at University of Ottawa on July 6 and July 11, 2012 (at the beginning and ending of Evolution 2012). The workshop is not part of the meeting and everyone is welcome (up to the capacity of the computer room reserved).

1. I have booked a computer room (Cube 104) between 8:30 am and 4:30 pm on Jul. 6 and Jul. 11. Cube is a small building that has the shape of cube, and it is labelled as Cube in the Google map at the following link

http://maps.google.com/maps/place?ftid=-0x4cce0509d6e48153:0xb83238f19fd6be3f&qE.420526,-75.680233&hl=en&vedAwQ-gswAA&sa=X&ei=-mjbfT-PfM-aiwAGMtf2LDg 2. The workshops will start at 9 am, with a lunch break between 12 noon and

1:30 pm, and resume at 1:30 pm. I will be with you during the morning and afternoon sessions.

3. The workshop will include DAMBE function demonstrations, presentation of essential but minimal theoretical background, and hands-on practices, all done in an informal and interactive manner. The topics will be as originally announced, i.e.,

-routine phylogenetic analyses and dating methods (both the conventional dating with internal node calibration and tip-dating which is used mainly for viral sequences sampled over different years)

-phylogeny-based comparative methods.

-evolutionary genomics

4. The workshop is free, but with the associated evils of no coffee, no cookies and no lunch. There is a drinking water fountain outside the computer room.

5. DAMBE is a comprehensive software package for molecular biology and evolution. It is freely available from my web site at: http://dambe.bio.uottawa.ca/dambe.asp The computer room has 27 seats. Currently 14 people have expressed interest in participating, so more participants can be accommodated. If you have colleagues who might want to attend the workshop, please let me know. Please also keep me informed of your change of plan. Thanks.

Best Xuhua

Xuhua Xia Professor Biology Department University of Ottawa Rm 278 Gendron 30 Marie Curie, Ottawa, Ontario Canada K1N 6N5 Tel: (613) 562-5800 ext 6886 http://dambe.bio.uottawa.ca http://www.biology.uottawa.ca/details.php?lang=eng&id1 Xuhua.Xia@uottawa.ca

Drosophila dates

In October 2011 I asked the following two questions (original email follows below) with the request that people do so without reference to the literature.

[1] When was the most recent common ancestor of D. melanogaster and D. simulans? and [2] When was the most recent common ancestor of the subgenera Sophophora and Drosophila

I have tried in several ways to incorporate all the estimates and their uncertainty - Here is my best go at headline values:

* D.melanogaster-D.simulans * Range of point estimates: 1-7 Mya Total 95% density of estimates, accounting for their confidence intervals: 0-9 Mya

* Sophophora-Drosophila * Range of point estimates: 7-100 Mya Total 95% density of estimates, accounting for their confidence intervals: 5-110 Mya

I have tried to capture the reported uncertainty is this figure: http://www.biology.ed.ac.uk/research/groups/obbard/Data/Drosophila_Date_survey.pdf.

For comparison, the estimates given in Tamura et al (2004)MBEv21 are 5.4[3.2-7.5]Mya and 63[39-87]Mya respectively, and the estimates given by Russo et al (1995)MBEv12 are 2.3[1-3.6]Mya and 40[33-46]Mya (95% bounds assuming normally distributed uncertainty).

My original objective was to establish the figures (if any) that the Drosophila community carry around in their heads, and the survey was motivated by the widespread use of dates that differ by nearly a factor of two (e.g. in back-to-back papers) but elicit no comment.

I received approximately 70 responses, around 40 of which provided either ranges or point estimates for both dates (some points included confidence intervals, as requested). I excluded responses from which I couldn't glean bounds or points, e.g: "a) A long time ago and b) Longer than a)."

Papers/books that were mentioned specifically by respondents were:

Moriyama, E.N., and J. R. Powell. 1997. Synonymous substitution rates in Drosophila: mitochondrial versus nuclear genes. J. Mol. Evol. 45(4):378-391.

Tamura, K., S. Subramanian, and S. Kumar. 2004. Temporal patterns of fruit fly (Drosophila) evolution revealed by mutation clocks. Mol. Biol. Evol. 21:36-44. (mentioned twice)

Jeffrey R. Powell (1997) "Progress and Prospects in Evolutionary Biology: The Drosophila Model" Oxford University Press, 4 Sep 1997 - 562 pages

A special prize goes to the person who responded "for question (1) 3.5 Ne generations where Ne is the effective population size of mel, or equivalently 1.5 Ne generations where Ne is the effective population size of sim." but when asked to convert to years suggested "Ok, 20 thousand years ago." This answer was excluded.

A big thank you to all who took part!

Darren

—– Original Email—–

*Without* looking at the literature, please attempt to answer the following questions: [1] When was the most recent common ancestor of Drosophila melanogaster and Drosophila simulans? [2] When was the most recent common ancestor of the subgenera Sophophora and Drosophila (from example, the MRCA of D.melanogaster and either D. virilis or D. mojavensis. This is the date at the root of the 12-genomes phylogeny).

My aim is to survey the community's opinion (including any errors or misapprehensions), not to directly survey the literature. So PLEASE answer questions [1] and [2] without looking them up first. If you wish, you can also name any paper that you might have in mind when you give your answer - but again PLEASE DO NOT look at that paper to check your answer. All answers will be treated anonymously, and the results published here in due course. If you distrust point estimates (as you should) please give confidence intervals. These could be a point estimate plus-or-minus a standard error, or a point estimate with 95% confidence intervals, or a flat stepped distribution of your choice (for example, "anywhere between X and Y million years ago"). I am also happy to take a multi-spiked distribution ("either X or Y million years ago"), including one with a zero-bound ("less than Z million years ago") or any specific distribution of your choice (e.g. paste in the R-code). If you have absolutely no informed opinion, but you have persisted in reading this far anyway, you are clearly the sort of person whose wild guess I would like to hear about. Please just take a guess (with any error distribution you feel is appropriate) and just let me know that it is an uninformed guess. Thank you for taking the time to read this email, and I look forward to hearing any and all (un)informed guesses.

–

Darren Obbard Institute of Evolutionary Biology University of Edinburgh, UK darren.obbard@ed.ac.uk http://www.biology.ed.ac.uk/research/groups/-obbard/ The University of Edinburgh is a charitable body, registered in Scotland, with registration number SC005336.

darren.obbard@ed.ac.uk

ESEB OutreachFund CallSept2012

ESEB Outreach Fund

The European Society for Evolutionary Biology (ESEB) welcomes applications to the ESEB Outreach Fund for projects that promote evolution-related activities. With a total annual budget of 15000 Euro, the goal of this initiative is to improve public knowledge about evolution globally.

Applications for funding will be accepted for educational initiatives that promote evolution, development of evolutionary material (books, films, websites) intended for a general audience, public outreach seminars, public exhibitions, etc.

The application form can be found onwww.eseb.org (click on the "Outreach Fund" link). Applications will be accepted twice yearly (deadlines March 15, September 15) and should be submitted by email to U. Friedrich<office@eseb.org> (Subject: Outreach).

– Ute Friedrich ESEB office Manager DEE, Le Biophore University of Lausanne CH-1015 Lausanne Switzerland Email:office@eseb.org

European Society for Evolutionary Biology www.eseb.org "U. Friedrich" <office@eseb.org>

Free ebooks on evolution

Having just discovered my Kindle app (mine's on an Android tablet, they are available for most/all tables and smart phones) I took a look at what's available at Amazon's Kindle Store - and noticed *many* books with a $0.00 price tag - including:

Insectivorous Plants by Charles Darwin (Kindle Edition - May 1, 2004) -

On the Origin of Species By Means of Natural Selection, or, the Preservation of Favoured Races in the Struggle for Life by Charles Darwin (Kindle Edition - Mar 1, 1998)

The Descent of Man by Charles Darwin (Kindle Edition - Mar 24, 2011) -

Lots more! They may be interesting and/or useful.

–henry schaffer

Henry Schaffer <hes@unity.ncsu.edu>

Frontiers Biogeography

Frontiers of Biogeography - Open Access journal

Frontiers of Biogeography is published by the International Biogeography Society (www.biogeography.org) and the University of California's eScholarship system (http://escholarship.org/uc/fb).

Our hybridization of the Society Journal and Open Access publishing models enables Frontiers of Biogeography to provide both exceptionally low publication fees ($200 per article, with waiver or partial-waiver options) and free access to all content for all readers.

Volume 4 issue 1 is now available at http://escholarship.org/uc/search?entity=3Dfb;volume=3D4;issue=3D1 and we encourage you to submit Opinion, Perspective, or Review Articles and Research Letters on the geographical variation of life at all levels of organization. This includes, but is not limited to, studies on temporal and/or evolutionary variation in any component of biodiversity if they have a geographical perspective, as well as studies at more local scales if they have a spatially-explicit component. Papers may study aerial, freshwater, marine, subterranean, or terrestrial biogeography of extant and/or extinct taxa spanning the entire tree of life and all time periods.

A sample of the articles published in Frontiers of Biogeography includes:

Losing time? Incorporating a deeper temporal perspective into modern ecology Felisa A. Smith & Alison G. Boyer (2012) Frontiers of Biogeography v.4 (1) http://escholarship.org/uc/item/3bg6583c Individual variation and weak neutrality as determinants of forest diversity Brian Beckage et al. (2012) Frontiers of Biogeography v.3 (4) http://escholarship.org/uc/item/5xv4k3tr Musings on the Acropolis: terminology for biogeography Samuel M. Scheiner (2011) Frontiers of Biogeography v.3 (2) http://escholarship.org/uc/item/4jr46958 We encourage you also to consider the journal for advertising events, jobs, and other matters relevant to ecologists, evolutionists and biogeographers. Frontiers of Biogeography has exceptionally low rates ($50) for advertising by institutions, which includes a quarter page advertisement in the online open access journal, complemented by free additional feeds to Facebook and Twitter communities, and the option for a more detailed free posting on the IBS Blog; links to all these resources are provided from the IBS homepage (http://www.biogeography.org).

Please consult the Frontiers of Biogeography website (http://escholarship.org/uc/fb) or contact our Editorial Office at frontiersofbiogeography@gmail.com for further information.

Sincerely, Joaquín Hortal, Editor-in-Chief Michael Dawson & Richard Field, Deputy Editors-in-Chief

Frontiers of Biogeography Editorial Advisory Board: Miguel B. Araújo, Lawrence R. Heaney, David G. Jenkins, Richard J. Ladle, & Mark V. Lomolino

Guyana EntomologyVolunteer

We are looking for a field assistant who can pay their own way in a collecting trip to Guyana for the dates of July 18-August 18, 2012. Total expected cost to the individual would be about $2200 US. The work will include collection of dragonflies, cockroaches, termites, and arachnids for phylogenetic and ecological studies. (See our blog for some pictures and stories about our previous trips: http://warelabatrutgers.blogspot.com/) We will be working in the tropical forests near the Atlantic coast and in the more remote inland tropical savannahs. Applicants must be physically fit and able to rope climb into the canopy (training and supplies for this will be provided). Vaccinations for Typhoid, and Yellow Fever REQUIRED for US applicants (others highly recommended). Please send resume and contact information for 2 professional references to dominice@pegasus.rutgers.edu. If you are interested please respond ASAP.

Dominic Evangelista

Dominic Evangelista <dominicev@gmail.com>

NESCent Academy call for course proposals

PROPOSALS FOR SHORT COURSES IN EVOLUTIONARY BIOLOGY

Do you have an idea for a short course in evolutionary biology? The NESCent Academy is a series of hands-on workshops aimed at a graduate students, postdocs and faculty. We are now accepting proposals for courses at the National Evolutionary Synthesis Center (NESCent). Courses are generally 7-10 days in duration and offered on-site at NESCent in Durham, NC during the summer break. NESCent provides the venue and logistics support, while PIs develop and deliver content.

We are particularly interested in topics that are not covered in regular graduate curriculum (for example, novel analysis methods, new data source, cross-disciplinary topics).

For more information and how to submit a proposal:

https://academy.nescent.org/wiki/Proposing_a_course Karen Cranston, PhD Training Coordinator and Informatics Project Manager nescent.org

Karen Cranston <karen.cranston@nescent.org>

NSF at Ottawa

NSF will be at Evolution Ottawa on Sunday, July 8, 12:15 - 1:15 pm in Rm. 108; feel free to bring along your conference lunch. We will discuss the new preproposal process for submissions to DEB and IOS core programs and will answer questions about other NSF opportunities. NSF program directors from Evolutionary Processes (Elizabeth Friar, George Gilchrist, Leslie Rissler, Sam Scheiner) and Systematics and Biodiversity Science (Maureen Kearney) plan to be present. We will also be available for personal meetings throughout the conference.

George W. Gilchrist, Ph.D. Program Director, Evolutionary Processes Division of Environmental Biology National Science Foundation 4201 Wilson Blvd, Suite 635 Arlington, VA 22230 Phone: 703.292.7138 Fax: 703.292.9064 Email: ggilchrist@nsf.gov

“Gilchrist, George W.” <ggilchri@nsf.gov>

PuertoRico FieldVolunteer AnoleResearch

Field Volunteer Needed: Ecology and adaptation in Anolis spp. in urban habitats Department of Biology, University of Massachusetts Boston

I am looking for 1 field assistant on short notice for an upcoming field trip to Puerto Rico from June 10-July 1, 2012 (3 weeks). The fieldwork involves capturing wild Anolis lizards from urban and natural habitats as part of my dissertation research. This opportunity is unpaid, but all expenses (airfare, food, lodging, and incidentals) will be covered. For more information about the Revell lab, see: http://faculty.umb.edu/liam.revell/ If interested, please contact Kristin Winchell: Kristin.Winchell001@umb.edu with a brief summary of why you are interested in this position and your CV. Deadline for applications is this Saturday, June 2.

kmwinchell@gmail.com

Ride to Ottawa

Good day,

If someone is interested in organizing (or already is) a road trip to Evolution Ottawa 2012 through Chicago, drop me an email kraman2@uic.edu. It’s more fun (and cheaper) to do this with more people.

Peace

Karolis Ramanauskas Graduate Student Department of Biological Sciences University of Illinois at Chicago 840 W. Taylor St. SEL 4093 M/C 067 Chicago, IL 60607

kraman2@uic.edu

Software LAMARC update

Dear LAMARC users:

We have just released LAMARC version 2.1.8. This version corrects two serious bugs affecting previous results, and also offers two important new features: inference of population splitting, and accomodation of SNP data derived via a panel.

Previous versions of LAMARC contained a a very serious bug in inference of migration rates. Inference of each migration rate was, due to this bug, a composite of information about the rate from A to B and information about the rate from B to A. This led to numerically incorrect results and in some but not all cases to reversing the apparent direction of asymmetrical migration. All LAMARC migration results must be considered suspect and should be rerun.

We deeply regret this error and apologize to those whose research it has affected.

We have also corrected a bug in inference of growth rates which could cause spurious peaks and confidence or support interval boundaries in cases where negative growth was considered. While most results which inferred strongly positive growth would be unaffected by this bug, results involving negative growth may have been affected, as may confidence interval boundaries extending into negative growth.

Version 2.1.8, besides fixing these bugs, introduces two new features.

First, LAMARC can now infer the time of population splitting for scenarios where populations have diverged from a common ancestor as well as the post-split migration rates. Scenarios with multiple populations are possible if the branching tree of populations is presumed to be known.

Second, LAMARC now offers a correction for use of SNP data derived using a panel-based SNP chip. Uncorrected use of panel-derived data will understate Theta due to loss of rare SNPs which were missed in the panel. The correction leads to nearly unbiased inference from panel-based data.

LAMARC's speed in likelihood-based runs has also been improved significantly.

LAMARC can be obtained from our web site at:

http://evolution.gs.washington.edu/lamarc.html We provide executables for Linux, Mac OSX, and 32-bit and 64-bit Windows, as well as source code for compiling on other systems.

Sincerely,

The LAMARC Development Team Mary Kuhner Bob Giansiracusa Jim McGill Elizabeth Walkup Jon Yamato

lamarc@uw.edu

Software MOL COANC

Dear Evoldir members,

A new release (3.0) of MOL_COANC is already available to download from the web page http://dl.dropbox.com/u/5714008/Fernandez.htm .

This programme is intended to estimate the genealogical coancestry between a group of contemporaneous individuals (i.e. none of them can be ancestor of other individual in the same set) from the genotype for a number of codominant markers, following the approach presented in Fernández & Toro (Molecular Ecology 2006). The underlying idea is constructing a pedigree by creating virtual' ancestors of the target (genotyped) individuals which maximises the correlation between the molecular coancestry matrix calculated from markers and the genealogical coancestry obtained for that particular pedigree. As stated in the original paper, this method has several advantages over other coancestry estimators: i) as the method implies explicit reconstruction of a genealogy, it always yields congruent coancestry matrices (in opposition with pairwise methods); ii) it needs no assumptions about the allelic frequencies of the used markers and no previous knowledge of the population structure (e.g. only FS families exist); iii) it allows for complex relationships between individuals as it is able to construct deeper' genealogies.

- Main novelty of this release is the possibility of dealing with hermaphroditic and monoecious species. Consequently, we can force the software to create ancestors with separate sexes (i.e. they permanently act as males or females, as in previous versions) or allow for any kind of mating design, assuming they can act as males or females each time they mate.

