EvolDir

April 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

AMNH NewYork StudentConservation Oct10-12 CallAbstracts

Abstracts Wanted! Conservation Science Conference at AMNH!

STUDENT CONFERENCE ON CONSERVATION SCIENCE-NEW YORK (SCCS-NY) American Museum of Natural History New York City October 10-12, 2012 $100 USD cbc.amnh.org

The conference is designed for graduate students, postdoctoral fellows, and early-career professionals pursuing or considering the field of conservation science. (Undergraduate students conducting thesis-level research may also apply.)

All Disciplines are Welcome! Whatever your focusXbiology, sociology, medicine, economics, architecture, the lawXif it has a relevance for conservation, we want to hear your perspective! Join fellow conservation students and conservation professionals from around the world to network, exchange ideas, and receive feedback from leaders in science, policy, academia, and management at one of the worlds preeminent scientific and cultural institutions.

Application Deadline for Talks, Speed Talks, and Posters: Monday, April 2. Non-presenting attendees may register until September.

The Student Conference on Conservation Science was created in 2000 by the University of Cambridge, and is currently held annually in Cambridge, New York, and Bangalore, India. The 2012 SCCS-NY is hosted by the Center for Biodiversity and Conservation at the American Museum of Natural History. Collaborating institutions include Cambridge University, Columbia University Earth Institute,Yale School of Forestry and Environmental Studies, and Princeton University.

To learn more, visit the SCCS-NY site or follow us on Facebook.

Fiona Brady <brady@amnh.org>

Ankara IntlStdCongressEvol Sep29-Oct1

Dear Sir/Madam

We are the members of Biology and Genetic Student Club in Middle East Technical University (METU) at Ankara/Turkey.

We will organize 1st International Student Congress of Evolutionary Biology. 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.

Congress will be held on 29-30 September, 1 October 2012 at METU. It will include 6 sessions. One of them consist presentations of academicians on "View of the Theory of Evolution in Turkey and World". Other 5 session include BSs, MSc and PhD students' presentations and academicians moderate the sessions (total 20 oral presentations also poster presentations). Also 2 plenary talks will take place in congress. Prof. Eva Jablonka from Tel Aviv University accepts to give a plenary talk. For other talk, we contact to Prof. John Endler.

Then, we apply for help to you. Even without financial aid, we ask you to other assistance, such as announcement of the congress. Also, recognition of the Congress and take place under the umbrella of SSE, will be great honor for us.

If you would like to review, I can send the promoting file of Congress.

Sincerely yours...

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>

Berlin SEAsianGatewayEvol Mar11-15

2nd Southeast Asian Gateway Evolution Meeting

March 11-15, 2013, Berlin, Germany

The Museum für Naturkunde Berlin and the Humboldt University will host the second International conference on Southeast Asian Gateway Evolution (SAGE 2013).

This meeting focuses on the origin, diversification, and conservation of Southeast Asia's megadiverse fauna and flora against the background of the region's complex geology and climate history. We aim to attract climatologists, biogeographers, palaeontologists & geologists to this multidisciplinary meeting and look forward to welcoming you in Berlin in March 2013.

Time schedule and deadlines

30 June 2012 Call for workshops & symposia closes

1 August 2012 Abstract submission and online registration opens

30 November 2012 Deadline for submission of abstracts and early registration

Please visit the conference website for more information and updates: www.sage2013.org. A pdf of the first circular can be downloaded from the website.

Dr. Thomas von Rintelen

Coordinator of DNA Laboratory & Curator of DNA collection

Museum für Naturkunde Leibniz-Institut für Evolutions- und Biodiversitätsforschung an der Humboldt-Universität zu Berlin Invalidenstraße 43 10115 Berlin Germany

Tel.: +49-(0)30-2093 8428 Fax: +49-(0)30-2093 8565 E-mail: thomas.rintelen@mfn-berlin.de

Internet: http://www.naturkundemuseum-berlin.de "Rintelen, Thomas von" <Thomas.Rintelen@mfn-berlin.de>

Chicago GalaxyCommunity Jul25-27 Registration

We are pleased to announce that early registration is now open for the 2012 Galaxy Community Conference (GCC2012, http://galaxyproject.org/GCC2012). GCC2012 will be held July 25-27, at the UIC Forum, in Chicago, Illinois. The conference will feature two full days of presentations, discussions, lightning talks, and breakouts. We have also added a new full day of training this year, featuring 3 parallel tracks with four workshops each, covering seven different topics.

The Galaxy Community Conference is for: * Sequencing core facility staff * Bioinformatics core staff * Bioinformatics tool and workflow developers * Bioinformatics focused principal investigators and researchers * Data producers * Power bioinformatics users

This event is about integrating, analyzing, and sharing the diverse and very large datasets that are now typical in biomedical research. GCC2012 is an opportunity to share best practices with, and learn from, a large community of researchers and support staff who are facing the challenges of data-intensive biology. Galaxy is an open web-based platform for data intensive biomedical research (http://galaxyproject.org) that is widely used and deployed at research organizations of all sizes and around the world.

Registration is very affordable, especially for post-docs and students. You can can save an additional 40% by registering on or before June 11.

Conference lodging can also be booked. Low-cost rooms have been reserved on the UIC campus. You can also stay at the conference hotel, at a substantial discount arranged for conference attendees. There are a limited rooms available in both, and you are encouraged to register early, if you would like to take advantage of these.