- In the case of non separated sexes it is also possible to allow or not for selfings, depending on the physiology of the species.

- Now the maximum number of ancestors per generation has not to be constant but can be define separately. This way the previous information on the demographic history of the population can be accounted for (e.g. number of founders, known bottlenecks or expansions) and more accurate solutions can be found. Notice that a larger number of possible ancestors will (unnecessarily) enlarge the space of feasible solutions reducing the efficiency of the optimisation algorithm.

- It is possible to establish a predefined coancestry matrix between founders. This feature permits to account for a real knowledge of the origin of the oldest known ancestors or to compare different hypothesis about the foundation of the population (i.e. from related or unrelated individuals).

Thank you

Jesús Fernández Martín Departamento de Mejora Genética Animal 34-91 3471487 Instituto Nacional de Investigación y 34-91 3478743 (FAX) Tecnología Agraria y Alimentaria (INIA) jmj@inia.es Crta. A Coruña Km. 7,5 28040 Madrid (SPAIN)

http://dl.dropbox.com/u/5714008/Fernandez.htm

jmj@inia.es

Software Positive selection

Dear all,

as you may know, due to the confounding effect of demography, it is extremely difficult to detect recent positive Darwinian selection reliably in a natural or domestic population. Recently, we proposed a novel method. This method has been mathematically proved that the demographic factors, including population size expansion and bottleneck, do not affect the test.

Notably, it's a single-locus based approach. That means, to detect positive selection reliably, all you need is just a short piece of nuclear DNA, say several hundred base pairs. The sample size should be >= 21 (diploid) individuals.

The logic behind the method is: the confounding effect of varying population size can be completely removed if we only examine tree topology. Then two very simple sampling strategies remove the confounding effect of hidden population structure. Those two sampling strategies are:

1) The minimum sample size from each sampling location should be at least 2 or 3, calculated as alph * (n - 1) / 2. Alpha is the significance level, n the sample size.

2) Assuming your sampling locations do not cover the whole species distribution area, and these uncovered areas are separated into several isolated regions due to natural barriers. Then try to collect one individual/chromosome from each isolated (and uncovered) regions. Those individuals will be used as migrant detectors. Usually, 2 or 5 migrant detectors should be enough.

The method has been described in: Haipeng Li (2011). A new test for detecting recent positive selection that is free from the confounding impacts of demography. Mol Biol Evol 28:365-375.

The software can be download freely from http://www.picb.ac.cn/evolgen/softwares/ Yours sincerely,

Yuting Wang (wangyuting@picb.ac.cn)

&

Haipeng Li (lihaipeng@picb.ac.cn)

Haipeng Li, Dr. Laboratory of Evolutionary Genomics CAS-MPG Partner Institute for Computational Biology Chinese Academy of Sciences Yue Yang Road 320 Shanghai, 200031 China

Tel: +(86)-21-54920460 Fax: +(86)-21-54920451

lihaipeng@picb.ac.cn

Software RAxML server

Dear Community,

The new RAxML-Light code, see:

http://bioinformatics.oxfordjournals.org/content/early/2012/05/24/bioinformatics.bts309.abstract is now also available as web-service thanks to the efforts of the great colleagues at the San Diego Supercomputer Center and support by the NSF iPlant collaborative.

To use this service you will first need to create an iPlant login here:

https://www.iplantcollaborative.org/user/register and subsequently log in on the CIPRES portal using your iPlant credentials:

http://www.phylo.org/portal2/login!input.action Cheers,

Alexis

Dr. Alexandros Stamatakis Research Group Leader HITS, Heidelberg Adjunct Professor, Dept. of Ecology and Evolutionary Biology, University of Arizona at Tucson www.exelixis-lab.org alexandros.stamatakis@gmail.com

Special Issue

Dear all,

we are pleased to announce that our special issue on Ecological Speciation of the International J of Ecology is accessible online (open access).

All of the papers in the special issue can viewed here: http://www.hindawi.com/journals/ijeco/si/213683/ And the entire issue can be downloaded as a single PDF here: http://downloads.hindawi.com/journals/specialissues/213683.pdf Happy reading,

Marianne Elias, Rui Faria, Zachariah Gompert and Andrew Hendry

– Marianne Elias CNRS researcher, UMR CNRS 7205 Muséum National d'Histoire Naturelle Département Systématique et Evolution 45 Rue Buffon, CP50, 75005, Paris, France tel: +33 1 40 79 37 90 fax: +33 1 40 79 56 79 http://www.mnhn.fr/oseb/ELIAS-Marianne,279 melias2008@googlemail.com melias2008@googlemail.com

Woody plants

What percentage of plant species are woody?

Woody versus herbaceous is one of the major axes of life history variation in plants. We sought to find the answer to the seemingly simple question: what percentage of plant species in the world are woody? We asked a small group of botanists this question and got an extraordinarily wide variety of answers. In addition to tallying up the species numbers, we (here "we" refers to myself along with Rich Fitzjohn, Amy Zanne, Will Cornwell and others involved with our NESCent working group: "Tempo and Mode of Plant Trait Evolution") thought it would be interesting to survey biologytypes to see if a general consensus answer exists. Please take a couple of seconds to fill out our questionnaire. Thanks! Answer coming out soon in a journal near you.

Our questionnaire is here< https://docs.google.com/spreadsheet/viewform?formkey=dDBDOXpUeGpXSWJESmV0TjNrWHFEMUE6MQ >

Thanks a lot for your help.

cheers, matt

Matt Pennell <mwpennell@gmail.com>

PostDocs

Austin Texas EvolutionaryGenomicsOfCancer

The Center for Computational Neuroscience at NeuroTexas Institute at St. David's HealthCare seeks a highly motivated individual who is interested in the genetics and genomics of glioblastoma multiformae (GBM). Of particular interest, is the development of evolutionary-genetic models suitable for studying the dynamics of and selective forces acting on mutations within growing GBM tumors and related bioinformatic approaches for model validation using DNA/RNA sequence data from GBM tumors.

The two-year position is available immediately. A PhD with a focus in computational biology, bioinformatics or genomics is required; individuals with PhD's in computer science, engineering, mathematics, or physics and at least two years of related post-doctoral research experience (computational biology or biological modeling research) are also encouraged to apply. Ideal candidates will be familiar with evolutionary theory and modeling, DNA/RNA sequence analysis and bioinformatics, and systems biological modeling. Previous knowledge and experience with cancer genomics and modeling is an additional plus.

NeuroTexas Institute is a highly multidisciplinary clinical, research and educational institute affiliated with St. David's HealthCare in Austin, TX. The Institute enjoys an open and highly productive relationship with the adjacent University of Texas at Austin (UT). There are many opportunities to build collaborative research projects and interact with members of the UT community.

Please submit a letter of intent, curriculum vitae and the names and addresses of two references to:

Dr. Matthew C. Cowperthwaite Center for Computational Neuroscience NeuroTexas Institute at St. David's HealthCare 1015 East 32nd Street, Suite 404 Austin, Texas 78705 E-mail: matthew.cowperthwaite@stdavids.com

Matthew.Cowperthwaite@stdavids.com

CIFAR Canada MicrobialBiodiversity

CIFAR Junior Fellowship Integrated Microbial Biodiversity Program

The Canadian Institute for Advanced Research brings together top international researchers to tackle many of the most interesting and pressing questions of our time. Our Junior Fellow Academy offers gifted, early career researchers the unique opportunity to participate in CIFARs global research network and to closely collaborate, and be mentored by, some of Canadas and the worlds best researchers.

Junior Fellows take part in one of CIFARs innovative research programs, where researchers meet regularly to establish new frameworks for thinking about the world with the potential to improve human health and the environment, transform technology, build strong societies, understand human culture and even chart the universe. To enhance leadership skills within an interdisciplinary network of peers, CIFAR also brings together Junior Fellows from all twelve programs for separate Academy meetings.

CIFAR is seeking an exceptional early career researcher to fill a Junior Fellowship in its Integrated Microbial Biodiversity Program, beginning in January 2013 or later. The fellowship will be supervised by one or more program members and held in conjunction with a formal postdoctoral appointment at the members home institution. Candidates are strongly encouraged to identify and contact the program member(s) they wish to work with before submitting an application.

The Integrated Microbial Biodiversity Program seeks to create a fundamentally deeper understanding of the diversity of microbial life, interactions among microbes, and interactions between microbes and macroscopic life. It provides a unique environment where experts on diverse microbial groups and levels of organization come into sustained, prolonged contact through annual program meetings, smaller question-driven workshops, symposia, and trainee exchanges. The membership includes 20 researchers from 13 institutions, including seven across Canada, five in the U.S., and one in Europe. Visit www.cifar.ca/integrated-microbial-biodiversity for more information.

Eligibility:

Individuals who have completed their PhD no more than three years before the Fellowship starting date are eligible to apply. The successful candidate will have an outstanding record of accomplishment in an area of interest to the program, excellent communication skills, strong potential to collaborate with program members and ability to contribute to the programs mission. He/she will also display a strong interest in connecting with peers from other disciplines through the Junior Fellow Academy.

Duration:

Funded for two years, as below. For three additional years, CIFAR will cover the cost for Junior Fellow Alumni to attend Academy meetings.

Value:

$70,000 CDN/US per year for salary and benefits $5,000 CDN/US per year for research support *US dollar values apply if the Junior Fellowship is held outside of Canada.

How to Apply:

Applications will be submitted through an online application system. Instructions are posted at www.cifar.ca/JFA. Application deadline: September 4, 2012.

CIFAR is strongly committed to diversity within its community, and especially welcomes applications from visible minority group members, women, Aboriginal persons, persons with disabilities, members of sexual minority groups and others who may contribute to further diversification of ideas.

Lori Dunn Event & Meeting Co-ordinator Programs Department Canadian Institute for Advanced Research (CIFAR) 180 Dundas Street West, Suite 1400 Toronto, ON M5G 1Z8 Tel.: (416) 971-4880 Fax: (416) 971-6169 email: ldunn@cifar.ca www.cifar.ca ldunn@cifar.ca

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Edinburgh EvolAsexualReproduction

Postdoc: Evolutionary genomics of asexual reproduction (Edinburgh, UK)

Two postdoctoral research associate positions are available to work on our project 'The evolutionary genomics of sexual recombination'. This is a large, 3-year, NERC-funded project based in the Universities of Edinburgh and Hull, UK. Using modern evolutionary comparative genomics approaches we aim to study the rate and pattern of genome sequence change with and without the action of meiosis, and across different levels of inbreeding. The project will be carried out in a phylogenetic design, on a newly generated nematode multi-genome data set, leading to advances in understanding the role of reproductive mode in shaping the structure and diversity of genomes. This advert refers to the first of the two postdoctoral posts, based in Edinburgh, UK.

The puzzling predominance of sexual reproduction amongst animals has been repeatedly identified as one of the major outstanding questions in biology and has received an enormous amount of study. Meiotic recombination is one of the fundamental forces of evolution and plays a very significant role in both generating and mixing the genetic diversity present in sexual organisms. Recombination is also suggested to be instrumental in shaping the content of eukaryotic genomes. We are embarking on a three year project to study the role of breeding system and recombination in shaping the content and diversity of animal genomes using an exceptionally powerful natural system - the Root Knot Nematodes (Meloidogyne spp.). We will, for the first time, be able to take a comparative genomic view of radically different reproductive modes in a phylogenetic design. Together these studies will give us a novel and powerful understanding of the role sexual reproduction plays in shaping genome cont ent.

The goals of the project are to generate complete, annotated genome sequences for a set of Meloidogyne species (at least 16 genomes), carefully chosen to represent independent evolutionary contrasts in reproductive mode, and then to use these whole genome data to characterise the effect of organismal breeding system on abundance, diversity and distribution of transposable elements between amphimicts, automicts, and apomicts. We will also test for adaptive evolution of genes and gene families using statistical birth and death model of gene family evolution, and test sequence based signatures of adaptive evolution and relate these to loci involved in either reproduction or plant-parasite interactions.

PDRA1-GENOME ASSEMBLY, ANNOTATION, AND ANALYSIS; UNIV OF EDINBURGH

Applicants with a strong background in evolutionary genomics, bioinformatics and genome analysis are invited for the position of Postdoctoral Research Associate to build, annotate and analyse new genome datasets. The post-holder will use advanced computational tools and hardware to assemble, validate and annotate novel genome sequences from Illumina data, and perform comparative analyses of these genomes in a phylogenetic framework.

The project is based in the lab of Prof. Mark Blaxter, within the University of Edinburgh Institute of Evolutionary Biology and in close association with the GenePool Genomics Facility. The Institute houses a large and diverse group of researchers, provides excellent facilities, and is a dynamic environment for research in evolutionary biology. The GenePool is one of the UKs leading next generation sequencing facilities, and is involved in a very wide range of next-gen projects using Illumina and other technologies. The University has a major compute grid resource, which will be used extensively. You must have, or shortly obtain a PhD in genomics, bioinformatics, evolutionary genomics, population genomics or other relevant subject. An excellent understanding of next generation data analysis and genome assembly and molecular evolutionary analysis would be advantageous. Understanding of the challenges of large data, and of the key issues in population genomics would be welcome.

Vacancy Reference: 3015830 Expiry Date: 09-Jul-2012 Informal enquiries to Prof Mark Blaxter: mark.blaxter@ed.ac.uk Further Information: http://goo.gl/rD8w3 Application: http://www.jobs.ed.ac.uk/vacancies/index.cfm?fuseaction=vacancies.detail&vacancy_ref015830&go=GO Start date 17 August 2012 or as soon as possible thereafter.

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

Mark.Blaxter@ed.ac.uk

EwhaWomansU TheoPopGenetics

A postdoctoral position in the area of computational/theoretical population genetics is available in the lab of Dr Yuseob Kim at Ewha Womans University, Seoul, Korea. The major aim of research in this lab is to detect and understand adaptive evolution in nature, particularly in species causing human infectious diseases. The position will be associated with either 1) developing theoretical/statistical tools for detecting selective sweeps in animals and applying them to genomic data, 2) modeling the population genetic dynamics of malaria parasites to understand the determinants of the rate of drug resistance evolution, or 3) evolutionary genetic analyses of influenza viruses. Other research topics related to adaptive evolution (positive Darwinian selection) proposed by the candidate can be considered. Candidates are expected to have completed a PhD in biology, mathematics, statistics, computer science or related field, with strong mathematical, computer-programming and/or bioinformatics skills.

Ewha Womans University is located in central Seoul and a major research-oriented University in Korea. Ewha provides an excellent research environment with beautiful and lively campus and is surrounded by areas of vibrant student culture and very safe environment for foreign students. Division of EcoScience is a comprehensive academic unit devoted to ecology and evolutionary biology and home to numerous international students and postdoctoral researchers. The official language of the lab is English. Other information can be found in our lab website (http://home.ewha.ac.kr/ykim).

Please e-mail your application (research interest, CV, contact information for two referees) to yuseob@ewha.ac.kr. Informal inquiry about the position, lab and living in Korea is welcomed. Applications will be accepted until August 31.

Yuseob Kim Assistant Professor Division of EcoScience Ewha Womans University Ewhayeodae-gil 52, Seodaemun-gu, Seoul 120-750, Korea Tel: +82 3277 3435

Yuseob Kim <yuseob@ewha.ac.kr>

FordhamU SeedBankEvolution

Postdoctoral Associate, Project Baseline: a seed bank for the study of evolution

A postdoctoral position is available in the lab of Steve Franks in the Department of Biology at Fordham University in New York. The position will involve work on Project Baseline, an initiative to collect seeds of multiple target species to analyze evolutionary responses to changes in climate.

Responsibilities include traveling throughout the eastern US to field sites, collecting seeds and environmental data, analyzing data, helping to supervise undergraduate students and other collectors, coordinating with collaborative investigators located in Minnesota, Colorado and California, and conducting research leading to publications. This position offers opportunities to design an independent project related to Project Baseline, as well as to participate in other career-development activities.

Qualifications include a Ph.D. in Botany, Ecology, Evolution or a related field; skills in plant identification; written and oral communicational skills; organizational, time and task management skills; proficiency with logistics; and the ability to travel for extended periods of time and work in the field under a variety of conditions. Experience in quantitative or ecological genetics, GIS, or climate or niche modeling would be useful.

The salary is commensurate with experience and includes benefits. The start date for the position is on or after October 15, 2012. Review of applications will begin August 15, 2012. The initial appointment will be for one year, and may be renewed for up to an additional 18 months. The position is based at the Rose Hill campus of Fordham University in the Bronx, New York.

To apply, please send a cover letter including current contact information, CV, and contact information for 3 references by e-mail to Steve Franks (franks@fordham.edu). PDF files are preferred. Inquiries may also be sent to this e-mail address. Please reference position number A06375 in the e-mail subject line and in the cover letter.

For more information on Project Baseline, see Franks et al. 2008, The resurrection initiative: Storing ancestral genotypes to capture evolution in action. BioScience 58: 870-873, as well as the project website, http://www.baselineseedbank.org/.

Fordham University is an equal opportunity/affirmative action institution. Qualified applicants of all backgrounds and career goals are encouraged to apply.

SteveFranks <franks.steve@gmail.com>

Harvard HumanBioinformatics

Hi,

I am currently seeking applicants to play a leading role in a large-scale analysis of loss-of-function variants in human protein-coding genes, as part of a new translational genomics group (http://www.macarthurlab.org) jointly based at Massachusetts General Hospital and the Broad Institute of Harvard and MIT. This position will involve developing tools for functional annotation of genetic variation data from over 20,000 sequenced exomes, as well as working with RNA sequencing data from multiple projects.

Applications for both postdoctoral training positions or staff scientist roles are welcome. The details of the position are below - please email me at macarthur@atgu.mgh.harvard.edu with a CV and cover letter if you're interested.

Best wishes,

Daniel MacArthur

About the position The MacArthur lab < https://sites.google.com/site/dgmacarthur/ > is a new research team based within the Analytic and Translational Genetics Unit < http://atgu.mgh.harvard.edu/ > (ATGU) at Massachusetts General Hospital and closely affiliated with the Broad Institute of Harvard and MIT. The successful candidate will become a part of the Broad Institute community, interacting extensively with other members of the Program in Medical and Population Genetics < http://www.broadinstitute.org/mpg >. You will work with population geneticists, clinicians, statisticians, computational biologists, industry partners and others in a unique and collaborative intellectual environment, and have access to new informatic and experimental technologies being developed in the world's leading center for human genomics.

We are looking for an ambitious, intellectually curious individual who is comfortable with integrating large, complex data-sets, and excited about the future of genomic medicine. Applicants do not necessarily have a formal background in academic research - a PhD is not required for applicants for the bioinformatics specialist position - but should be prepared to apply rigorous computational approaches to complex biological problems, and enthusiastic about communicating their work to both scientific and lay audiences.

Principal duties and responsibilities This role will focus on exploring the impact of natural loss-of-function (LoF) mutations in human protein-coding genes. Our group has recently published an article in the journal *Science* < http://www.sciencemag.org/content/335/6070/823.full > on the systematic identification of LoF variants from next-generation sequencing data < https://sites.google.com/site/dgmacarthur/lof >. You will work with ATGU members and other collaborators in developing an informatic pipeline for the identification and filtering of LoF variants from genome and exome sequencing data. This position will involve using data from large-scale RNA sequencing experiments and databases of known disease mutations to refine probabilistic models of the functional impact of genetic variants. You will coordinate the application of the completed analysis pipeline to exome sequencing data from over 20,000 individuals.

Ultimately, we aim to perform large-scale genotyping of LoF variants to identify the effects of these genetic changes on human traits and disease risk - an approach we have dubbed the Human Knockout Project. You will have a chance to be involved in the design and execution of this ambitious project, which we anticipate will uncover the function of many currently uncharacterized human genes. You will also contribute to the development of an integrated pipeline for the annotation of clinical sequencing data currently being generated by the ATGU and collaborators, and to the application of this pipeline to sequencing data from hundreds of Mendelian disease patients to discover novel disease-causing mutations.

The candidate will be expected to contribute to the writing of high-impact scientific publications and funding applications, to travel to and present their work at international conferences, and to actively seek collaborations with other researchers around the world. This position may also involve some supervision of graduate students and research technicians.

Skills required

- A good working knowledge of biology and human genomics; - Direct experience with large-scale data from genotyping and next-generation sequencing technologies, including familiarity with analysis tools such as SAMtools and GATK; - Ability to work in a unix environment, with demonstrable experience in high-level programming using C/C++ and experience with scripting languages such as Perl or Python;

— / —

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

LMU Munich EvolutionaryGenetics

Postdoc position in Plant Evolutionary Genetics at LMU Munich (Germany)

A postdoctoral position is open for (up to) three years in the Biology Department at the University of Munich LMU for someone interested by molecular evolution and population genetics in plants (wild tomato species). The applicant will be based in the Section of Evolutionary Biology in the group of Prof. Wolfgang Stephan. The applicant will pursue research on molecular adaptation of wild tomato species to abiotic stress such as drought tolerance or cold resistance. These species are found in a wide range of habitats (high mountains, deserts) in South America, and are thus a good model to study plant adaptation at the genome level. The objective of the postdoctoral period is to use high-throughput sequencing to detect natural selection involved in adaptation to different habitats. The applicant is also expected to perform functional validation at candidate genes. The project involves thus molecular and quantitative genetic assays of wild tomato accessions, and inferences from molecular population genetics and evolution.

Applicants must have completed their PhD before starting the position. We seek highly motivated candidates with a strong record of accomplishment from their Master/PhD thesis work. Ideally, applicants should have some experience with molecular genetic techniques, and a strong background in population genetics, evolution and statistics.

The Ludwig-Maximilian University of Munich is rated the best in Germany by international standards. The Department of Biology comprises research groups working on both plant and animal genetics. The Section of Evolutionary Biology also includes the group of Prof. J. Parsch working on evolution of gene regulation in Drosophila melanogaster, and the group of Prof. D. Metzler developing statistical and mathematical methods in population genetics. Our recent publications on adaptation in wild tomatoes include:

Xia, H., L. Camus-Kulandaivelu, W. Stephan, A. Tellier, and Z. Zhang (2010): Nucleotide diversity pattern of local adaptation at drought-related candidate genes in wild tomatoes. Mol. Ecol. 19: 4144-4154

Fischer, I., L. Camus-Kulandaivelu, F. Allal, and W. Stephan (2011): Adaptation to drought in two wild tomato species: the evolution of the Asr gene family. New Phytologist 190: 1032-1044

Tellier, A., S.J. Laurent, H. Lainer, P. Pavlidis, and W. Stephan (2011): Inference of seed bank parameters in two wild tomato species using ecological and genetic data. PNAS 108: 17052-17057

Hörger, A. C., M. Ilyas, W. Stephan, A. Tellier, R.A.L. van der Hoorn, and L.E. Rose (2012): Balancing selection at the tomato RCR3 guardee gene family maintains variation in strength of pathogen defense. PLoS Genet. (in press)

Mboup, M., I. Fischer, H. Lainer, and W. Stephan (2012): Trans-species polymorphism and allele-specific expression in the CBF gene family of wild tomatoes. Mol. Biol. Evol. (in press)

The start date is summer or fall 2012. Applications will be reviewed until the position is filled. To apply please email 1) a CV, 2) a short statement of research interests and experience describing your qualifications for this position, and 3) contact information for three references.

Contact: Prof Wolfgang Stephan (stephan@bio.lmu.de) Section of Evolutionary Biology, LMU BioCenter, Grosshaderner Str. 2, 82152 Planegg-Martinsried, Germany Tel: +49 89 2180 74 102, Fax: +49 89 2180 74 104, www.evol.bio.lmu.de hutter@zi.biologie.uni-muenchen.de

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MaastrichtU EvolutionTropicalTrees

Research in the natural sciences is changing rapidly. With the recent advent of massive parallel (next generation) sequencing, gigabytes of data per day are generated. However, the use of these data in certain areas of plant biology (e.g. systematics and phylogenetics) is still fairly limited and its possibilities are underinvestigated for non-model organisms.

We are looking for a post doctoral fellow to join the Maastricht Science Programme at the faculty of Humanities and Sciences of Maastricht University. The position will focus on next-generation sequencing of plant (plastid) genomes as a basis for research on tropical tree diversity in the South American Amazon. Plastid genomes of c. 150 species of tropical trees will be generated and their evolution studied. Also this genomic data set has to be mined to explore its additional potential. Furthermore, the successful applicant should contribute to the sequencing and analyses of transcriptomes of tropical trees as part of a newly emerging systems biology research theme at Maastricht University.

Requirements

The ideal candidate is a highly motivated postdoctoral fellow and has experience with (different) next generation platforms and high throughput variation analysis. The candidate should hold a PhD in (plant) molecular biology or related fields, and have a strong publication record. A strong bioinformatics background and experience in working with large datasets (such as next-generation sequencing) is a firm requirement. Also prior wet lab experience and experience with DNA extraction and sequencing from difficult templates is required. Conditions of employment

The terms of employment of MaastrichtUniversityare set out in the Collective Labour Agreement of Dutch Universities (CAO). Furthermore, local UM provisions also apply. For more information look at the website www.maastrichtuniversity.nl/ , A-Z Terms of Employment.

Contract type: Temporary, 2 years, 01-09-2012 until 01-09-2014 Organisation

http://www.maastrichtuniversity.nl/ Maastricht University is renowned for its unique, innovative, problem-based learning system, which is characterized by a small-scale and student-oriented approach. Research at UM is characterized by a multidisciplinary and thematic approach, and is concentrated in research institutes and schools. Maastricht University has around 14,500 students and 3,800 employees. Reflecting the university's strong international profile, a fair amount of both students and staff are from abroad. The university hosts 6 faculties: Faculty of Health, Medicine and Life Sciences, Faculty of Law, School of Business and Economics, Faculty of Humanities and Sciences, Faculty of Arts and Social Sciences, Faculty of Psychology and Neuroscience.

Additional information

More information on this application can be received from Dr. Roy Erkens: roy.erkens@maastrichtuniversity.nl, +31 43 38 81 182 and at http://www.academictransfer.com/employer/-UM/vacancy/14121/lang/en/?utm_campaign=-ENfeed&utm_term=%23job&utm_content=-%23vacancy&utm_source=twitterfeed&utm_medium=twitter Roy H.J. Erkens VENI-researcher and Lecturer Biology Maastricht Science Programme roy.erkens@maastrichtuniversity.nl www.maastrichtuniversity.nl Researcher ID < http:/-/www.researcherid.com/rid/B-9961-2008 > and Personal webpage < http://www.royerkens.nl/ >

Kapoenstraat 2, 6211 KW Maastricht P.O. Box 616, 6200 MD Maastricht, The Netherlands T +31 43 38 81 182 or +31 43 38 85 190 F +31 43 38 83 570

"Erkens Roy (MSC)" <roy.erkens@maastrichtuniversity.nl>

Montpellier EvolutionAgressiveness

An 18-months post-doctoral position is available in Montpellier, France, from Septembre 2012. The proposed research will be conducted as part of the BIOFIS project (Pest and invasive species: from individual to population and species) granted by Agropolis Foundation. Using several tools including experimental approaches, this project aims at disentangling *key question regarding invasive success*: role of *admixture events* and of *genetic bottlenecks*, *evolution of particular traits during spatial expansions*. In our team, the post-doctoral researcher will address these questions on two *fungal species responsible for major emerging diseases of plants*: /Magnaporthe oryzae/ and /Mycosphaerella fijiensis/ attacking rice and banana, respectively. On */Magnaporthe oryzae/*, using *experimental evolution*, the post-doctoral researcher will study the*role of initial genetic variability of the inoculum* on the invasive success on resistant hosts, and will seek for aggressiveness traits having evolved during invasion. On */Mycosphaerella fijiensis/*, he/she will contribute to study the *evolution of aggressiveness traits in natural population during a spatial expansion* from one hand, and *during an admixture event* on the other hand.

The applicant will join the BecPhy group (Evolutionary Biology of Phytopathogenic Fungi) of the BGPI Research Unit (Biology and Genetics of Plant-Pathogen Interactions). To evaluate emergence risks and define new and durable control strategies, our group aims at *understanding how populations of phytopathogenic fungi adapt*. Using theoretical and experimental studies in epidemiology and evolutionary biology, we address the origin of emerging fungal diseases, the importance of the different evolutionary forces in the adaptive process, the genetic constraints on traits involved in adaptation, and the epidemiological and adaptive dynamics in fungal populations in agrosystems.

Applicants must hold a PhD and have a strong background in evolutionary biology. An expertise in experimental evolution and in the study of evolution of adaptive traits is required.

Nous proposons un contrat post-doctoral de 18 mois à Montpellier, France, avec prise de fonction à partir de septembre 2012. Le travail de recherche proposé sera réalisé dans le cadre du projet Biofis (≪ Bioagresseurs et espèces invasives : de l'individu à la population, à l'espèce ≫)financé par la Fondation Agropolis. Ce projet aborde, entre autres par des études expérimentales sur différentes espèces invasives, des *questions clés liées au succès invasif*: rôle des *événements d'admixture* et des *goulots d'étranglement*, *évolution de certains traits lors des expansions spatiales*. Dans notre équipe, le post-doctorant abordera ces questions sur deux espèces de *champignons responsables de maladies émergentes majeures de plantes*: /Magnaporthe oryzae/ et /Mycosphaerella fijiensis /respectivement pathogène du riz et du bananier. Pour */Magnaporthe oryzae/*, le post-doctorant étudiera, par des approches d'*évolution expérimentale*, le *rôle de la variabilité génétique initiale *de l'inoculum**sur le succès invasif sur des hôtes résistants, et recherchera les traits d'agressivité sélectionnés au cours de l'invasion. Pour */Mycosphaerella fijiensis/*, il/elle contribuera à l'étude de *l'évolution de traits d'agressivité dans des populations naturelles* *au cours d'une expansion spatiale* d'une part, et au cours d'un *événement d'admixture* d'autre part.

Le post-doctorant sera intégré à l'équipe BecPhy (Biologie Evolutive des Champignons Phytopathogènes) de l'UMR BGPI (Biologie et génétique des interactions plantes-pathogènes). Pour évaluer les risques d'émergence et pour définir de nouvelles stratégies de lutte durables, l'équipe *a pour objectif de comprendre comment les populations de champignons phytopathogènes s'adaptent. *Nous combinons approches théoriques et expérimentales en épidémiologie et biologie évolutive, pour étudier l'origine des maladies fongiques émergentes, l'importance des différentes forces évolutives dans l'adaptation, les contraintes génétiques sur les traits impliqués dans l'adaptation, et les dynamiques épidémiologique et adaptative des champignons dans les agrosystèmes.

Les candidat(e)s devront être titulaires d'une thèse. Ils devront disposer de solides connaissances en biologie évolutive, et disposer d'une expertise dans les domaines de l'évolution expérimentale et l'étude de l'évolution de traits adaptatifs.

Contacts:

Elisabeth FOURNIER (elisabeth.fournier@supagro.inra.fr)

Jean CARLIER (jean.carlier@cirad.fr)

Elisabeth Fournier, Chargée de Recherche UMR BGPI TA A 54/K Campus International de Baillarguet 34398 Montpellier cedex 5

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Montpellier PlantEvolutionaryGenomics

A post-doc position in plant evolutionary genomics is available in Montpellier (France).

The post-doctorate scientist will participate to the ARCAD program (2009-2013), “Agropolis Resource Center for Crop Conservation, Adaptation and Diversity” (www.arcad-project.org) and will work on the project “Comparative population genomics in wild and crop plants”.

“Comparative population genomics of the evolution of GC-content in angiosperms”

The aim of the project is to analyse the evolutionary forces (mutational bias, selection, biased gene conversion) affecting GC-content dynamics in several species distributed over the angiosperm phylogeny, including several monocot and eudicot species. The candidate will analyze large polymorphism and divergence dataset issued from high-throughput sequencing of transcriptomes to test population genetics predictions (mutation bias vs selection vs GC-biased gene conversion) and to infer population genetic parameters (selection/conversion intensity, mutational bias).

Performance period: 18 months from July 2012 (or later) Location: The post-doctorate will be located both in the ISE-M lab (http://www.isem.cnrs.fr/spip.php?rubrique380&lang=en) and in the AGAP unit in Montpellier (http://www.montpellier.inra.fr/centre_et_unites/unites_et_campus/les_unites_du_centre/agap) Salary: Commensurate with qualifications and experience, benefits included. Gross salary around 2400â¬(3600$)

Application Please send a detailed CV, a letter of motivation, and two referents' names. Contact: Sylvain Glémin and Jacques David Email : sylvain.glemin@univ-montp2.fr and jacques.david@supagro.inra.fr

Sylvain Glémin

Chargé de Recherche - CNRS Institut des Sciences de l'Evolution. CC64 Université Montpellier II Place Eugène Bataillon 34095 Montpellier cedex 5 France Tel : 04 67 14 35 87

Page personnelle: http://sylvain.glemin.pagesperso-orange.fr/ Page ISEM: http://www.isem.univ-montp2.fr/ Sylvain Glemin <sylvain.glemin@univ-montp2.fr>

NCStateU BiolComplexity 2

NC State University Distinguished Postdoctoral Fellow in Biological Complexity

North Carolina State University is embarking on a new university-wide interdisciplinary initiative in biological complexity encompassing systems genetics, behavioral neurogenetics and neurogenomics, genome-environment interactions, ecological genetics, systems ecology, climate change, computational biology and bioinformatics.

Associated with the new initiative in biological complexity is a distinguished postdoctoral fellowship program. Applicants are expected to be near completion of a terminal doctorate degree, have a strong research record with evidence of exceptional scholarship, and embrace interdisciplinary research. Fellows will receive competitive stipends and independent research funds to initiate an innovative research program with guidance from a multidisciplinary mentoring committee in areas covered by the initiative in biological complexity.

To apply for a fellowship, go to jobs.ncsu.edu, search jobs, and enter position number 100730 under keywords. Provide a cover letter, curriculum vitae, a three-sentence statement of the most significant scientific problem(s) to be addressed in the near future, and statements of research interests. Three letters of recommendation should be sent to trudy_mackay@ncsu.edu. Review of applications will continue until the position is filled.

NCSU is an AA/EO employer. All qualified applicants will receive consideration for employment without regard to race, color, national origin, religion, sex, age, veteran status or disability. In its commitment to diversity and equity, NC State University seeks applications from women, minorities, and persons with disabilities. NC State welcomes all persons without regard to sexual orientation. ADA Accommodations: please call 919-515-5727.