Abstract submission is also open, from now through April 16. Abstract submissions on any topic of interest to the Galaxy community are strongly encouraged. See the Abstracts page for details.

Dave Clements, on behalf of the GCC2012 Organizing Committee

PS: Please help get the word out. A flyer and graphics are at http://wiki.g2.bx.psu.edu/Events/GCC2012/-Promotion . – http://galaxyproject.org/GCC2012 http://galaxyproject.org/ http://getgalaxy.org/-http://usegalaxy.org/ http://galaxyproject.org/wiki/ Dave Clements <clements@galaxyproject.org>

Columbia Metagenomics May7-8

The Organizing Committee would like to invite you to attend a *free* Symposium on “Frontiers in Metagenomics” to be held in the beautiful Monsanto Auditorium at the Christopher S. Bond Life Sciences Center on the University of Missouri campus in Columbia, Missouri from May 7-8, 2012.

The objective of the Frontiers in Metagenomics Symposium is to expose you to a dazzling range of current applications which will be presented by a stellar group of accomplished scientists. The symposium will span the Kingdoms of Life and will address both the generation and analysis of metagenomic data.

Due to the generous sponsorship of the Mizzou Advantage Program and the Stadler Genetics Symposium, there will be no charge to attend. However preregistration is required by April 23, 2012 due to space limitations and there will be a $40 charge to attend the spectacular symposium dinner that will be held at Les Bourgeois Vineyards and Winery situated on the bluffs overlooking the Missouri River in Rocheport, Missouri.

Symposium information and registration details can be found at the website:www.muconf.missouri.edu/-metagenomics/index.html If you require more information, please do not hesitate to contact me.

Best regards on behalf of the Frontiers in Metagenomics Symposium Organizing Committee: Michael Calcutt, Perry Gustafson, Mark McIntosh, Melanie Mormile, Daniel Oerther, Chris Pires, Jack Schultz, Gary Stacey and Judy Wall.

We hope to see you in Columbia!!!!

Jerry Taylor Curators’ Professor and Wurdack Chair in Animal Genomics Division of Animal Sciences University of Missouri 920 East Campus Drive Columbia, MO 65211-5300 Voice: (573) 884-4946 E-mail: taylorjerr@missouri.edu

taylorjerr@missouri.edu

Edinburgh EvolutionMaternalEffects May9 reminder

Dear Colleagues,

This is a reminder of the May 9, 2012 Symposium on

Maternal Effects on Health and Fitness

at the Ashworth Laboratories, University of Edinburgh, UK.

The list of speakers, and preliminary schedule with titles is below.

10:00: Sylvain Gandon (Montpellier, France) Evolution of host defenses against pathogens: space, mothers and drugs

10:30: Romain Garnier (Montpellier, France) Persistence of maternal antibodies: theoretical and experimental approaches

11:00: Per Smiseth (University of Edinburgh, UK) Parental Defenses against Microbes

12:00: Tom Little (University of Edinburgh, UK) Adaptive Maternal Effects in Daphnia

12:30: Tessa Roseboom, (Amsterdam, NL) Maternal under-nutrition during gestation and health of the (grand)offspring: the Dutch famine birth cohort study

14:00: Sylvia Pedroni (University of Edinburgh) Obesity and pregnancy: effects on maternal metabolism and inflammation

14:30: Phillip Heeb (Toulouse, France) Reaction norms in differential allocations: Females trade-off male attractiveness with self maintenance

15:00: Alasdair Leslie (Oxford, UK) The Role of HLA in Paediatric HIV infection and Control

16:00: Ariel Lindner (Paris, France) Non-genetic Determinants of Bacterial Life History

16:30: Laura Galloway (Virginia, USA) Multiple sources of maternal effects contribute to adaptive evolution in plants

You can register via our website: http://-ciie.bio.ed.ac.uk/node/336. Registration is free, but please do register as it allows us to calculate numbers for the free lunch, coffee etc.

Yours, Tom

Tom Little Wellcome Trust Senior Research Fellow in Basic Biomedical Sciences Institute of Evolutionary Biology Kings Buildings University of Edinburgh EH9 3JT UK

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http://www.biology.ed.ac.uk/research/groups/tlittle/

Tom Little <TOM.LITTLE@ed.ac.uk>

FieldMuseum Chicago PlantEvolution Apr20

Friday, April 20 at the Field Museum

www.chicagoplantscience.org The Chicago Plant Science Symposium is a one-day meeting intended to highlight the cutting edge of research in plant evolution, ecology, and conservation. The program includes lunch and a post-conference mixer. Best of all, registration is free!

The theme of the symposium this year is Major Evolutionary Transitions. In their ~450 million years of evolution, land plants have confronted and overcome a wide range of challenges, such as dealing with the environment and interacting with other organisms, either competitively or cooperatively. The seven invited speakers are united by the common thread that their research investigates some aspect of these major evolutionary transitions or events in the history of land plants. The talks span evolution, ecology, and paleontology, and include perspectives from molecular, morphological, and functional data.

The speakers this year are:

Jody Banks, Purdue University What a comparison of the Selaginella genome to others tells us about the early evolution of plants

Norman Wickett, Chicago Botanic Garden New insights in the evolution of parasitic plants

Nathan Muchhala, University of Nebraska-Lincoln Bats, birds, and bellflowers: the evolution of specialized pollination in the Neotropics

Elizabeth Kellogg, University of Missouri-St. Louis The grass menagerie

Bonnie Jacobs, Southern Methodist University Cenozoic evolution of Africa's tropical ecosystems

Kevin Boyce, University of Chicago What the flowers did - terrestrial environments and ecology before and after angiosperm evolution

Thomas Taylor, University of Kansas Fungi as a driving force in land plant evolution: evidence from the fossil record

Questions: Contact the co-organizers, Patrick Herendeen (pherendeen@chicagobotanic.org) or Rick Ree (rree@fieldmuseum.org); or visit www.chicagoplantscience.org We look forward to seeing you in April!