Trudy F. C. Mackay, PhD, FRS William Neal Reynolds and Distinguished University Professor of Genetics Department of Genetics North Carolina State University Campus Box 7614 Raleigh, NC 27695-7614 Tel: 919-515-5810 Fax: 919-515-3355 Email: trudy_mackay@ncsu.edu

Trudy Mackay <trudy_mackay@ncsu.edu>

SangerInst ComparativeParasites

THREE-YEAR POST-DOCTORAL FELLOWSHIP IN COMPARATIVE INSIGHTS INTO PARASITE GENE FUNCTION

Applications are invited for a three-year post-doctoral fellowship held jointly at the Sanger Institute and EMBL-European Bioinformatics Institute under these institutes' "ESPOD" fellowship programme (http://www.ebi.ac.uk/training/postdoc/ESPOD).

The above webpage includes a link to an abstract of this project (and others in the programme). Full project details are available at http://tinyurl.com/c3pgoka. The successful candidate will work in the Goldman Group at EMBL-European Bioinformatics Institute (http://www.ebi.ac.uk/goldman) and Matt Berriman's Parasite Genomics group at the Sanger Institute (http://www.sanger.ac.uk/research/projects/parasitegenomics).

Applications should be sumitted by e-mail to Tracey Andrew <tandrew@ebi.ac.uk> by Wednesday 15 August 2012. Please contact Nick, Matt, or James Cotton (james.cotton@sanger.ac.uk) with informal queries.

James Cotton Senior Scientist Wellcome Trust Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridge. CB10 1SA UK

james.cotton@sanger.ac.uk 01223 494864

jc17@sanger.ac.uk

StanfordU EvolutionaryGenomics

Stanford University, Evolutionary genomics

A postdoctoral position is available in the lab of Hunter Fraser. Our lab combines 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. Familiarity 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 10 labs. To apply, please email a CV and cover letter to hbfraser[at]stanford.edu. The position can begin immediately.Salary and benefits are very competitive. For further information please see the labs website, http://www.stanford.edu/~hbfraser/ . Hunter Fraser Assistant Professor Department of Biology Stanford University Stanford, CA hbfraser[at]stanford.edu

Hunter Fraser <hbfraser [at] stanford.edu>

Switzerland BirdEvolution

Post-doctoral researcher in bird migration ecology

We are seeking a highly motivated post-doctoral scientist to join our team at the Swiss Ornithological Institute. Within the migration ecology department, we investigate the ecology of (small) long-distance migratory birds, focussing on the whereabouts during the non-breeding period and their consequences. More specifically, within the research project, we aim at (1) analysing individual (geolocator-derived) tracking data, (2) describing movement patterns in relation to individual state and environmental factors, (3) developing models to identify causal relations between individual behaviour and environmental factors

Requirements: PhD in ecology, evolutionary biology or biostatistics. The ideal candidate has a strong background in animal migration ecology and experience with (statistical) migration models, e.g. network models, as shown with a proven track record. Preference will be given to candidates with excellent statistical and programming skills (preferably in R) and good skills in scientific writing. The successful candidate is expected to work within the team as there are several existing datasets to be analysed.

The position is initially for 2 years, with the possibility of a one-year extension. Salary is according to the regulation of the Swiss Ornithological Institute. The intended starting date is November 2012 but can be negotiated if required. Place of work is Sempach, Switzerland.

Applications should be electronically submitted as one PDF or Word file to Felix Liechti (felix.liechti@vogelwarte.ch), Swiss Ornithological Institute, Seerose 1, CH-6204 Sempach, Switzerland, before 31 August 2012 and include a letter of motivation detailing research interests and experiences, a current CV and contact information of three academic referees. Interviews will tentatively take place in September. Questions should be directed to felix.liechti@vogelwarte.ch.

The Swiss Ornithological Institute is a non-profit foundation supported by the public. It is the largest private field research institute in Switzerland. We regularly work together with different universities in Switzerland and abroad. The Swiss Ornithological Institute serves as counselling office for the public, media and authorities, works out scientific facts in ornithology and provides arguments for the conservation of birds. Together with our partners, we make sure that nature benefits from the existing knowledge and law. Further information can be found at http://www.vogelwarte.ch/ . Dr. Felix Liechti Programmleiter Vogelzugforschung Tel. +41 41 462 97 82 (Direct) Fax +41 41 462 97 10 felix.liechti@vogelwarte.ch http://www.vogelwarte.ch/home.php?lang=d&cap=projekte&subcap=vogelzug Schweizerische Vogelwarte Seerose 1 CH-6204 Sempach Switzerland

Liechti Felix <felix.liechti@vogelwarte.ch>

UAlabama AlgalGenomics

POSTDOCTORAL POSITION IN ALGAL GENOMES DEPARTMENT OF BIOLOGICAL SCIENCES, THE UNIVERSITY OF ALABAMA A 2-year postdoctoral position is available in the laboratory of Juan Lopez-Bautista at The University of Alabama. The successful candidate will participate in a Research Stimulation Program and will be involved in the analyses of algal genomes, sequencing, editing, annotation, assembling and phylogenomic analyses. The candidate will also help the PI mentor graduate students and manage an active lab working on algal biodiversity, systematics and evolution. The candidate will have the opportunity to develop collaborative research project(s) in the area of algal phylogenomics. Minimum qualifications: 1) A Ph.D. in biology or related field; 2) previous research experience and a strong publication record; 3) familiarity with basic scripting languages such as Perl and Python, and experience with Unix operating systems; and 4) strong interpersonal skills and the ability to work as part of a team.

APPLICATION DEADLINE: 1 August 2012. Position starts 1 September, 2012.

TO APPLY: Apply online at the UA staff job application site: http://jobs.ua.edu/ The specific job is Requisition # 0805053 (a general postdoc application form, create a logon ID, and submit documentation). Interested individuals should provide with a cover letter, a CV, a 2-page (maximum) statement of interest including research background and goals, and contact details for three individuals who could provide a confidential letter of recommendation.

Upload all required materials to the site and additionally send the same materials to Juan Lopez-Bautista at jlopez@ua.edu

Info on the University of Alabama can be found here: http://www.ua.edu/ Lopez-Bautista's lab information can be found here: http://www.as.ua.edu/phycolab/ The University of Alabama is an equal opportunity/affirmative action employer.

Juan M. Lopez-Bautista, Associate Professor and 2012 PSA President The University of Alabama, Department of Biological Sciences 500 Hackberry Lane, Mary Harmon Bryant Hall #309 Tuscaloosa, AL 35487-0345 http://www.as.ua.edu/phycolab Ph Office (205) 348-1791; Labs (205) 348-4263/5844

jlopez@ua.edu

UAlabama EvolutionaryBiol

Postdoctoral Position in Evolutionary Biology

Department of Biological Sciences, University of Alabama

A 1-year postdoctoral position is available in the laboratory of Leslie Rissler at the University of Alabama. The successful candidate will aid in projects involving biogeography, conservation genetics, and the landscape ecology of amphibians and reptiles. The candidate will also help the P.I. mentor graduate students and manage an active lab working on diverse grant-supported projects. The candidate will have the opportunity to develop collaborative research project(s) that are linked to an ongoing NSF-funded project that examines the impact of the environment on neuroendocrine responses and genetic diversity across a latitudinal gradient in natural populations of the wood frog. MINIMUM QUALIFICATIONS: 1) A Ph.D. in biology or related field with a focus on evolution, population genetics, biogeography, ecology, conservation, behavior, and/or systematics; 2) previous research experience and a strong publication record; 3) field experience and familiarity with IACUC procedures; and 4) strong interpersonal skills and the ability to work as part of a team. ADDITIONAL PREFERRED QUALIFICATIONS: 1) experience doing stress response work in the lab and/or field; 2) experience with GIS and modeling using Maxent or similar algorithms; 3) molecular biology experience (microsatellites, SNPs, sequencing, etc. with associated skills in the analysis of these types of data); 4) programming in R and/or 5) curatorial experience.

APPLICATION DEADLINE: 1 August 2012 (or until filled). Position starts ~ 1 October 2012.

To Apply: Apply online at the UA staff job application site: http://jobs.ua.edu/. The specific job is Requisition # 0805053 (a general postdoc application form for the university). Applicants must have been awarded a Ph.D. degree by the application deadline date. Interested individuals should send a cover letter, a CV, a 2-page (maximum) statement of interest including research background and goals, and contact details for three individuals who could provide a confidential letter of recommendation. Upload all required materials to the site but also send the same materials to Leslie Rissler at Rissler@as.ua.edu.

Info on the University of Alabama can be found here: http://www.ua.edu/ Rissler's lab information can be found here: http://web.mac.com/ljrissler/lab/ rissler@as.ua.edu

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UArizona DiseaseBioinformatics

*Postdoctoral Fellowship in Bioinformatics of Next-Generation Sequencing and Disease***

The University of Arizona Genetics Core (UAGC) in cooperation with Michael Hammer's Lab in the ARL Division of Biotechnology at the University of Arizona is seeking a post-doctoral fellow interested in joining our cutting-edge team with emphasis on research and diagnostics of severe sporadic diseases in children, such as those involving epilepsy, autism, and other neurological/neuromuscular disorders. The position involves gene mapping using exome and whole genome sequencing, the characterization of newly identified disease genes and pathways, and the evolution of such genes and pathways through comparative analyses in primates.

*Tasks *The candidate will work with groups housed in both the UAGC nextgen core facility in the BIO5 Keating Building and in the Hammer lab. The candidate will (a) implement workflows for whole-exome and whole-genome sequence data, (b) perform bioinformatics analysis in collaboration with our research group and various clinicians within the University of Arizona Medical Center (UAMC), and (c) develop new methods and approaches for the analysis of whole genome sequence data. The workflows will include methods for pre-processing, identification of sequence variants, comparisons to and integration with public databases, statistical analyses, and data visualization. The candidate will use these workflows to analyze data and to associate variants with both monogenic and complex diseases. The candidate will be expected to author scientific publications based on results of data analysis and on methods that have been developed.

*Requirements *We are looking for an enthusiastic communicative team player with - a PhD in genomics, bioinformatics, or a relevant scientific discipline; - strong background in bioinformatics; - experience with the analysis of next generation sequence data is very useful but not mandatory; - experience with the statistical packages such as R; - good programming skills (e.g., Perl, Java) and knowledge of Unix; and - good English language and communicative skills.

Applicants should have experience in one or more of the following areas: statistical genetics, bioinformatics, computer science, or mathematics. Experience in neuroscience is seen as particularly useful and the ability to work in an interdisciplinary team is expected.

We offer competitive post-doctoral salaries and benefits. The University of Arizona is an EEO/AA Employer - M/W/D/V.

*To Apply: *

All applicants must apply through the University of Arizona online application process by completing an appointed personnel application with contact information for three references and attaching a letter of interest and curriculum vitae. To view the online posting and to apply, go to www.uacareertrack and search postings using job #50278, or go to the quick link at www.uacareertrack.com/applicants/-Central?quickFind 5009. The posting will remain open until filled, and review of applications will begin June 6, 2012. In addition to completing the required online application process, qualified candidates are encouraged to email curriculum vitae and statement of interest to mfh at email dot arizona dot edu <mfh@email.arizona.edu> , attention: Dr. Michael Hammer, with "Postdoc " in the subject line.

Michael Hammer <hammeruofa@gmail.com>

UBergen EvolutionaryEcology

Postdoctoral fellow in evolutionary (fisheries) ecology University of Bergen, Norway

The 4-year position in evolutionary fisheries ecology is available at the research group EvoFish at the Department of Biology, University of Bergen. EvoFish is an international group working at the interface of evolutionary ecology and fisheries biology, with fisheries-induced evolution as one of our key areas.

We are looking for applicants with good quantitative skills (statistics and/or modelling) and preferably with some knowledge of life-history theory and fisheries biology.

For more information on the position, please see the official announcement: http://-www.jobbnorge.no/job.aspx?jobid=84695 For more information on EvoFish, please see our homepage: http://www.uib.no/rg/evofish Mikko Heino Mikko.heino@bio.uib.no

Mikko Petteri Heino <Mikko.Heino@bio.uib.no>

UBirmingham Biostatistics

UNIVERSITY OF BIRMINGHAM School of Biosciences

Research Fellow (100%) Fixed term for 12 to 36 months Salary from £27,578 to £38,140 a year.

A Post-Doctoral Research Fellow position is available for experts in Biostatistics / Computational Biology, who will make significant contributions to the field of Environmental Genomics at the University of Birmingham, School of Biosciences. We are seeking prospective candidates that have demonstrated research interests in computational methods for statistical inferences from high-dimensional data.

The successful candidate will work within a vibrant, interdisciplinary, research team that uses high-throughput genomics technologies and the ecological model species Daphnia to study environmental effects on genomic structures and gene functions, and to understand how natural populations adapt to cope with environmental challenges, including climate change. Specifically, the Post-Doctoral Research Fellow will develop theory and statistical methods for analyzing genomic-scale population genetic data in an evolutionary context. This may include solving problems of large-scale multiple testing, of discovering gene-environment interaction mechanisms from high-dimensional sparse networks, of identifying signatures of natural selection from genome sequences of structured populations, of identifying the conditional dependency of gene expression from genetical genomics (eQTL) data, or from associating population-genomic variation to environmental conditions. Overall, the hired applicant will benefit from the academic life of the School and will gain experience at mentoring early career scientists in the lab.

Applicants should hold a PhD in biostatistics, computational biology, bioinformatics, systems genetics or related disciplines; have experience in analyzing population genetics or genomics data.

Post is available from October 2012

Closing date: 25 June 2012 or until filled Reference: 47469

Informal enquiries about these posts can be addressed to Professor John Colbourne by email at: jcolbour@indiana.edu, or Professor Mark Viant (tel: +44 (0)121 414 2219, email: M.Viant@bham.ac.uk).

To obtain further details and submit an electronic application online visit: http://www.hr.bham.ac.uk/jobs Valuing excellence; sustaining investment

"Colbourne, John" <jcolbour@indiana.edu>

UBirmingham CladoceraTaxonomy

UNIVERSITY OF BIRMINGHAM School of Biosciences

Research Fellow (100%) Fixed term for 24 months Salary from £27,578 to £38,140 a year.

A Post-Doctoral Research Fellow position is available for experts in morphology, physiology, life-history, ecology and taxonomy of the Cladocera, who will make significant contributions to the field of Environmental Genomics at the University of Birmingham, School of Biosciences. We are seeking prospective candidates that have demonstrated research interests in biodiversity issues as they relate to the biogeography, conservation and adaptive evolution of these important constituents of freshwater ecosystems.

The successful candidate will work within a vibrant, interdisciplinary, research team that uses high-throughput genomics technologies and the ecological model species Daphnia to study environmental effects on genomic structures and gene functions, and to understand how different species and natural populations adapt to cope with environmental challenges, including climate change. Specifically, the Post-Doctoral Research Fellow will play essential roles at linking genomics data to the species biology and ecology. This will include studying the developmental morphology of Daphnia to anchor omics data that are sampled throughout the species life-span; curating the Daphnia live animal collection for research by the Daphnia Genomics Consortium; leading sampling expeditions to discover evolutionary novelties tied to specific ecological conditions; and coordinating a long-term project to sample genome sequences representing the global diversity of Cladocera species. Overall, the hired applicant will benefit from the academic life of the School, will gain experience at mentoring early career scientists in the lab, and is expected to win an independent research fellowship after two years.

Applicants should hold a PhD in taxonomy, comparative biology, biogeography of Cladocera or related disciplines; have extensive fieldwork experience.

Post is available from October 2012

Closing date: 25 June 2012 or until filled Reference: 47470

Informal inquiries about these posts can be addressed to Professor John Colbourne by email at: jcolbour@indiana.edu, or Professor Mark Viant (tel: +44 (0)121 414 2219, email: M.Viant@bham.ac.uk).

To obtain further details and submit an electronic application online visit: http://www.hr.bham.ac.uk/jobs Valuing excellence; sustaining investment

"Colbourne, John" <jcolbour@indiana.edu>

UChicago ComputationalGenomics

A postdoc position is available in the Gilad lab in the Human Genetics department at the University of Chicago.

We are looking for applicants skilled in empirical and computational genomics. Postdocs in the Gilad lab can choose to work on one of our existing research projects (more details available on our website: http://giladlab.uchicago.edu), or propose to develop a new project altogether. Interested applicants should send their CV and arrange for three reference letters to be emailed directly to Yoav Gilad (gilad@uchicago.edu).