Rick and Pat

Richard Ree <rree@fieldmuseum.org>

Fribourg Switzerland RapidEvolution Sep6-7

Dear colleagues,

It is with pleasure to announce this forthcoming 2-day Symposium on Rapid evolution during Biological Invasions. The meeting will last two days and will take place at our Department of Biology in Fribourg, Switzerland, on Thursday and Friday, 6-7 September 2012.

The 2-day symposium is mainly run by presentations of invited international experts and PhD students (especially from two Swiss Doctoral Programs), but it is open to all interested researchers. The website link is as follow:

http://www.unifr.ch/biol/ecology/CUSO/EEday2012/index.html and is now open for registration and abstract submission,

Greatly looking forward to meet you soon,

Heinz Müller-Schärer

Prof. Dr. Heinz Müller-Schärer Département de Biologie/Ecologie & Evolution Université de Fribourg/Pérolles Chemin du Musée 10 CH-1700 Fribourg, SWITZERLAND Tel: + (41) (0) 26-300 88 35 direct Tel: + (41) (0) 26-300 88 50 secr. Fax: + (41) (0) 26-300 96 98

E-mail: heinz.mueller@UNIFR.CH http://www.unifr.ch/biol/ecology/ http://www.unine.ch/nccr

patrik.mraz@unifr.ch

Galveston QuantitativeGeneticsGenomics Feb16-17

Quantitative Genetics and Genomics Gordon Research Seminar will be held on February 16-17 2013 in Galveston, Texas. This year's theme is 'Genetics of Complex Phenotypes'

Gordon Research Seminars are 2-day meetings for graduate students and post docs to discuss and present cutting-edge work and network with peers and leaders in their field. This GRS takes place before the related Gordon Research Conference.

Speakers will be selected from the submitted abstracts. Students or postdocs who are interested in the conference should apply at http://www.grc.org/programs.aspx?year=2013&program=grs_quant We will likely be able to cover the registration costs for some of the participants. Registration includes dinner Saturday, breakfast and lunch on Sunday, and the Saturday stay at the Hotel Galvez.

Please see the conference website for more details: http://www.grc.org/programs.aspx?year=2013&program=grs_quant Thank you!

Suzanne McGaugh

Suzanne McGaugh Biology Department Box 90338 Duke University Durham, NC 27708

http://www.duke.edu/~sm252/ Suzanne McGaugh <suzanne.mcgaugh@duke.edu>

IowaStateU StatMethods NGS May11

Registration and abstract submission are now open for the "Conference on New Statistical Methods for Next Generation Sequencing Data Analysis" to be held at Iowa State University in Ames, IA on May 11, 2012. The conference will provide a platform to discuss the latest statistical research in next generation sequencing data analysis and promote collaborations among researchers with interest and expertise in this area.

Co-sponsors include the American Statistical Association, the Institute of Mathematical Statistics, and the Department of Statistics, the Office of Biotechnology, and the Laurence H. Baker Endowment at Iowa State University. Please visit http://www.stat.iastate.edu/-Conference2012/ for more information.

kdorman@iastate.edu

IST Austria HumanEvolution May7 Registration

The deadline for registration for the upcoming Young Scientist Symposium on human evolution at IST Austria is fast approaching!

Human evolution is a topic that lends itself to a variety of approaches, such as genetics, cognition, the evolution of language and palaeontology, including extensive informatic applications. With this symposium we aim to bring together people from diverse academic backgrounds and give participants the opportunity to hear about research that they would perhaps not normally experience.

We are pleased to announce the following confirmed speakers: Bence Viola (MPI Leipzig, DE) Bill Sellers (Manchester, UK) Eörs Szathmáry (Budapest, HU) Daniel Nettle (Newcastle, UK) Johannes Krause (Tübingen, DE) (Plus one more TBC)

This one-day event is organised by the students and postdocs of IST Austria, and will take place on May 7th at the Institute of Science and Technology Austria, 18km North of Vienna. Registration is free and includes lunch, and a shuttle bus will be provided too and from Vienna free of charge. There will also be an opportunity for a campus tour if you wish to take a look at the rest of what goes on at IST Austria.

The deadline for registration is April 5th.

We are especially keen to give scientists at the start of their career the opportunity to interact with top scientists, and as the day will also include a question and answer session with the speakers at the end of the day on the future of human evolution, so that students can pitch their questions directly to the experts. The event is aimed at all scientists with an interest in evolutionary biology, and in particular young scientists are encouraged to register!

For more information and to register for this event, please see the following website: http://www.ist.ac.at/-young-scientist-symposium-2012 Note that registration is strictly limited to 140 people. Unfortunately as this is a free event, we are unable to provide funding for travel for delegates or assist with VISAs or accommodation.

Tom Ellis PhD student Barton Group Am Campus 1 Institute of Science and Technology Austria A-3400 Klosterneuburg Austria

0043 (0) 2243 9000 3008

tom.ellis@ist.ac.at

KansasCity ArthropodGenomics May30-Jun2 LastCall

One week remains (Fri, 3/30 deadline) to Register, Submit Abstracts, and Reserve Hotel for the Arthropod Genomics Symposium and i5kWorkshop, May 30-June 2, Kansas City

- Sixth Annual Arthropod Genomics Symposium and i5k Community Workshop*-* MAY 30 to JUNE 2, 2012 Kansas City Marriott on the Country Club Plaza http://www.ksu.edu/agc/symp2012

Print this e-mail from a PDF (http:/-/www.k-state.edu/agc/symp2012/images/-Announcement#5.pdf)

You still have time to register before Friday, March 30, at the early bird rates and make arrangements to attend!!!

Key deadlines: Friday, March 30 - Early Discount Registration Friday, March 30 - Hotel Reservations at the Marriott on the Country Club Plaza Friday, March 30 - Poster Abstracts to display a poster Friday, May 18 - Registration at regular rates. Registration will continue to be accepted after May 18, if space is available.

The symposium focuses on new insights gleaned from analyzing arthropod genomes and is designed for scientists interested in genomic studies of Arthropods, both model organisms and those of agricultural or health relevance. The program will include platform presentations, a welcome reception, a bioinformatics-related workshop and arthropod genomics-related poster sessions. Postdoctoral, graduate, and undergraduate students are also encouraged to attend. Sessions conclude Saturday evening, followed by an optional Kansas City Barbecue banquet.

--*-*-* i5k Community Workshop*-*-*-*-*- MAY 30, 2012 (Wednesday morning) to MAY 31, 2012 (Thursday afternoon) "i5k Community Workshop: An international effort to sequence 5,000 of the world's key arthropod species." The Workshop will aim to bring together biologists, informaticists, and policy-makers to discuss and contribute to advance planning for the i5k initiative. Plans for the i5k Workshop include presentations by top genomics and bioinformatics researchers and representatives from the primary sequencing centers, followed by training and breakout sessions focused on i5k and other successful insect genome projects. The Workshop will conclude with a discussion of white papers and programmatic steps needed to enact i5k projects.

REGISTRATION: Register ONLINE by accessing this link (http://www.k-state.edu/agc/symp2012/register.html) or visit the Register tab on the Symposium website, www.k-state.edu/agc/symp2012 .

Registration Rates for Non-Students: Arthropod Genomics Symposium ONLY- $375 ($475 after 3/30/12) i5k Workshop ONLY - $100 ($150 after 3/30/12) Combined Symposium and i5k Workshop - $425 ($575 after 3/30/12)

Registration Rates for Students: Arthropod Genomics Symposium ONLY- $175 ($250 after 3/30/12) i5k Workshop ONLY - $50 ($100 after 3/30/12) Combined Symposium and i5k Workshop - $200 ($300 after 3/30/12)

HOTEL ROOMS at the Kansas City Marriott on the Country Club Plaza can be reserved for the low rate of $121/night at: http://www.k-state.edu/agc/symp2012/hotel.html POSTER SESSIONS are planned for Friday and Saturday. Please follow the guidelines at http://www.k-state.edu/agc/symp2012/images/AbstractGuidelines.pdf and submit your abstract by March 30, 2012.

BIOINFORMATICS WORKSHOP: Friday, June 1, 5:30-7:30 p.m. Terence Murphy, NCBI/NIH, "How to submit your sequencing project to NCBI" Dan Lawson, EMBL-EBI, "Making your genome useful to a wider audience"

KEYNOTE SPEAKER: Gene E. Robinson Entomology and Institute for Genomic Biology, University of Illinois at Urbana-Champaign "Understanding the Relationship between Genes and Social Behavior: Lessons from the Honey Bee"

FEATURED SPEAKERS: Volker Brendel Department of Biology and School of Informatics and Computing, Indiana University "Vertical Integration of Genomic Information"

William E. Browne Biology, University of Miami Niche Partitioning in the Pelagic Zone and the Evolution of the HyperiidAmphipods

Angela E. Douglas Entomology, CornellUniversity "From Metagenomes to Function in Animal-microbial Symbioses"

Giles E. Duffield Biological Sciences and Eck Institute for Global Health, University of Notre Dame "Circadian and Light Regulation of the Mosquito Transcriptome"

MiodragGrbic Biology, The University of Western Ontario, London, Canada and Research Center of Vine- and Wine-related Science, Logroño, Spain "The Genome of the Two Spotted Spider Mite Tatranychusurticae: New Model for Plant-pest Interactions"

Marc S. Halfon Biochemistry, University at Buffalo-State University of New York and NY

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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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Lund EvolutionaryConstraint Aug18

ISBE Post Conference Symposia (August 18 2012) - stress as evolutionary and behavioral constraints V where are we now?

Dear EvolDir members,

Like several others before us, we would like to take the opportunity to advertise a post-conference symposium of this years ISBE meeting in Lund (see http://www.isbe2012lund.org/ for information about the meeting).

The symposium stress as evolutionary and behavioral constraints V where are we now? is one of six post-conference symposia that will be held on Saturday, 18 August 2012.