Yoav Gilad Dept. of Human Genetics University of Chicago 920 E. 58th Street - CLSC 325C Chicago, IL 60637, USA Office: +1-773-702-8507 Lab: +1-773-834-1984 Fax:+1-773-834-8470 Email: gilad@uchicago.edu WWW: http://giladlab.uchicago.edu/ yoav.gilad@gmail.com

UChicago EvolutionDiversityPatterns

Postdoctoral Scholar, University of Chicago

Seeking a postdoctoral scholar to participate in an ongoing collaborative research project (D. Jablonski-K. Roy-J. W. Valentine) on the evolutionary history and future of modern spatial patterns of diversity, such as the latitudinal gradient. Marine bivalves will be used as a model system due to their excellent fossil record, ecology diversity and highly resolved taxonomy. Research involves quantifying present-day biogeographic patterns, quantifying the Cenozoic spatial and evolutionary dynamics underlying them, and relating these patterns to environmental change. Postdoctoral scholar will assist in analyses and modeling of diversity dynamics, and take the lead on some new research projects. Experience in some combination of modeling, statistical, phylogenetic, and spatial (GIS) analyses and/or database management required. Familiarity with paleontological, climatic and/or biogeographic data is preferable. One-year appointment renewable for one or more additional years. Starting date negotiable but prefer summer to early fall 2012. Requires either Ph.D in hand or dissertation submitted and approved for degree. Please email a letter documenting research interests and experience, a CV, and the email addresses of two references to Dr. Andrew Z. Krug (akrug@uchicago.edu) at the University of Chicago. Applications required by July 1, 2012 for full consideration. The *University of Chicago is an equal opportunity**/*affirmative action employer, and encourages applications from under-represented minorities and women.

Andrew Krug <akrug@uchicago.edu>

UCLondon ComparativeGenomics

UCL Research Fellowship in Comparative Genomics or Comparative Developmental Biology (EvoDevo).

The Department of Genetics, Evolution and Environment at University College London (UCL) is offering a research fellowship in the field of Comparative Genomics or Comparative Developmental Biology. The funding (up to 2 years) is intended to support exceptional early career scientists, allowing them time to apply for further independent fellowship funding from UK Research Councils and Charities. The highly motivated fellow will be expected to have demonstrated their potential through a record of publication in leading journals. We also welcome applications from candidates who already hold research fellowships.

We are open to applications from candidates using theoretical and/or experimental approaches, with no restriction on organism or level of biological organization studied. Potential research areas of interest might include, but are not restricted to: evolutionary genomics; regulatory genomics; comparative developmental genetics; bioinformatic and systems approaches to evolution.

Details of the Departments activities can be found at www.ucl.ac.uk/gee Expression of interest should be directed to Prof Max Telford, (m.telford@ucl.ac.uk) or Dr Paola Oliveri (p.oliveri@ucl.ac.uk). Applicants should submit a CV, including a statement of their research interests and plans, and the names and addresses of three referees.

Closing date: 6th July 2012

Max Telford Professor of Zoology Department of Genetics, Evolution and Environment, University College London, Darwin Building, Gower Street, London WC1E 6BT, UK. Tel: +44 (0)20 7679 2554 (Internal: 32554) Fax: +44 (0)20 7679 7096 http://www.ucl.ac.uk/biology/academic-staff/telford/telford.html a new open access journal EvoDevo: http://www.evodevojournal.com/ Telford & Littlewood: Animal Evolution. OUP < http://ukcatalogue.oup.com/product/9780199570300.do >

Software to align Nucleotide sequence according to Amino Acid translation TranslatorX < http://www.translatorx.co.uk >

Files and software for downloading: < http://web.mac.com/maxtelford/iWeb/Work/Downloads.html >

Mrimpatient: If you cant wait to see latest result of MrBayes analysis. Xstem and Ystem: Software for 2y structure data in rRNA phylogenetic analyses. MtZoa and MtHydro : new amino acid substitution matrices Hacked version of MrBayes using these matrices

Xenoturbella You Tube video < http://uk.youtube.com/watch?v=yJXNcoxL2Xs >

The Linnean Society of London < http://www.linnean.org/ >

“Telford, Max” <m.telford@ucl.ac.uk>

UEdinburgh PopulationGenomics

Post Doctoral Research Associate in population genomics

A NERC-funded postdoctoral position for up to 3 years is available at the Institute of Evolutionary Biology to develop and apply methods for demographic inference for genomic data. The project represents an excellent opportunity to combine advancement of theory with exploration of empirical data in haploid systems.

The project has two aims. First, to develop new inference methods (in collaboration with project partners Prof Nick Barton (Institute of Science and Technology Austria) and Prof Mike Hickerson (Queens College - City University of New York)); and second, to use these methods to reconstruct the Pleistocene history of two natural insect communities from population genomic data.

Genomic data will be processed and assembled by a project-dedicated bioinformatician.

We are seeking a highly motivated researcher with a strong background in either population genetics theory and/or analysis of high-throughput sequencing data. Interest in both coalescent theory and model-based inference are essential, although the balance of theoretical and empirical work is flexible and can be adjusted to fit the interests of the candidate. The candidate will be based in Edinburgh with Prof. Graham Stone's group and Dr. Konrad Lohse, with strong links with project Co-PI Prof. James Cook at the University of Reading and the NERC Genepool facility, Edinburgh.

Applicants must have, or shortly obtain a PhD.

For an introduction to the population genetic exploration of the oak gallwasp system see Stone GN et al. (2012), Current Biology 22:1-6 for an overview of a possible theory framework for genome analysis see Lohse et al. (2011) Genetics 189, 977V987 .

Interested candidates are invited to contact Konrad Lohse (Konrad.lohse@ed.ac.uk) or Graham Stone (graham.stone@ed.ac.uk) informally if they wish to discuss the project.

Closing date; August 13th

We encourage all applicants to apply online at www.jobs.ed.ac.uk. The application process is quick and easy to follow, and you will receive email confirmation of safe receipt of your application. The online system allows you to submit a CV. Applicants are requested to submit two references as an attachment to their application (if appropriate).

This is a re-advertisement V previous candidates (unless contacted directly) need not apply.

Professor Graham Stone Chair in Ecology Institute of Evolutionary Biology, The King's Buildings, West Mains Road, Edinburgh EH9 3JT

http://www.gallwasp.org/ tel +44 131 6507194 fax +44 131 6506564

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GRAHAM STONE <gstone@staffmail.ed.ac.uk>

UGroningen TheoreticalEvolEcol

PhD position or Postdoc Theoretical Evolutionary Ecology (1,0 fte)

Vacancy number 212054H

Job description

In many organisms individuals differ systematically in their dispersal behaviour. Moreover, individual variation in dispersal is correlated with other traits, including metabolism, activity, aggressiveness, boldness, sociability, behavioural flexibility and learning ability. Although such correlation structures ("dispersal syndromes") have been described for many species, neither their evolutionary emergence nor their ecological, evolutionary and genetic consequences are well understood. By means of a theoretical approach (using analytical models and individual-based computer simulations) the project will address questions such as: Why are the dispersal syndromes in different species remarkably similar in some respects and remarkably different in others? What are the consequences of variation in dispersal for social evolution (e.g., cooperative breeding) and the mating system? What are the implications of non-equilibrium dynamics for the genetic structure of a population and for the estimation of pedigrees, relatedness and fitness?

The project is designed as a 4-year PhD project; however, we also welcome applications from exceptional postdoctoral researchers for a 3-year position. The close collaboration between theoretical and behavioural researchers, along with access to the long-term Seychelles warbler dataset, provides a unique opportunity to forge a link between conceptual models and real-world data.

Requirements - MSc in Theoretical Biology, Behavioural Ecology, Evolutionary Biology or related discipline (for a PhD candidate) or a PhD in any of these disciplines (for a postdoc) - research experience in areas related to model development and analysis, individual-based simulations or dynamical systems (desired for a PhD candidate; essential for a postdoc) - working knowledge of programmes like C++, Maple/Mathematica/Matlab or R; excellent programming skills (desired for a PhD candidate; essential for a postdoc) - excellent academic record (as shown by a list of examination marks); proven ability to plan and prioritize work and to work to and meet deadlines; strong commitment to excellence in research and teaching - ability to develop creative approaches to problem solving; creativity, curiosity, and ambition; proactive attitude; ability to implement new methods and ideas - excellent organisational and interpersonal skills; ability to work in a team consisting of scientists, students and technical assistants with different backgrounds - excellent communication skills: effective paper writing skills (demonstrated by publications) and ample experience with delivering presentations - good command of the English language (oral and written).

Conditions of employment The University of Groningen offers the PhD a salary of ? 2,042 (scale 50, number 0) gross per month in the first year, up to a maximum of ? 2,612 (scale 50, number 3) gross per month in the final year, based on a full-time position. The position requires residence in Groningen and must result in a PhD thesis within the 4-year contract period. A PhD training program is part of the agreement and the successful candidate will be enrolled in the Graduate School of Science. The successful candidate will first be offered a temporary position of 1.5 years with the perspective of prolongation for another 2.5 years. After the first year, there will be an evaluation on the perspectives of the successful completion of the PhD thesis within the next three years. If these perspectives are poor, the contract may not be renewed.

The University of Groningen offers the postdoc a gross salary depending on qualifications and experience, ranging between ? 2,744, gross (scale 10, number 3) per month and a maximum of ? 3,755 (scale 10, number 12) gross per month for a full-time postdoctoral job. This position is defined according to the UFO function profile 'researcher'. After the first year there is an assessment interview; continuation of the project for the next two years is dependent on successful performance during the first year.

Starting date: The preferred starting date is 1 June 2012. The position will be filled as soon as suitable candidates have been found.

Application You can apply for this job by sending your application including a letter of motivation, a curriculum vitae, a list of examination marks, a publication list, and the names and addresses of three academic referees who are willing to provide letters of reference (upon request) before 1 April 2012, 24:00 CET.

Organisation This research project “Causes and consequences of variation in dispersal behaviour” is a collaborative effort of the research groups Theoretical Biology and Behavioural Ecology and Self-organization (BESO), which both are part of the Centre for Ecological and Evolutionary Studies at the

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

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UJyvaskyla Finland EvolutionaryDevBiol

A Post-Doctoral Researcher is being recruited to work in the project: Larval polymorphism and evolutionary transitions in developmental mode with Dr. Emily Knott at the University of Jyvaskyla, Finland. The project aims to identify factors that influence larval polymorphism in the polychaete worm Pygospio elegans. The project is funded by the Academy of Finland.

The Post-Doctoral researcher position is available beginning September or October 2012 for a highly motivated individual with a background in evolutionary developmental biology. The post-doctoral researcher will be involved in transcriptomic and epigenetic analyses. Experience in bioinformatics and / or microscopy is a plus. Some travel and work abroad will be required during the project. The post-doctoral researcher will have the opportunity to lead PhD and MS level students and participate in teaching, if desired. Candidates should have good organizational, writing and presentation skills and should be able to work well both independently and in a team environment. The position is available for 2 years with possibility of a 1 year extension.

The research takes place in the Ecology and Evolutionary Biology division in the Department of Biological and Environmental Science at the University of Jyvaskyla https://www.jyu.fi/bioenv/en/divisions/eko . Additional information about Emily Knott's research can be found https://www.jyu.fi/bioenv/en/divisions/eko/research/Knott_group/index.html .

To be considered for the post, please send a letter of motivation and your CV, including the names, email addresses and phone numbers of three referees who could provide a statement of your suitability for the position, to emily.knott@jyu.fi<mailto:emily.knott@jyu.fi> by 30th June 2012.

K. Emily Knott University Lecturer Department of Biological & Environmental Science P.O. Box 35; Survontie 9; Ambiotica C4 40014 University of Jyvaskyla FINLAND

emily.knott@jyu.fi

UKansas PhylogeneticSoftware

Two positions for postdoctoral researchers are available in the laboratory of Dr. Mark Holder in the Department of Ecology and Evolutionary Biology at the University of Kansas (Lawrence, KS). The duration of each position is two years. The research projects that fund the position focus on developing improved methods of conducting multiple sequence alignment and phylogenetic inference. In particular, designing new algorithms and statistical models for updating large gene trees in light of new sequence data is an important target for the work. The postdoctoral researchers will be expected to contribute to the software efforts of a multi-institutional collaborative effort to integrate phylogenetic estimates across the entire tree of life (http://opentreeoflife.com). Candidates will be expected to have completed a PhD in Biology, Statistics, Computer Science or a related field. Preferably the candidate will have experience in Python and either Java, C, or C++.

The ideal candidate will be enthusiastic, motivated, have a strong background in phylogenetics, and have experience implementing statistical inference techniques in software as demonstrated by materials submitted through the application process, work experience, and letters of reference, and/or previous publications.

Apply to: https://jobs.ku.edu and use the “Search postings” to search for position number 00065509.

Currently the URL for the posting is at: https://jobs.ku.edu/applicants/jsp/shared/position/JobDetails_css.jsp?postingId=447330 (but that may change if the posting has to be amended, and searching for the position number should remain a reliable manner to find the listing).

Review of applications will begin on June 20, 2012 and will continue until the positions are filled. For more information, see the Holder web page at: http://phylo.bio.ku.edu/

KU is an EO/AA employer.

Sincerely, Mark Holder

mtholder@ku.edu http://phylo.bio.ku.edu/mark-holder Department of Ecology and Evolutionary Biology University of Kansas 6031 Haworth Hall 1200 Sunnyside Avenue Lawrence, Kansas 66045

lab phone: 785.864.5789

fax (shared): 785.864.5860

mtholder@ku.edu

UKentucky EvolGenomics

Postdoc in Evolutionary Genomics at the University of Kentucky

The Linnen lab at the University of Kentucky is seeking a full-time postdoctoral researcher to contribute to ongoing work on the genetics, ecology, and demography of adaptation and speciation in pine sawflies (genus *Neodiprion*). Depending on the skills and expertise of the successful applicant, this research position will involve some combination of the following: fieldwork, behavioral studies, genetic crosses, population genetics, phylogenetics, and genomics. For additional details about current research in the lab, please visit our website: http://www.uky.edu/ ˜ cli242/Linnen_Lab/Home.html . We encourage applications from independent and creative individuals who are motivated by a desire to address fundamental questions in evolutionary biology. The ideal candidate will have a strong background in evolutionary or population genetics and experience with generating and analyzing next-generation sequence data. We are also looking for someone who is personable and enthusiastic about working in a collaborative environment. A PhD in a related field (e.g., biology, evolution, genetics, genomics, etc.) is required.

Interested candidates should send a letter describing research interests and experience, a full CV, and contact information for three references. Applications and all queries should be sent to catherine.linnen@uky.edu. Priority will be given to applications received by August 1. Start date is flexible and funding is guaranteed for 1 year, with subsequent years renewable depending on progress.

Catherine R. Linnen, Ph.D. Assistant Professor Department of Biology University of Kentucky 200A Thomas Hunt Morgan Building Lexington, KY 40506 website: http://www.uky.edu/ ˜ cli242/Linnen_Lab/Home.html Phone (lab): 859-323-3160 Phone (cell): 617-970-7717 clinnen@gmail.com

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UKonstanz EvolutionaryBiol

Postdoc positions are available in the lab of Axel Meyer (http://www.evolutionsbiologie.uni-konstanz.de/-index.php?section=10) and the Zukunkftskolleg http://www.zukunftskolleg.uni-konstanz.de/en/about-zukunftskolleg/concept/ at the University of Konstanz in Germany

The Zukunftskolleg ("College of the Future") at University of Konstanz offers several kinds of new and attractive postdoctoral fellowship schemes (2-5 years in duration) that offer not only salaries, but also a research allowance and other types of support that are supposed to help young researchers' transition into academic independence.

For more information and application procedures see:

http://www.zukunftskolleg.uni-konstanz.de/-aktuelles/ausschreibungen/ The deadline for applications is 26.8.2012

The starting date of the 2-year fellowships is flexible and could begin soon after the deadline - the 5-year fellowships would commence March 1. 2013.

The Meyer-Lab is working on various aspects of evolutionary biology. We are looking for applications from Ph.D. biologists, ideally with prior experience in bioinformatics, molecular evolution or population genomics. We have recently received funding through an ERC advanced grant for work on the comparative genomics of parallel evolution of repeated adaptive radiations of cichlid fishes in Nicaragua (see: Elmer and Meyer. 2011. Adaptation in the age of ecological genomics: insights from parallelism and convergence. Trends in Ecology and Evolution 26: 298-306). This system is one our major research foci in the lab, but we welcome applications from evolutionary biologists interested in speciation, genomics, population genetics and population genomics - liking cichlids and knowing a thing or two about fishes is a plus, of course.

For publications of the Meyer-lab see:http://www.evolutionsbiologie.uni-konstanz.de/-index.php?section' Excellent working conditions are available in terms of space, equipment, departmental facilities and internal and external financial support for research expenses. The lab has state-of- the-art facilities for molecular and developmental biology, including Illumina and Roche FLX 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 southern border of Germany, adjacent to Switzerland. The annual gross salary (depending on prior experience) is about 58,000 Euros (about 73.000 US$) before taxes and other deductions. Habilitation is possible. Additional information can be obtained from a.meyer@uni-konstanz.de, (tel.+49 7531 84163, fax + 49 7531 883018) or from our www page.http://www.evolutionsbiologie.uni-konstanz.de . Prof. Axel Meyer, Ph.D. Lehrstuhl für Zoologie und Evolutionsbiologie Department of Biology Building M, Room M806 University of Konstanz 78457 Konstanz Germany

fon + 49 (0)7531 88 4163 fax + 49 (0)7531 88 3018

secretary: Ingrid.Bader@uni-konstanz.de tel. + 49 (0)7531 88 3069

www.evolutionsbiologie.uni-konstanz.de We are hosting the annual meeting of the German Zoological Society in Konstanz (Sept. 21- 24th 2012) Check out the program: http://cms.uni-konstanz.de/dzg/home/ Axel Meyer <axel.meyer@uni-konstanz.de>

UMichigan PredatorPreyGeneVariation

UMichigan.MolecularGenetics

A postdoctoral research position is available in Tom Dudas lab at the Department of Ecology and Evolutionary Biology, University of Michigan. The main thrust of the project that will be conducted is to characterize genes that are involved in predator-prey interactions and interpret patterns of variation of these genes. The primary responsibilities of the postdoc are to generate and analyze sequence datasets. Please visit the Duda labs website to learn more about activities in his laboratory at the following address:

http://www.ummz.lsa.umich.edu/mollusks/labs/-duda/index.html Potential candiates should have demonstrated proficiency in RNA-seq or other high-throughput sequencing approaches as well as the analyses of data generated using these methods.