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. Participants who wish to present a 15-minute oral contribution should send a title and a short abstract to either Michi Tobler (michael.tobler@biol.lu.se) or Caroline Isaksson (caroline.isaksson@biol.lu.se). Registration, more information and detailed program will be posted at http://www.isbe2012lund.org/post-conference-symposia . 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 Epost: michael.tobler@biol.lu.se

Michael Tobler <Michael.Tobler@biol.lu.se>

LundU BehaviourEvolution Aug12-17 Registr 2

Dear all,

This is kind reminder that “early bird” registration and Abstract submission to ISBE 2012 (International Behavioural Ecology Congress, Lund, Sweden) is approaching. We welcome everybody to this meeting and we hope that many will take the opportunity to visit our beatiful country and city this coming August.

Here you will find information how to register and link:

http://www.isbe2012lund.org/registration/ Here you can submit Abstracts for either oral talks or posters:

http://www.isbe2012lund.org/call-for-abstracts/ We have also now decided about the post-conference symposia that will be held the day after the regular ISBE-meeting, on August 18 2012. Here is more information:

http://www.isbe2012lund.org/post-conference-symposia/ Once again: We wish you all very welcome to Lund in August and this meeting!

Best wishes,

Erik Svensson & Anders Hedenström

(Scientific Committé, ISBE 2012)

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

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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 NonAdaptiveSpeciation Aug18

ISBE Post Conference Symposia (August 18 2012) -The Role of Behaviour in Non-adaptive and Non-ecological Speciation’

Invited speakers:

Mark McPeek (Dartmouth College, USA) Kerry Shaw (Cornell University, USA) John Wiens (SUNY Stony Brook, USA)

Admission to this symposium is free of charge. Contributors who wish to present a 15-minute oral contribution should send a title and short abstract to Maren Wellenreuther (maren.wellenreuther@biol.lu.se)

This meeting is funded by the European Science Foundation’s (ESF) < http://www.esf.org/index.php?id=3D4757 > Frontier’s of Speciation Research FrontSpects < http://www.iiasa.ac.at/Research/EEP/FroSpects/ >, and will be one of several post-conference symposia the day after The International Behavioural Ecology Congress (“ISBE 2012”) < http://www.isbe2012lund.org/ > that will take place between August 12 and August 17 2012.

Background:

During the past decade, the ecological theory of adaptive speciation and radiation has received considerable attention. At the core of the ecological theory lies the idea that incipient species are formed as a direct or indirect result of niche-based ecological differences and divergent natural selection.

However, more recently non-ecological and non-adaptive speciation has moved back into the focus of many researchers, particularly those working on groups like birds, marine fish, amphibians and insects. The reason for this shift is that evolutionary diversity in some groups is less likely to have resulted from divergent ecological selection. Species in these aforementioned groups are often ecologically similar and show a high degree of niche conservatism, yet speciation obviously happens also in these groups of animals.

Behavior might play a crucial role in driving speciation processes in these groups, including learned mate preferences, sexual selection and sexual conflict. The role of behavior, whether it is through niche conservatism, mating behaviours or learning, makes the study of non-ecological and non-adaptive speciation processes especially interesting for behavioral ecologists. This symposium intends to foster greater communication between speciation researchers and behavioral ecologists.

Organizing committee:

Prof. Erik Svensson < http://www.lu.se/phenotypic-evolution/people/principal-investigator/erik-svensson >

Dr. Machteld Verzijden

Dr. Maren Wellenreuther

Ms. Anna Runemark

WWW

http://svenssonresearchlaboratory.blogspot.com/2011/07/esflund18aug2012.html http://www.isbe2012lund.org/post-conference-symposia/ Maren Wellenreuther

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Homepages ** < http://www.isbe2012lund.org/post-conference-symposia/ >* http://marenwellenreuther.com/index.html http://www.lu.se/o.o.i.s/26164 I support WINGS http://www.lu.se/wings/working-group/maren-wellenreuther-coordinator- Lund Postdoctoral Society *http://ced2.srv.lu.se/lupodnew/contact.aspx* maren.wellenreuther@gmail.com

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Mainz BiodivEvolBiol Sep16-19

21st International Symposium “Biodiversity and Evolutionary Biology” of the German Botanical Society (DBG).

September 16th - 19th 2012 | Mainz (Germany)

The Institut für Spezielle Botanik und Botanischer Garten of Johannes Gutenberg-Universität Mainz and the section “Biodiversity and Evolution” of the German Botanical Society invite you to participate in the 21st International Symposium “Biodiversity and Evolutionary Biology”.

The symposium is intended to provide the opportunity for stimulating exchange for botanists interested in plant systematics, morphology, phylogeny and evolution. We are looking forward to interesting talks and posters on your latest research and to lively discussions, and hope to learn much about the latest developments in our field.

Please visit: www.biodivevol2012.uni-mainz.de Conference Fee (conference dinner not included): Regular: 210 euro ; Students: 110 euro

Online registration and submission of Abstracts will be open from 1st May until 1st July 2012 at: www.biodivevol2012.uni-mainz.de Organizing Committee: Regine Claßen-Bockhoff, Berit Gehrke, Gudrun Kadereit, Joachim W. Kadereit, Angelika Schmitt, Christian Uhink

Contact: 21.SymposiumDBG@uni-mainz.de

Our meeting will be followed (20th - 23rd September) by the “Jahrestagung des Verbands Botanischer Gärten” (annual meeting of the Association of Botanic Gardens in Germany). More information at: www.botgarten.uni- mainz.de/1074.php.

Preliminary program

Sunday 16th September afternoon - Excursion to the “Mainzer Sand” (relict steppe flora) 5 p.m. onwards - Welcome and registration with “Weck, Worscht und Woi” in the Botanic Garden

Monday 17th September - Symposium: Evolution of Mountain Floras - invited speaker: Ch. Körner/Basel: Why is biological diversity in mountains higher than in lowlands? - Symposium: Next Generation Sequencing in Plant Systematics and Evolution - invited speakers: T. Hankeln/Mainz: Next-Generation sequencing: a technical introduction; A. Liston/Corvallis: Next generation sequencing for plant systematics and evolution - Symposium: Mechanisms of Speciation - invited speaker: H.P. Linder/Zürich: Speciation mechanisms, speciation rates, and phylogenies - Plenary talk - B. Gemeinholzer/Gießen: Accessing and sharing biodiversity data - the next generation research

Evening: informal gathering in the Botanic Garden.

Tuesday 18th September - Symposium: Evolution of Tropical Floras - invited speaker: T. Pennington/Edinburgh: Phylogeny, ecology and the historical assembly of tropical forests - Symposium: Pollination and Dispersal Biology - invited speaker: A. Cocucci/Córdoba (Argentinia): The bull in the milkweed: evidence of animal-like male-male competition in plants - Open Symposium (topics not specified) - Plenary talk - E.Beck/Bayreuth: (Why) Do we need legal regulations for biodiversity research? - Meeting of the section "Biodiversity and Evolution" of the German Botanical Society

Conference Dinner

Wednesday 19th September - Poster Session - Symposium: Evolution of Mediterranean and Arid Floras - invited speaker: B.G. Baldwin/Berkeley: Evolutionary patterns and processes in the California Floristic Province - Symposium: Ontogeny: from Meristems to Phenotypic Diversity - invited speaker: L. Ronse de Craene/Edinburgh: Evolution of perianth and androecium in Caryophyllales: a complex story - Plenary talk - H. Hurka/Osnabrück: Ex situ plant conservation strategies - pros and cons - Exploring Mainz: Museum of Antique Shipping/Roman Mainz/Chagall church windows/Gutenberg-Museum

Evening: informal gathering in the Botanic Garden.

Thursday 20th September - Workshop: How to deal with inflorescences in systematics and floral ecology?

The workshop offers a forum for discussion and for practical inflorescence analysis.Participants are welcome to bring their own material. Early registration is required. Contact: R. Claßen-Bockhoff (classenb@uni-mainz.de).

gehrke@uni-mainz.de

Manchester GenomeEvolution May11

We are pleased to announce that the third annual Molecular and Genome Evolution Symposium will take place at the Faculty of Life Sciences, The University of Manchester on Friday 11th May, with an expected start around 09h30.

The remit of the symposium is broad and includes all aspects of molecular and genome evolution, including from computational methods, theoretical work, and wet-lab experiments. The symposium will be a day long event consisting of a series of talks, a poster session, and two plenary lectures from:

Frank Jiggins (Cambridge) "The molecular evolution of Drosophila and viruses", and Erich Bornberg-Bauer (Muenster) "Evolutionary dynamics and adaptive benefits of emergence and modular rearrangements of protein domains"

The remainder of the day will be made up from a selection of short submitted talks along with some other hand picked talks. We encourage anyone interested to attend the symposium and, if they wish, to submit an abstract. The best abstracts will be selected to give talks, with the remainder invited to present posters. All talks and posters will also be considered for a prize, presented at the drinks reception following the symposium. We are particularly keen to give PhD students and post-docs a chance to present their work, although all abstract submissions are welcomed.

Lunch will be provided free of charge and there will also be a free drinks reception with the poster session. There are limited places so please register for the symposium online at the URL http://tinyurl.com/ManMage2012 (full URL: https://survey.ls.manchester.ac.uk/-TakeSurvey.aspx?SurveyID=3D94KI4725). If you have any questions about the symposium please contact me (simon.whelan@manchester.ac.uk) or Karen Reeson (karen.m.reeson@manchester.ac.uk).

Please pass this message on to anyone else that may be interested

Regards,

Simon Whelan

– Simon Whelan | T: +44-(0)161-3068901 | F: +44-(0)161-2755586 Computational and Evolutionary Biology, University of Manchester Michael Smith Building, Oxford Road, Manchester, M13 9PT, UK http://www.ls.manchester.ac.uk/-people/profile/index.aspx?PersonID=3D1716 simon.whelan@manchester.ac.uk

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Marseilles EvolutionaryBiol Sep18-21

Dear All,

It is my pleasure to announce that registration and abstract submission for the 16th Evolutionary Biology Meeting at Marseilles, September 18-21, 2012, is open. Please visit the web site of the meeting http:/-

/sites.univ-provence.fr/evol-cgr where you will find all relevant information.

The following subjects will be discussed:

- Evolutionary biology concepts and modelisations for biological annotation; - Biodiversity and Systematics; - Comparative genomics and post-genomics (at all taxonomic levels); - Functional phylogeny; - Environment and biological evolution; - Origin of Life and exobiology; - Non-adaptative versus adaptative evolution; - The ≪ minor ≫ phyla: their usefulness in evolutionary biology knowledge; - Convergent evolution

Looking forward to your participation.

Best wishes,

Marie-Hélène Rome

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

MNHN Paris EvolutionConstraints Jun20-22

Dear colleagues,

We are pleased to announce thesymposium organised at the Muséum National d'Histoire Naturelle

*This international symposium*aims to:

*/1.initiate discussion/*on the concept of constraints acting at different organisational levels. ,

*/2.share and discuss results/*of present and fossil examples in a comparative framework at molecular, genomic, developmental, functional, behavioural and ecological levels.