Candidates should also have expertise in molecular evolutionary and/or population genetic methodologies.

Applications should be sent to tfduda@umich.edu and include a CV, description of research interests and experiences, PDFs of relevant publications and contact information for two to three references. Applications from women and members of underrepresented groups in science are especially encouraged to apply.

The University of Michigan is a nondiscriminatory, affirmative action employer.

Tom Duda Department of Ecology and Evolutionary Biology 1109 Geddes Avenue Ann Arbor, MI 48109

tfduda@umich.edu

"Duda, Thomas" <tfduda@umich.edu>

UNewMexico EvolutionaryGenomics

Postdoctoral Research Fellow in Caenorhabditis elegans Evolutionary Genetics and Genomics Department of Biology University of New Mexico

Applications are invited for a postdoctoral research position in the laboratory of Vaishali Katju in the Department of Biology at the University of New Mexico. Our lab employs molecular and bioinformatic tools to study evolutionary processes at the level of genomes and populations (both experimental and natural). Presently we are analyzing genetic changes during experimental evolution in C. elegans as well as a copy number variants in natural populations of C. elegans. The project details are flexible, but will focus on analyzing of whole-genome sequences of natural and experimental C. elegans populations in order to characterize the ensuing molecular changes (including structural variants) and their role in shaping genome evolution. Preference will be given to candidates with a strong background in computational biology, molecular evolution, population genetics and statistics. Familiarity with experimental use of C. elegans, analysis of high-throughput sequencing data or quantitative/statistical genetics is a plus.

Additional information: Please visit our lab website (http://biology.unm.edu/katju/-Katju_Lab_Website/Home.html) or contact me directly vkatju@unm.edu to discuss research options in greater detail.

Application Instructions: E-mail your application to vkatju@unm.edu as a single pdf file containing your CV with publications, contact details of 3-5 referees, a letter describing your research interests and why you would be an exceptional candidate for this position.

Salary: A competitive salary commensurate with experience is guaranteed for one year with subsequent years renewable depending on performance.

Environment: The Department of Biology at UNM is located in Castetter Hall on the main campus, which includes modern lab and computational facilities. The Department has an exceptionally strong concentration in ecology and evolutionary research. Our research team also benefits from a close collaboration with Dr. Ulfar Bergthorsson, an evolutionary geneticist at UNM, and access to next-generation sequencing and microarray facilities through Dr. Donald Moerman, Professor and Director of the C. elegans Reverse Genetics Core Facility at the University of British Columbia and Dr. Robert Waterston, Professor and Chair of the Department of Genome Sciences at the University of Washington.

vkatju@unm.edu

UNorthCarolina Charlotte BioinformaticsGenomics

At the University of North Carolina at Charlotte (UNCC), Department of Bioinformatics and Genomics, we seek two postdoctoral fellows with recent Ph.D. degrees.

Valuable experience includes: 1) development of workflows for analyses of next generation sequence data.

and

2) publication of results.

The fellows will work with a variety of stakeholders with backgrounds in biology, public health, and computer science towards mutual research goals.

Please send curriculum vitae and contact information to unccpostdoc@gmail.com

Dan Janies <unccpostdoc@gmail.com>

UoExeter HostParasiteGenomics

On behalf of a project with Prof Mike Boots University of Exeter...

3yr Post-doc 'Resource availability and the evolution of host resistance to parasites'

http://www.jobs.ac.uk/job/AEQ066/associate-research-fellow-or-research-fell ow/

The College of Life and Environmental Sciences wishes to recruit an Associate Research Fellow or Research Fellow to work with Professor Mike Boots on a new research project that is funded by a NERC responsive mode grant. This NERC funded post is available from September 2012 for duration of three years. The successful applicant will be the key researcher on a proposal entitled "Resource availability and the evolution of host resistance to parasites: within individuals, trade-off shapes and the genetic basis of resistance." All organisms are subject to infection and have to invest resources into mechanisms that either prevent infection or that clear infections that enter the body. However, the availability of resources in the wild is finite and differs across environments. This is important because parasites are critical to natural, agricultural and human populations and an understanding of the expression and evolution of host defence is crucial to the management of infectious disease in both natural and managed systems. The project will take an experimental approach to examine the role that resource availability plays: (1) in individual immune responses; (2) in shaping the genetic variability and trade-off relationships; and (3) in constraining the evolution of resistance. The project will examine the evolution of resistance to parasites using the Indian meal moth and its granulosis virus as a model system, where we have demonstrated ability to control both resource availability and pathogen infection. The moth will be genome sequenced and a combination of resequencing, gene-expression and new quantitative techniques will be used to examine fundamental questions on the shape of trade-off relationships. The successful candidate will be based Biosciences in Falmouth, Cornwall but collaborate researchers based in Liverpool and Oxford. The successful applicant will be able to present information on research progress and outcomes, communicate complex information, orally, in writing and electronically. Applicants will have a PhD in evolutionary biology and be able to demonstrate sufficient knowledge in host-parasite interactions and/or the analysis of sequence and expression data or quantitative genetics. Applicants must be able to work independently, organise time and manage technicians. For further information please contact Professor Mike Boots on Tel. 01326 25 5735 or e-mail m.boots@exeter.ac.uk.

– Prof Steve Paterson Institute of Integrative Biology University of Liverpool Liverpool, L69 7ZB, UK Tel +44 151 795 4521 Fax +44 151 795 4408 Mob +44 797 024 7668 s.paterson@liv.ac.uk http://www.liv.ac.uk/-genomic-research/ S.Paterson@liverpool.ac.uk

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UParisSud PlantEvoDevo

Post-doc position at the Laboratoire Ecologie, Systématique et Evolution, Université Paris-Sud, Orsay, France

Research area A post-doctoral position in the field of plant evo-devo is available for one year at Université Paris-Sud, starting in October 2012. The successful candidate will take part in a research project on floral symmetry in Proteaceae, funded by a consortium of universities and involving three research labs (see below). Using RNA-Seq, a reference transcriptome of Grevillea flowers will be constructed. The candidate will be in charge of its bio-analysis and use this transcriptome to seek homologues of candidate genes known to be involved in floral bilateral symmetry in model species such as snapdragon. He/she will study expression profiles of selected candidate genes using in situ hybridization and RT-PCR techniques. He/she will also contribute to the study of floral development in four species of Proteaceae with contrasted floral symmetry, using SEM and micro-CT scanning technology.

Required Qualifications Experience in bio-analysis of sequences (basic knowledge in sequence alignment, search of homology, gene families and molecular evolution) Experience in plant molecular biology (especially RNA work) Experience in floral development Excellent level of English (written and spoken) and good interpersonal skills (French not required, but useful)

Preferred Experience Experience in in situ hybridization on plant tissues

Place of employment and place of work The place of employment is Université Paris-Sud, located near the city of Orsay, in a beautiful green campus which is also a botanical garden, and easily accessed via a short comute from Paris. The research fellow will spend most of his/her time at Laboratoire Ecologie, Systématique et Evolution (ESE, Bâtiment 360, 91405 Orsay cedex, France), working closely with Sophie Nadot and Hervé Sauquet. He/she will also have strong interactions (and spend short periods of time) with Etienne Delannoy's team at URGV (Unité de recherches en Génomique

Végétale, INRA, Université d'Evry Val d'Essonne) and Catherine Damerval's lab (UMR de Génétique Végétale, INRA/CNRS/UPS, Ferme du Moulon), both of which are located close to Orsay and Paris. This project also involves external collaborators at the Royal Botanic Gardens in Sydney (Australia) and the University of Vienna (Austria).

For more information, see: http://www.ese.u-psud.fr/-?lang=3Den (ESE lab) http://www.u-psud.fr (Université Paris-Sud) http://www.versailles.inra.fr/urgv/- (URGV) http://moulon.inra.fr/index.php/en/team/-gear (UMR GV) Further information on the position may be obtained from Professor Sophie Nadot, phone +33 169155665, sophie.nadot@u-psud.fr

Application Interested candidates should contact sophie.nadot@u-psud.fr and send a CV including research interests, a list of publications and the names and contact information for two references.

Deadline All applications must be received by 15 August 2012.

"' Sophie Nadot Ecologie, Systematique et Evolution, UMR 8079 Universite Paris-Sud Batiment 360 F-91405 Orsay cedex

Tel : +33 (0)1 69 15 56 65 Fax : +33 (0)1 69 15 46 97 Page perso : http://www.ese.u-psud.fr/-article206.html Page equipe : http://www.ese.u-psud.fr/rubrique4.html – Hervé Sauquet

Maître de Conférences / Assistant Professor Université Paris-Sud 11 Lab. Écologie, Systématique, Évolution (ESE) CNRS UMR 8079, bât. 360 91405 Orsay, France Tel/Fax: +33 169154991/+33 169154697 E-mail:herve.sauquet@u-psud.fr

herve.sauquet@gmail.com

UPennsylvania HumanEvolutionaryGenomics

The University of Pennsylvania is offering an Academic Diversity Fellowship Program which seeks to attract promising scholars and educators from different backgrounds, races, ethnic groups, and other diverse groups whose life experience, research experience and employment background will contribute significantly to Penn's academic excellence. Detailed information is available at the following URL:

http://www.upenn.edu/research/research_site/-postdoc_diversity.html The Tishkoff lab is seeking potential candidates for this position. We are integrating genomic, transcriptomic, metabolomic, and epigenomic analyses in a large sample of ethnically diverse Africans with the aim of using an evolutionary and systems biology approach towards understanding the genetic architecture of a number of adaptive traits for which we have detailed phenotype data. We are also interested in inferring demographic history of Africans, and testing models of human evolutionary history using large genome-scale datasets.

Interested candidates for this and for other potential postdoctoral fellowship opportunities should contact:

Dr. Sarah Tishkoff Departments of Genetics and Biology University of Pennsylvania tishkoff@mail.med.upenn.edu

http://www.med.upenn.edu/tishkoff/
tishkoff@mail.med.upenn.edu

USalford SeafoodIdentification

We invite applications for a 2-year post-doctoral position, to work on seafood genetic identification in Dr Mariani's lab at the University of Salford, Manchester. The project is primarily funded by the EU Interreg Atlantic area and offers the opportunity to interact with collaborators in Spain, Portugal, France, Ireland and Germany.

The ideal candidate will hold a PhD in Evolutionary Biology, Genetics, Ecology, Marine Biology, or other relevant subjects, and will have a proven track-record in publishing in international peer-reviewed journals. He/she will also exhibit strong skills in molecular genetics techniques and bioinformatics, and will have a positive, communicative, dynamic personality, suited to work as part of a team.

Dr Mariani's lab at Salford University - still twinned with its previous base at University College Dublin - contributes to a broad range of investigations in population and conservation genetics and fisheries biology (for details: http://www.els.salford.ac.uk/staff/-profile.php?staffid=151).

The University of Salford, in Manchester's metropolitan area, has recently invested in new state-of-the-art facilities, including a dedicated building for teaching, research and innovation, within the new MediaCityUK complex (http://www.salford.ac.uk/MediaCityUK).

To apply, please send a covering letter, a full CV, and names and contact details of two referees, all in one single file, named with your surname, to: s.mariani@salford.ac.uk

Closing date: July 10th. Interviews: early August. Start date: September 2012, with limited flexibility. Gross salary: >30,000 £

Dr Stefano Mariani Reader in Wildlife Biology School of Environment & Life Sciences Peel Building, Room 316 The University of Salford M5 4WT, UK Tel. +44.161.2956913 http://www.els.salford.ac.uk/-staff/profile.php?staffid=151 Mariani Stefano <S.Mariani@salford.ac.uk>

USouthampton MolEvolBioinformatics

Location: Highfield Campus, University of Southampton, UK. Salary: £27,578 to £30,122 Full Time Fixed Term Closing Date: Friday 15 June 2012 Interview Date: Monday 25 June 2012 Reference: 119512BJ

You are invited to apply for the post of Research Fellow to work closely with Dr Richard Edwards on a BBSRC-funded project to develop and apply computational tools for the prediction of protein motifs that mediate protein-protein interactions.

Many protein-protein interactions are mediated by Short Linear Motifs (SLiMs): short stretches of proteins (5-15 amino acids long), of which only a few positions are critical to function. These motifs are vital for biological processes of fundamental importance, such as signalling pathways and targeting proteins to the correct part of a cell.

This position represents an exciting opportunity to join one of the early pioneers in the growing field of SLiM prediction. The primary objective of this project is to integrate a number of leading computational techniques to predict novel SLiMs and, in so doing, add crucial detail to protein-protein interaction networks. This will generate a valuable resource of potential SLiMs, including defined occurrences and interactions.

The project will use a number of computational and sequence analysis techniques. Basic programming skills are essential. Experience with database design, HPC and web programming are desirable. You will be required to develop a thorough knowledge of SLiM-mediated protein-protein interactions and should therefore be comfortable with biological literature, biochemistry, molecular evolution and structural biology.

A background in either computer science or biology, with a PhD in a relevant subject area, is essential. Previous research experience (PhD or Postdoctoral) in computational biology is highly desirable. Candidates with a computer science background must demonstrate an interest and aptitude for molecular biology. Similarly, candidates with a biology background must demonstrate an interest and aptitude for computer programming.

You should be an enthusiastic researcher, a good team-worker and an excellent communicator. Project management skills and independent research experience are desirable.

For informal enquiries, contact Richard Edwards, email: R.Edwards@soton.ac.uk. More information about the lab and on-going research can be found at: http://www.southampton.ac.uk/~re1u06/ . The position is full-time and available immediately for a period of up to two years.

The closing date for this position is 15 June 2012. Please apply online through www.jobs.soton.ac.uk or alternatively telephone 023 8059 2750 for an application form. Please quote reference number 119512BJ on all correspondence. In addition to submitting your CV, please enclose a personal statement highlighting your research interests and experience, as outlined in the accompanying Further Particulars. Please note that the project is 100% computational.

Dr Richard Edwards Lecturer (Bioinformatics & Molecular evolution) Centre for Biological Sciences University of Southampton B85/3041, Life Sciences Building Highfield Campus Southampton SO17 1BJ Tel: +44(0)23 8059 4344 email: r.edwards@southampton.ac.uk http://www.southampton.ac.uk/~re1u06/ R.Edwards@soton.ac.uk

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USouthBohemia CzechRep AquaticEvo

Postdoctoral fellow in the field of anthropogenic impact on populations in aquatic habitats

One postdoctoral position focusing on modelling the ecological and evolutionary consequences of human impact on aquatic ecosystems is available in the newly established group of Dr. David Boukal at the Faculty of Science, University of South Bohemia, Ceske Budejovice (Czech Republic). The position is defined broadly and can be tailored to individual interests. Our ongoing theoretical work focuses mainly on size-, stage- and trait-based approaches to population dynamics and community assembly and on fisheries management and fisheries-induced evolution. Ongoing experiments deal with predator-prey interactions, life histories and phenotypic plasticity in freshwater insects, and community assembly in small pools.

Basic qualifications are a PhD in ecology, mathematics or a related field, obtained after 28 March 2008, and a strong interest in quantitative ecology. Previous experience in fisheries, fish/insect population dynamics, studies of life history evolution or community dynamics is a plus. Candidates must be fluent in English (corresponding to CAE or equivalent) or Czech language. Young researchers interested in both experimental and theoretical work are particularly encouraged to apply.

The position is funded through a European Social Fund project, and the salary is highly competitive. The position is available from 1 September 2012 for up to 34 months and includes funding for 4-5 months to stay in Prof. Mikko Heino's group at the University of Bergen, Norway (www.uib.no/rg/evofish) and/or Dr. Andrew Beckerman's group at the University of Sheffield (www.beckslab.staff.shef.ac.uk).

To apply, please send a CV including the list of publications, research statement and contacts of two previous supervisors/colleagues to boukal@entu.cas.cz or dboukal@prf.jcu.cz. The call will be open until 15 July 2012 or until the position is filled. Shortlisted candidates will be interviewed in the second half of July and final decision made immediately afterwards.

For more information, visit www.entu.cas.cz/boukal/-job.html or e-mail David Boukal (boukal@entu.cas.cz).

David Boukal <boukal@entu.cas.cz>

UToronto EvolutionPlantPhenols

Post-doc position in chemical ecology of polyphenols in the Salminen lab: "Evolution and global distribution of plant polyphenol-based pro-oxidant defenses"

Polyphenols are a group of specialized metabolites that are produced by practically all global plant species. One of the most important polyphenol functions is their ability to serve as plants' chemical defense against e.g. herbivorous insects. However, the true mechanisms responsible for the polyphenol activities have been a target of ongoing debate. One of the most apparent types of defense mechanisms - polyphenol oxidation triggered by either high gut pH or plant oxidase enzymes - has received only a little attention. Thus we have a gap in our knowledge of (1) what are the active (or inactive) pro-oxidant polyphenols, (2) how are the pro-oxidant polyphenols (and pro-oxidant activity) distributed in the plant kingdom, and (3) how are the pro-oxidant polyphenol molecules and pro-oxidant activity evolved in ecologically relevant families and genus.

Position The post-doc will be part of the Natural Chemistry Research Group working in the Salminen lab (Laboratory of Organic Chemistry and Chemical Biology, University of Turku, Finland). The lab is equipped with the latest high-quality instruments needed for the modern studies of chemical ecology. Recently, the Salminen lab has created a UPLC-MS/MS based method that is able to (1) reveal all the polyphenol classes, (2) quantify the individual polyphenols and (3) reveal and quantify the individual pro-oxidant polyphenols (active and inactive ones) present in any plant species or sample. This method is currently being used to reveal the individual pro-oxidant polyphenols present in more than 1500 plant species that have been collected around the globe and distributed along the plant tree of life. A special emphasis is given for ecologically relevant species of Oenothera, Quercus and Eucalypts, to reveal both the micro- and macroevolution of polyphenol-based pro-oxidant defences in plants. The post-doc will join this exciting and challenging task, and will coordinate the data production and handling. The project will involve interdisciplinary collaborations with leadings scientists from around the globe and the post-doc may visit their labs either in Cornell University (New York, USA), University of Toronto (Toronto, Canada) or Australian National University (Canberra, Australia). He/she will be able to boost his/her career by writing many high-quality papers related to e.g. (1) the polyphenol oxidation hypothesis, (2) the micro- and macroevolution of polyphenol-based pro-oxidant defences, (3) the latitudinal herbivore defence hypothesis, and (4) methodology related to these advanced chemical ecology techniques.

Requirements We are seeking a highly motivated, team-oriented post-doc with a strong interest in chemical ecology, chemistry and plant-herbivore interactions. Applicants should hold a PhD (chemistry, chemical ecology or equivalent) and must have a proven experience in the field of chemical ecology, both in the lab work and writing of scientific papers. Experience with chemical methods such as LC, LC-MS, 96-well plate reader and/or any other methods related to polyphenol chemistry would be highly beneficial. Knowledge of statistical methods and the ability to handle large data sets will be beneficial as well. Good knowledge of spoken and written English is required.

Conditions The position will start in September 2012 at the earliest. The position will be for a maximum of four years, but could be filled for a shorter period, if needed. The salary is fixed according to the guidelines of the University of Turku for teaching and research personnel at the level 4-6. The mobility of a foreign post-doc may be enhanced by an additional mobility grant.

Application Deadline: July 15, 2012. To apply, send a cover letter explaining your interest in this position, a complete academic record, CV and addresses of 2-3 potential academic referees to: prof. Juha-Pekka Salminen (j-p.salminen@utu.fi).

c.thomsen@utoronto.ca

UUppsala CompGenomicsEndosymbioticBacteria

Researcher in comparative genomics of endosymbiotic bacteria:

http://www.uu.se/jobb/others/-annonsvisning?tarContentId=3D196228&languageId=1 The position is for at least 1 year and will be filled as soon as possible.

The Department of Cell and Molecular Biology is one of the most international, broad and distinguished bio molecular departments in Europe, comprising six research programs with about 125 employed. This position is within the program in Molecular evolution.

Project description: The aim of the project is to identify the genetic components of the endosymbiotic bacterium Wolbachia that are responsible for the induction of cytoplasmic incompatibility (CI) using genome sequencing and comparative genome analyses. More information can be found under: http://www.icm.uu.se/faculty-research/Molecular-Evolution/People/lisa-klasson/?languageId=1 Requirements: The candidate should have a PhD in bioinformatics, molecular biology or other relevant areas. Previous experience of working with next-generation-sequencing data and bioinformatic analyses, used to working in a Linux/Unix environment and familiarity with a scripting language such as Perl is highly desirable. Basic skills in molecular biology laboratory techniques are also desirable. The candidate needs to be proficient in both written and spoken English.

For inquiries regarding the positions please contact Lisa Klasson (lisa.klasson@icm.uu.se). The application should include a CV, a summary of research interest and contact details for at least 2 references.

You are welcome to submit your application no later than 6:th of July 2012

Dr. Lisa Klasson Molecular Evolution Department of Cell and Molecular Biology Uppsala University Box 596 SE-751 24 Uppsala Sweden phone: +46 (0)18 471 6403

guy.lionel@gmail.com

Vienna PopGeneticsPhylogeny

A two-year postdoctoral position is available in the group of Dr Carolin Kosiol at the Institute of Population Genetics at the Vetmeduni Vienna. My group works on probabilistic models of sequence evolution, comparative genomics, next generation sequencing, population genetic aspects of phylogenetics, molecular evolution and natural selection. The position will be associated with the project "Empirical codon models for comparative re-sequencing data" and is funded by a Stand-Alone Grant of the Austrian Science Foundation.

Candidates will be expected to have completed a PhD in Computational Biology, Mathematics, Statistics, Computer Science or a related field. Good bioinformatic skills and prior experience with either population genetics or phylogeny are essential. Preferably the candidate will have experience in C or C++ and a scripting language such as Python or Perl.

In recent years, Vienna has developed into one of the leading centers in evolutionary biology (http://www.evolvienna.at). In addition to a stimulating scientific environment, Vienna is also a quite liveable city with affordable housing, good public transport and an exciting cultural life.

Please send a letter of interest, C.V., and the names and contact details of two referees to Carolin Kosiol at carolin.kosiol@vetmeduni.ac.at. Questions and requests for more information should be directed to the same address. Review of applications will begin on 1 August, 2012 and will continue until the position is filled.

Carolin Kosiol Group Leader in Bioinformatics Institute of Population Genetics Vetmeduni Vienna Veterinärplatz 1 A-1210 WIEN, Austria Tel +43(0)1-25077-4331 E-mail: carolin.kosiol@vetmeduni.ac.at

Lab Website: http://i122server.vu-wien.ac.at/pop/Kosiol_website/kosiol_home.html Vienna Graduate School of Population Genetics: http://www.popgen-vienna.at Carolin Kosiol <carolin.kosiol@vetmeduni.ac.at>

Zurich PlantEvolution

Zurich-Basel Plant Science Center launched new international post doc fellowship programme PLANT FELLOWS

PLANT FELLOWS is a new international post doc fellowship programme in the field of plant sciences cofunded by the Marie Curie Actions - COFUND (FP7). PLANT FELLOWS is centrally managed at the Zurich-Basel Plant Science Center, a competence center of the three Swiss universities, the University of Zurich, the University of Basel and the ETH Zurich.

This post doc fellowship programme is open to applicants from all over the world and all research fields in plant sciences are eligible. 23 international universities and research institutions have been predefined as host organisations on the basis of their excellence in higher education and plant research.

PLANT FELLOWS offers more than 60 new post doc fellowships spread between three different mobility schemes (incoming, outgoing, reintegration) and a structured training programme, including workshops, dedicated training in complementary skills and industrial placements. Unique in its kind the fellows of the programme have the opportunity to obtain a PLANT FELLOWS Training Certification after successfully completing the whole training programme.

PLANT FELLOWS is operating through a system of three calls for participants: June and October 2012 as well as February 2013. The application submission deadline is 3 months after the publication of the call. The evaluation process will take place within a maximum period of 3 months. The fellow is expected to start his/her fellowship within 6 months after notification.

The first call will be open from June 1st 2012 until August 31st 2012 (3months) and you will find all necessary information on our homepage. In the download section of our website you will find the PLANT FELLOWS guide for applicants together with the obligatory application templates for the application process.

You can enter the online application portal via the PLANT FELLOWS website: http://www.plantfellows.ch For any questions you might have in the context of the fellowship program and the application process, please do not hesitate to contact the programme officer Mrs. Romy Kohlmann. (romy.kohlmann@usys.ethz.ch)

Romy Kohlmann, M.A. - Programme Officer PLANT FELLOWS - Zurich-Basel Plant Science Center - ETH Zürich, LFW B 51 - Universitätstrasse 2 - 8092 Zürich phone: 0041 44 632 47 96 - fax: 044 632 18 26 (Monday-Thursday)

Rosario Garcia Gil <M.Rosario.Garcia@slu.se>

WorkshopsCourses

ArcadiaNatlPark EvolutionaryMedicine Aug6-10

*Evolutionary Foundations for Medicine and Public Health: Focus on Infection and Cancer < http://www.mdibl.org/courses/Evolution_and_Medicine/398/ >

August 6-10 at the Mount Desert Island Biological Laboratory, Bar Harbor, Maine

Registration < http://www.mdibl.org/courses/Evolution_and_Medicine/398/ > * CME credit available Discounted tuition for trainees Many enrolled "students" are leaders in their fields; this course will be appropriate for professional biologists and for practicing medical professionals as well as students.

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. Special expertise in evolutionary biology is not required, however those who have already studied evolutionary biology will have specialized opportunities. In order 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 undergraduate to postdocs will be warmly welcomed. For more information on evolution and medicine, see The Evolution and Medicine Review

Faculty

Randolph Nesse V University of Michigan (Course director) Douglas Brash X Yale University Carlo Maley V University of California San Francisco Athena Aktipis – University of California San Francisco and Arizona State University Andrew Read V Pennsylvania State University Mark SchwartzXNew York University Stephen Stearns V Yale University Robert Woods – University of Michigan

Description

This intensive one-week course will introduce strategies for applying core principles of evolutionary biology to problems in medicine and public health, with a special focus on infection and cancer. The course will not attempt to cover all possible applications, it will focus on a few examples. Some especially relevant principles include life history theory, host pathogen co-evolution, the regulation of defenses, developmental plasticity, and trade-offs shaping reproductive strategies. These principles 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 years course will have extensive special expertise available on topics related to cancer and infectious disease. Mornings will be devoted to lectures and structured discussions. After lunch, participants will gather in small groups for faculty led discussions on a number of specialized topics such as strategies to prevent antibiotic resistance, the role of infection in mental disorders, how social evolution theory might advance new chemotherapy strategies, how viral sequences get incorporated into genomes, the role of imprinting in controlling gene expression. Participants will be in small workgroups with faculty and others who share specialized interests. Most workgroups will investigate a specific topic, for instance, malignant melanoma, cervical cancer, breast cancer, sexually transmitted diseases, antibiotic resistance, or vaccine design. Other groups will address other topics such as strategies for educating physicians, creating curriculum materials, or current debates about levels of selection. Each group will develop a possible research or teaching project, for presentation on Friday. Individuals are also free to create their own projects. Late afternoons are not prescheduled, so participants can organize their own additional discussions and projects or pursue individual interests, including recreation in Acadia National Park. Several optional preplanned expeditions are available, including whale watching, and guided hikes in the park. More information about evolutionary medicine is at The Evolution and Medicine Review< http://evmedreview.com/ >

Tentative Schedule

Monday Tuesday Wednesday Thursday Friday *7-8 am* Self-serve breakfast available in Dining Hall Self-serve breakfast available in Dining Hall Self-serve breakfast available in Dining Hall Self-serve breakfast available in Dining Hall Self-serve breakfast available in Dining Hall *8-9 am*

Overview of core evolutionary principles

Nesse/Faculty

Evolution and Infectious Disease Read

Cancer: An introduction Brash

Infectious causes of cancer Read/Maley

Social evolution: Theory and applications to cancer progression

Aktipis *9-10 am*

Overview of core evolutionary principles

Nesse/Faculty

Evolution and Infection in the Clinic

Read

Cancer: Evolution

Maley

Regulation of Defenses

Nesse

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Basel MicrobiotaEvolution Sep12-14

Just a reminder that the WORKSHOP DEADLINE (for the lecture) IS APPROACHING!!!

The Organizing Committee would like to invite you to attend a 3-day international workshop on the "Evolution and Ecology of Host-Associated Microbiota" to be held at the Zoological Institute, University of Basel, Switzerland on September 12- 14, 2012. The major aim of this workshop is to provide a synthesis of the emerging evolutionary and ecological patterns governing the complex interactions of host-microbiota across different biological systems. We have invited leaders in the field of host-associated microbiota and microbial ecology to share their insights on the evolutionary and ecological principles that shape bacterial community structure and host-microbiota interactions.

This workshop is intended for undergraduate students, graduate students, postdoctoral researchers and early career investigators (100 slots available) who wanted to be exposed to the evolutionary and ecological concepts and bioinformatics tools being applied on the study of host-associated microbiota systems and microbial ecology. Together with the lecture, a hands-on tutorial (bioinformatic tools and approaches encompassing microbial ecology, comparative genomics, molecular evolution) will be provided on the analysis of complex sequence data sets derived from next-generation sequencing.

Thanks to the generous funding from ProDoc of the Swiss National Science Foundation and the University of Basel, we are only charging a minimal fee of CHF 150 for registration (includes 3 lunches, 1 social dinner, 2 social mixers and snacks during the entire workshop) or CHF 250 (+ tutorial on the analysis of next-generation sequences; 50 slots available). We also have arranged for a number of rooms around Basel ranging from youth hostel dormitories (CHF 32-79/ day) to 3-star hotels (CHF 160- 250/ day). Moreover, Basel/Mulhouse Airport is a hub for Easyjet, a budget airline in Europe. Application deadline for the tutorial is May 30 and for the lecture series is June 30, 2012. More information can be found at this website:http://evolution.unibas.ch/ebert/microbiota/index.htm Please direct any questions to the organizing committee: Marilou Sison-Mangus (m.sison@unibas.ch), Samuel Pichon (samuel.pichon@unibas.ch) and Dieter Ebert (dieter.ebert@unibas.ch)

Confirmed Speakers:

Bioinformatics and Computational Tools

1. KNIGHT, Rob (University of Colorado Boulder, USA) - computational tools for understanding the evolution of microbiota through time and space

2. CAPORASO Greg (Northern Arizona University, USA) - QIIME (Quantitative Insights Into Microbial Ecology) and microbiota dynamics

3. HUSON, Daniel (University of Tubingen, DE) - MEGAN (MetaGenome ANalyzer) and phylogenetic networks

4. QI Weihong (ETH Zürich, CH) - Trends and applications of next- generation sequencing technologies

Microbial Diversity and Symbiosis

5. DUBILIER Nicole (Max Plank Institute, Bremen, DE) - Symbioses of bacteria and hydrothermal vent organisms

6. BRUNE, Andreas (Max Plank Institute, Marburg, DE) - Insect gut microbiology and symbiosis

7. EBERT Dieter (University of Basel, CH) - Daphnia parasites and microbiota

Microbiota Dynamics and Evolution

8. GILBERT Jack (University of Chicago, USA) - Microbial community dynamics and function

9. JANSSON, Janet (LNL, DOE-JGI, USA)- bacterial diversity in the environment

10. LEE Carol Eunmi (University of Wisconsin-Madison, USA) - Copepod microbiota and invasion success

11. Van der MEER Jan (University of Lausanne, CH) - Genetic adaptation and evolution of bacteria in the environment

Genomics of Health- and Nutrition-Associated Microorganisms

12. SVANBORG Catharina (University of Lund, SE) - Host imprints on human- associated bacterial genomes

13. VORHOLT Julia (ETH Zürich, CH) - Physiology of plant-associated microbes (metaproteomics)

Bacteria- host interactions and evolution

14. ROSENBERG Eugene and ZILBER-ROSENBERG, Ilana (University of Tel Aviv, IL) - Coral microbial communities and the hologenome theory

15. POULSEN, Michael (University of Copenhagen, DK) - Multiple interactions between symbionts and host

16. HENTSCHEL, Ute (University of Würzburg, DE) - Mechanisms of interactions between sponges and their microbial communities

Marilou P. Sison-Mangus, PhD Postdoctoral Researcher Evolutionary Biology, Zoology Institute University of Basel Vesalgasse 1, 4051 Basel Switzerland

Tel no: 061 267 03 72

m.sison@unibas.ch

CIBIO Portugal EvolutionaryDataAnalysis Nov5-9

Workshop on Multivariate Data Analysis for **Ecology and Evolution in R*, CIBIO, Portugal, 5-9 November 2012

with the following link: http://webpages.icav.up.pt/-AK/WEBPAGE/multivarEE_inR.html Antigoni Kaliontzopoulou

CIBIO, Centro de Investigacao em Biodiversidade e Recursos Geneticos Campus Agrario de Vairao, 4485-661 Vairao PORTUGAL Department of Ecology, Evolution, and Organismal Biology Iowa State University, Ames, Iowa 50011, USA

Antigoni Kaliontzopoulou <antigoni@cibio.up.pt>

CollegedeFrance Paris PhylogeneticDiversification Oct22-23

Workshop: Phylogenetic approaches to diversification CIRB - College de France, Paris, October 22-23, 2012

The Center for Interdisciplinary Research in Biology (CIRB) at College de France is sponsoring a workshop on phylogenetic approaches to diversification, to be held on October 22-23.

In the past few years, phylogenies have played an increasing role in our understanding of the way ecological and evolutionary processes generate biological diversity. The goal of the workshop is to foster interactions between theoreticians working on the development of phylogenetic inference methods and empiricists applying these methods to large datasets.