Ideally, the symposium will foster new networks of researchers who will develop interdisciplinary discussions around new concepts on the origin, development and evolution of the forms of life.

Any organism is defined by the sum and integration of the specific "forms" which it displays at different levels of resolution, from the molecular to the ecological. These forms shape the capacity to generate variation and to evolve in different environments. Understanding how forms evolve and which constraints regulate these processes are central questions which remain largely unanswered. Interdisciplinary discussions between biologists, physicists, chemists and philosophers will help develop a new conceptual approach to the notions of "constraints" and evolution of forms. The integration of this new understanding in a comparative context will help improve our vision of evolution and adaptation in a geological timeframe.

This symposium is included into the ATM programme "/Formes possibles, formes réalisées/" directed by Pierre-Henri Gouyon and VincentBels from 2009 to 2012 at the *Museum National d'Histoire Naturelle *for contributing to supporting research on the origin, development, function, adaptation and evolution of form in biological systems.

*WHERE ?**GRANDE GALERIE DE L'EVOLUTION Muséum National d'Histoire Naturelle, France, *36, rue Geoffroy Saint-Hilaire 75005 Paris, FRANCE

*WHEN ? **20th – 22th June, 2012*

*WEBSITE for registration and abstract:*www.mnhn.fr/colloque/form2012 * Please feel free to contact us for any informations: _symposium.form@mnhn.fr_*

* *The organisers

Vincent Bels & Pierre-Henri Gouyon

Pierre-Henri Gouyon <gouyon@mnhn.fr>

Montpellier EvolutionCancer Apr11

Evolution and Cancer Conference - 11 April 2012

A one day conference on "Evolution and Cancer" will take place at < http://www.agropolis.fr/pratique/acces.php > Agropolis international in Montpellier, France on the 11th of April. The objective is to foster interdisciplinary research on the emergence, progression and therapies of cancer from a Darwinian perspective.

The conference will include 8 presentations and a round table discussion. Please consult http://www.darevcan.univ-montp2.fr/?page_id=221 for the final program (which will be posted shortly).

Attendance is by registration only at http://www.darevcan.univ-montp2.fr/?page_id=335 For additional information, please contact <fadela.tamoune@univ-montp2.fr> Fadela Tamoune

Michael Hochberg <mhochber@univ-montp2.fr>

Novosibirsk GenomeBioinformatics Jun25-29

Dear Dr. Golding!

For your attention here are news on the 8th International Conference on the Bioinformatics of Genome Regulation and Structure/Systems Biology (GRS\SB-2012) [Novosibirsk, Russia, June 25-29, 2012]

1) The registration to the Conference continues by science sections listed at the web-site http://conf.nsc.ru/-BGRSSB2012/en/. Thesis submission deadline is 6 April 2012.

2) The Program Committee and Editorial boards of the journals JBCB (http://www.worldscinet.com/jbcb/-) and CSBJ (www.csbj.org) have agreed about post-conference publication of papers on materials presented by BGRS\SB-2012 participants.

3) GRS\SB-2012 invited speakers:

Academician Konstantin Skryabin, "Bioengineering" Center, RAS, Moscow, Russia

Dr Yuriy Aulchenko, ICG SB RAS, Novosibirsk, Russia, and Erasmus MC, The Netherlands

Prof Ming Chen, Zhejiang University, Hangzhou, China

Prof Frank Eisenhaber, Bioinformatics Institute, A-STAR, Singapore

Prof Roman Efremov, Institute of Biochemistry, RAS, Moscow, Russia

Prof Fazel Famili, University of Ottawa, IIT/ITI, Canada

Prof Dr Robert Giegerich, Bielefeld University, Germany

Prof Igor Goryanin, Biomedical Cluster Skolkovo, Russia

Prof Vadim Govorun, Institute of Phys.-Chem. Medicine, Moscow

Prof Javier Guillen, AAALAC International, Pamplona, Spain

Prof Vladimir Ilyin, SINP MSU, Moscow, Russia

Prof Jaap Kaandorp, University of Amsterdam, Netherlands

Prof Lars Kaderali, Dresden University, Germany

Dr Olga Krebs, Heidelberg Institute for Theoretical Studies, Germany

Prof. Gordon Lauc, University of Zagreb, Croatia

Dr Vsevolod Makeev, Vavilov Institute of General Genetics RAS, Moscow, Russia

Prof Luciano Milanesi, ITBA, Italy

Prof Chanchal Mitra, Hyderabad University, India

Prof Eric Mjolsness, University of California, Irvine, USA

Prof Jan-Bass Prins, John Radcliffe Hospital, Oxford, UK

Dr Egor Prokhorchouk, "Bioengineering" Center, RAS, Moscow, Russia

Prof Andrey Rzhetsky, University of Chicago, USA

Dr Yijun Ruan, Genome Institute of Singapore, Singapore

Prof Maria Samsonova, State Polytechnic University, St. Petersburg, Russia

Prof Vladimir Sobolev, Weizmann Institute of Science, Rehovot, Israel

Prof Victor Solovyev, Department of Computer Science, University of London, UK

Prof Limsoon Wong, National University of Singapore, Singapore

Prof Jaroslaw Zola, Electrical & Computer Engineering, Iowa State University, USA

Complete list of speakers you'd see at the Science Program page at: http://conf.nsc.ru/BGRSSB2012/-scientific_program

4) Cultural program and social events includes local excursions and tours:

* Sightseeing excursion in the Akademgorodok, visiting museums; * Novosibirsk sightseeing tour by bus; * Excursion to the Novosibirsk Zoo (http://-www.zoonovosib.ru/?en); * Post-conference tour: Altai mountains: "Sites of Strength" (shifts 30/06 and 2/07/2012); * Post-conference tour: "Hello, Baikal!" (Lake Baikal, start 01/07/2012); * Post-conference tour: "Beauty of the Small Sea Straight" (Maloe More, Lake Baikal, start 30/07/2012).