The workshop will consist in 15 invited talks of 40 minutes (including questions), starting at 9:00 on Monday, October 22, and finishing at 13:00 on Tuesday, October 23.

Here is the website < http://-www.proba.jussieu.fr/dw/doku.php?id=-users:smile:phylosmile2012 > and the poster < http:/-/www.proba.jussieu.fr/dw/lib/exe/fetch.php?media=-users:smile:posterphylosmile2012.pdf > of the workshop.

Registration is free but required. Please register by sending an email to <amaury.lambert@upmc.fr> specifying that you would like to attend. The conference room has a limited capacity, so don't wait too long before registering!

A poster session will take place on the evening of Monday, 22. If you would like to present a poster, please send a title and abstract to <helene.morlon@cmap.polytechnique.fr>

List of speakers :

Alexandre Antonelli (U. Gothenburg) Folmer Bokma (U. Umeå) Fabien Condamine (Ecole Polytechnique, Palaiseau) Emmanuel Douzery (U. Montpellier) Rampal S. Etienne (U. Groningen) Susanne Fritz (Bik-F, Francfort) Olivier Gascuel (CNRS, Montpellier) Amaury Lambert (CIRB and UPMC Univ Paris 06) Alexander Pigot (EGI, U. Oxford) Susanne Renner (U. Munich) James Rosindell (Imperial College) Isabel Sanmartin (Real Jardin Botanico, CSIC, Madrid) Tanja Stadler (ETH Zürich) Mike Steel (U. Canterbury) Chris Venditti (U. Hull)

We are hoping to see you in Paris next October, please circulate the information!!

The organizers Amaury Lambert (CIRB and UPMC Univ Paris 06) Hélène Morlon (CNRS and Ecole Polytechnique)

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Amaury Lambert, professeur UPMC http://www.proba.jussieu.fr/pageperso/amaury SMILE group http://www.proba.jussieu.fr/ ˜ smile Stochastics& Biology group http://www.proba.jussieu.fr/˜psb amaury.lambert@upmc.fr

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LakeheadU AncientDNA

Practical DNA Training Course

A two-week (9 business days) intensive laboratory-based training course designed to teach participants fundamentals of molecular techniques including DNA extraction, amplification (using PCR), sequencing and interpretation.

This training course is offered at various times throughout the year and we will work with you to find a suitable time for training.

For more information please contact us at 807-343-8877 or paleodna@lakeheadu.ca or visit our website www.ancientdna.com . Thank you.

Karen.

Karen Maa Administrative Assistant Paleo-DNA Laboratory 1294 Balmoral Street, 3rd Floor Thunder Bay, Ontario P7B 5Z5 Telephone: 1-866-DNA-LABS or 1-807-343-8616

Karen Maa <kmaa@lakeheadu.ca>

Ottawa WomenInScience Evol2012 Jul8-9

Women in Science Workshops, July 8 & 9, Ottawa, 2012

At this year's Joint Congress in Evolutionary Biology in Ottawa, Canada, (http://www.confersense.ca/Evolution2012/index.htm) we are happy to announce two complementary workshops on issues relating to women in science. The first, held on Sunday, July 8, will focus on increasing diversity in evolutionary biology by advancing the leadership of women, and is targeted to faculty. The second, held on Monday, July 9, is the fourth annual "Symposium for women entering ecology and evolution" (SWEEET - http://www.ecoevo.ca/SWEEET/) with this year's theme focusing on career options beyond academia.

1. "Advancing diversity in evolution: faculty mentoring panel, discussion & social" Sunday, July 8, 7-8:30pm Host: Jenny Boughman, Michigan State University This event is focused on increasing diversity in evolutionary biology by advancing leadership of women in the sciences. How can we increase the success of women after they've been hired as faculty, so that more women get onto the tenure track, then receive tenure and go on to positions in academic and scientific leadership? There are many excellent programs and events for women graduate students and postdocs; these are much needed because moving from these stages into faculty positions is a critical juncture. However, very few programs or efforts are targeted at women at the next stages of their careers to help women position themselves to be leaders in their fields and at their institutions. This event hopes to begin filling that gap. Both genders and people from all ethnic backgrounds are invited to attend. Light refreshments will be served. A partial list of panelists includes: Michelle Dudash, University of Maryland Hanna Kokko, Australian National University Helen Rodd, University of Toronto Nina Weddell, University of Exeter

2. "Knowing your options and getting the job you want: career options beyond academia" Monday, July 9, 1:15 - 5pm followed by a social mixer with speakers Host: SWEEET 2012 (http://www.ecoevo.ca/SWEEET/2012meeting.html) SWEEET is a symposium intended to address issues that influence the advancement of women from postgraduate degrees into academic, government, NGO and industry positions

from backgrounds in ecology and evolution. The transition into a permanent job is a critical step that involves many challenges - many of these are particularly relevant to women, who tend to be under represented in scientific careers. At this year's SWEEET we will be discussing two related topics on the theme of career options outside of academia including "Tactical advice for moving your academic skills into a non-academic position" and "Carving your own niche - women in non-traditional careers in science". We are pleased to announce our exciting list confirmed speakers: Dr. Suzanne Fortier, President, NSERC Dr. Bronwyn Keatley, Senior Policy Advisor, Fisheries and Oceans Canada Dr. Lalita Acharya, Science and Technology Division, Library of Parliament Dr. Jenny Carpenter, Freelance journalist. The format of the symposium encourages active participation between speakers and the audience. Speakers will discuss their personal journey to their current career, challenges along the way and will provide advice to early-career scientists interested in keeping their career options open. We encourage and welcome women and men to attend.

erubidge@gmail.com

Prague 3 EvolDataAnalysis

EVOLTREE Summer School: Genetic Data Analysis >From Monday, 11. June 2012 To Friday, 15. June 2012

Tentative programme: Theory of linear mixed models, ASReml software basics and options, Breeding values, Multi environmental trials, Spatial analysis of field test data, Multivariate models, Imputing missing genotypes, Realized genomic relationships matrix, Genomic BLUP, Marker-trait associations, Genome-wide selection, Pedigree reconstruction from markers

Organisers: North Carolina State University Cooperative Tree Improvement Program, Czech University of Life Sciences

Further information: http://www.ncsu-feop.org/-GDA/ Registration: http://www.ncsu-feop.org/-GDA/registration_form.html Deadline: End of May. Late applicants, please contact Milan Lstiburek (istiburek@gmail.com) Location : Prague, Czech Republic

http://www.evoltree.eu/index.php/component/-jevents/icalrepeat.detail/2012/06/11/196/-/-

EVOLTREE Summer School: Genome-wide association studies using mixed models >From Wednesday, 5. September 2012 To Friday, 7. September 2012

Tentative programme: This course will provide a general background for statistical models used in association studies with an emphasis on mixed model approaches. Multi-trait and multi-locus extensions of models of genotype-phenotype association will be discussed with applications to data and hands-on examples. The course will cover both genotype- phenotype associations and genotype-environment associations and discuss parallels between these approaches. In addition, we will discuss downstream analyses (e.g., gene set and functional class enrichment and experimental work) that can be used to help validate association study results and to clarify the biological basis for the observed signals. Finally, participants will receive practical experience running analyses with a sample data set using R packages.

1. Introduction to mixed models with application to genotype-phenotype association studies 2. Another application of mixed models: genotype-environment association studies. 3. More complex models such as multi-trait and multi-locus models. 4. Range-wide versus population-specific analyses - pros and cons of using geographically restricted versus range-wide sampling 5. Methods for validating the results and integrating results with other genome-wide information (e.g, enrichment of likely functional variants, relevant candidate gene sets, experimental follow-up) and making biological interpretations 6. Practical experience using R with a sample data set

Location : Uppsala, Sweden

Organiser: Martin Lascoux (martin.lascoux@ebc.uu.se).

Deadline for registrations is August 15th, 2012

http://www.evoltree.eu/index.php/component/-jevents/icalrepeat.detail/2012/09/05/199/-/-
EVOLTREE Summer School: Population genetic and genomic approaches >From Monday, 24. September 2012 To Friday, 28. September 2012

Full title: Population genetic and genomic approaches to mitigate global climate change impacts on forest genetic resources and to breed more resilient trees

Description: Global climate change poses a major challenge for most boreal and temperate forests. Climate influences growth rate, adaptation and survival of forest trees. Global climate change can lead to both extinction of forests in more arid and colder environments and expansion in wetter and warmer ones. The fast changes in climate can also threaten forest genetic resources or make them more vulnerable. The proposed summer school will teach how the application of population genetics and genomics can help to tackle this challenge and guide forest protection and conservation programs aimed to mitigate undesirable effects of global climate change. It will also demonstrate how modern genomic selection can be used for breeding more resilient trees that will be productive in harsh and variable environments. The proposed summer school will teach also population genetics and genomics tools and methods that can be used to better characterize available forest tree genetic resources.

Topics: - Human and global climate change impacts on forest genetic resources - Genetic implications of forest management - Forest population genetics and genomics: an introduction to tools and methods - Association mapping of environmental and genetic variables - Spatial analysis in forest population genetics and ecogenomics - Gene flow, forest regeneration and assisted migration - Genomic selection for more resilient trees

Participants: PhD students and young scientists interested in the application of modern methods and approaches of population genetics and

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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

Sevilla ClimateChange Sep24-Oct5

The Estacion Biologica de Doñana (Sevilla, Spain) invites applications for its third international course on climate change entitled 'Ecological Consequences of Climate Change: Integrating Research Approaches' taking place from 24 September to 5 October 2012 in the heart of Doñana National Park. The course is open to students at the early postdoc, PhD and Master/advanced Diploma levels who are involved in global-change research. Its aim is to provide a synthetic overview upon different research perspectives ranging from paleoecology to population genetics, ecophysiology and bioclimatic modeling. The course will include lectures and practical exercises provided by an international panel of high-profile researchers, as well as field trips within the National Park.

Invited teachers:

Miguel Araujo, Museo Nacional de Ciencias Naturales (CSIC), Madrid, Spain. Keith Bildstein, Hawk Mountain Sanctuary, Pennsylvania, USA. Isabelle Chuine, CNRS-CEFE, Montpellier, France. Arndt Hampe, UMR1202 BIOGECO (INRA), Cestas, France. Fernando Valladares, Museo Nacional de Ciencias Naturales (CSIC), Madrid, Spain. Katherine Willis, University of Oxford, UK. Clive Finlayson, Gibraltar Museum, Gibraltar, UK.. Miguel Tejedo, Estacion Biologica de Doñana (CSIC), Sevilla, Spain.

Organizers: Juan José Negro, scientific deputy of Estacion Biologica de Doñana (CSIC), and Arndt Hampe (INRA).

The course language will be English. Support from the Gas Natural Chair 'Biodiversity Conservation under Climate Change' enables us to limit registration fees to 100 Euros and to cover all costs for transportation between Sevilla and Doñana National Park, accommodation and meals during the 2-weeks course. Applicants should provide a brief CV (max. two pages) as well as a statement (max. 500 words) about their research interests/current projects and why they would like to attend to the course. Application deadline is 05 July. Please send applications in a single pdf file and any related questions to Begoña Arrizabalaga (bego@ebd.csic.es).

Begoña Arrizabalaga <bego@ebd.csic.es>

Switzerland PhenotypeVariation Aug4-7

Dear colleagues,

We are pleased to announce our workshop on 'The evolution of consistent phenotype variation: alternative tactics vs. behavioural syndromes'. The workshop is to be held in Adelboden, a beautifully located village in the Swiss Alps, from August 04 to August 07, 2012. The target audience for this meeting is PhD students, advanced MSc students and post-docs in Ecology and Evolution.

The program of the workshop will consist of a combination of plenary talks by invited speakers and work performed in small groups, in which the participants will discuss a particular theme together with one of the invited speakers. The results of these small-group sessions will be presented to the other participants, followed by a plenary discussion. On the last day of the meeting all participants are invited to join in a scenic hike to one of the numerous lookouts or mountain peaks in the vicinity of Adelboden (there will be options for all grades of fitness and spirit of adventure), which will allow to experience pristine alpine landscapes and offer breath-taking views.

Besides others the invited speakers will be:

Rui Oliveira < http://www.ispa.pt/ui/uie/ibbg/-rui_oliveira.asp > (Centro de Biociências - ISPA, Portugal)

Bryan Neff < http://publish.uwo.ca/%7Ebneff/-index.htm > (University of Western Ontario, Canada)

Jacek Radwan < http://www.eko.uj.edu.pl/-molecol/index.php?option=3Dcom_content&view=-article&id=51&Itemid=32 > (Jagiellonian University, Poland)

Andy Sih < http://www.des.ucdavis.edu/research/-sihlab/ > (University of California, USA)

Olof Leimar < http://www.zoologi.su.se/research/-leimar/ > (Stockholm University, Sweden)

Jonathan Wright < http://www.ntnu.edu/ansatte/-jonathan.wright > (Norwegian University of Science and Technology, Norway)

Workshop description

The coexistence of alternative behavioural and life history tactics within a population is an evolutionary puzzle studied since decades by several biological disciplines, ranging from population genetics to eco-physiology and behavioural ecology. More recently, the consistent behavioural variation of individuals within a population generating unimodal trait distributions has received much interest, because directional selection should generate 'optimal' phenotypes or behavioural flexibility instead of a broad array of phenotypes specializing in different solutions to the same environmental or social challenge. It is currently not well understood which mechanisms are responsible for continuous or bimodal/multimodal trait distributions. This is partly due to the independent, parallel development of two research fields that focus either on alternative behavioural tactics or on behavioural syndromes/animal personalities. This meeting aims to combine these different research fields. Leading scientists from both fields will be invited to lecture on this issue and to supervise workshop groups of participants addressing the evolutionary mechanisms responsible for consistent phenotype variation within populations.

More details are available at:

http://behav.zoology.unibe.ch/index.php?pp=-3D56&p=3D130 Best wishes

Joachim Frommen and Michael Taborsky

Dr. Joachim Frommen Institut für Ökologie und Evolution Ethologische Station Hasli Wohlenstrasse 50a CH-3032 Hinterkappelen

joachim.frommen@iee.unibe.ch

UCalifornia SanDiego DrosophilaSpecies Oct18-21

Drosophila Species Workshop XI - October 18th - 21st, 2012

The Eleventh Drosophila Species Workshop will take place from Thursday, October 18th through Sunday, October 21st, 2012 at the UCSD campus in La Jolla, California. The workshop employs hands-on approaches and will focus on the chracteristics of the melanogaster, repleta, virilis, and obscura species groups, including how to identify species, aspects of their biology and reproduction, and husbandry. Workshop instructors include Patrick OGrady, Stephen Schaeffer, Masa Watada, Therese Markow, and Maxi Richmond. We are pleased to announce this year's keynote speaker will be Mariana Wolfner (Cornell University). Registration is $400 and includes all instruction and materials, a dinner with keynote talk by Mariana Wolfner, morning and afternoon refreshments and one lunch. Space is limited. To apply, please send a one-page statement of your research interests and why the workshop will be valuable to you to Dr. Maxi Richmond, UCSD Drosophila Species Stock Center: mrichmond@ucsd.edu. More information and schedules from previous years can be found on our website: https://stockcenter.ucsd.edu/-info/workshops.php . Maxi Polihronakis Richmond <mrichmond@ucsd.edu>

UGoettingen DrosophilaPopGenetics Jun14

Dear colleagues,

on June 14 2012 we organise a research seminar entitled âNew developments in quantitative and population genetics of Drosophila'.

Speakers and topics will be:

Trudy Mackay (North Carolina State University, Raleigh, USA): The genetic architecture of quantitative traits: Lessons from Drosophila

Ulrike Ober (Department of Animal Sciences, Georg-August-University Göttingen, Germany): Estimation of effective population size from linkage disequilibrium structure revisited

Thuy Ha (Centre for Statistics, Georg-August-University Göttingen, Germany): Tail estimation methods for the number of correct and false positive associations in the Drosophila Genetic Reference Panel

Stuart Barker (University of New England, Armidale, Australia: Population genetics and demography of Drosophila buzzatii in Australia

Robert Anholt (North Carolina State University, Raleigh, USA): The Yin and Yang of Canalization: Phenotypic Plasticity and Transcriptional Robustness

Christian Schloetterer (University of Veterinary Medicine, Vienna, Austria): Pool-Seq: from data analysis to biological insight

The full program can be downloaded at http://www.uni-goettingen.de/en/92842.html

The seminar will be held on Thursday, June 14 2012, from 10:15 - 15:30 in the Paulinerkirche, Papendiek 14, 37073 Göttingen, Germany (for a map see http://www.uni-goettingen.de/en/125332.html)

To cover the costs of coffee and refreshments, external participants will be charged an attendance fee of 10â¬*whichwillbecollectedonsite.*

The research seminar is open to all interested scientists. For registration please send a mail until June 8, 2012 to bstraus@gwdg.de

Best regards

Henner

Henner Simianer

Professor, Animal Breeding and Genetics Department of Animal Sciences Georg-August-University Goettingen Albrecht-Thaer-Weg 3, 37075 Goettingen Tel.: +49-551-395604, Fax: +49-551-395587 Email: hsimian@gwdg.de

http://www.uni-goettingen.de/tierzucht "Simianer, Henner" <hsimian@gwdg.de>

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.