Detailed information is at the Cultural Program page http://conf.nsc.ru/BGRSSB2012/en/cultural_program Please note: application for Russian visa may take more than month (depending on the country). Please, count days of pre- and post-conference tours in your visa application (if you wish to participate).

Contacts:

General questions and accommodation: bgrs2012@bionet.nsc.ru

Visa application: Dr Galina N. Kiseleva. ôÅl. +7(383)363-4987(*1338), kiseleva@bionet.nsc.ru

School for young scientists "Bioinformatics and System Biology": Victoria V. Mironova kviki@bionet.nsc.ru

Welcome to Novosibirsk in June!

Best regards,

Prof. Nikolay A. Kolchanov, Academician, Director of the Institute of Cytology and Genetics,

Siberian Branch of the Russian Academy of Sciences

BGRS\SB_2012 Chairman

Prof. Dr. Ralf Hofestaedt, Bielefeld University, Germany, BGRS\SB_2012 Co-chairman

Dr Tamara M. Khlebodarova, Academic secretary of BGRS\SB-2012

Svetlana V. Zubova, Local Organizing Committee

Organizing committee BGRSSB-2012 <bgrs2012@bionet.nsc.ru>

Ottawa Evol2012 MSI Faculty

Evolution 2012 MSI Faculty Travel Award - Application Deadline Approaching

Are you a biologist at a minority-serving institution? Apply now for a travel award to attend Evolution 2012 < http://www.confersense.ca/-Evolution2012/index.htm > in Ottawa, Canada.

The National Evolutionary Synthesis Center (http://www.nescent.org), with support from the Society for the Study of Evolution (http://-www.evolutionsociety.org/), is pleased to announce a travel award for faculty from Minority Serving Institutions (MSIs) to attend Evolution 2012. This year, the meeting will be the "1st Joint Congress on Evolutionary Biology", bringing together five of the world's largest academic societies devoted to the study of ecology and evolutionary biology: the American Society of Naturalists (ASN), the Canadian Society for Ecology and Evolution (CSEE) the European Society for Evolutionary Biology (ESEB), the Society for the Study of Evolution (SSE), and the Society of Systematic Biologists (SSB).

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

This award is intended to provide MSI faculty with an opportunity to present original research in evolution, systematic biology, evolutionary genomics/informatics, evolution education/outreach or other disciplines typically represented at the Evolution meetings. As such, your application must include a talk/poster title and abstract. In addition, you will be asked to provide a brief (1 page) statement describing how this award will contribute to your professional/scientific development, as well as provide benefit to your students and institution.

To apply, please visit www.nescent.org/-Evo2012facultyapp Application Deadline: March 31st, 2012 (Awards will be announced by April 9th, 2012)

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

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

"Weintraub, Jory P" <lviscrst@live.unc.edu>

Ottawa Evolution2012 Jul6-10

1st Joint Congress on Evolutionary Biology (i.e. Evolution2012 and more!) July 6-10, 2012 - Ottawa, Canada www.evolution2012.org REMINDER: EARLY REGISTRATION DEADLINE IS FAST APPROACHING (Apr. 30)

The 1st Joint Congress is a merging of the traditional 'Evolution' meeting (the annual meeting of the American Society of Naturalists, the Society for the Study of Evolution, and the Society of Systematic Biologists) with the annual meeting of the Canadian Society for Ecology and Evolution and the (normally biennial) meeting of the European Society for Evolutionary Biology. Along with a full range of topics in evolutionary biology, with the joint participation of the CSEE and the ASN, we look forward to increased representation of our ecologists.

IMPORTANT POINTS - Separate registration for several optional (and exciting) pre/post congress workshops is NOW OPEN (see http://www.confersense.ca/-Evolution2012/workshops.htm)

- Ottawa is a tourist city and accommodation is often in high demand. Booking hotel/residence NOW is STRONGLY RECOMMENDED. We have gone to substantial lengths to ensure that our conference hotel rates are the best possible; please book through our registration process and not via the hotels directly.

- Coming from outside CANADA? You WILL need a passport (INCLUDING IF YOU'RE DRIVING OR FLYING FROM THE USA).

- Most people will not require a visa; check here to find out for sure: http://www.cic.gc.ca/english/visit/-visas.asp#exemptions - Our new congress blog site is up and running and will soon feature all sorts of useful information (http://evolution2012ottawa.com/-wordpress/)

HIGHLIGHTS - The meeting will be held at the state-of-the-art, newly opened Ottawa Convention Centre, situated in the heart of downtown Ottawa.

- Optional pre/post congress tours now available for booking, including world-class whitewater rafting on the Ottawa River.

- Child care is available onsite at the congress venue (book now).

- Affordable residence accommodation at the University of Ottawa, only a short walk from the congress venue, along with an array of hotel options.

- A plenary address and two symposia sponsored by each society.

- Various optional pre/post-congress workshops/symposia, along with the iEvoBio satellite conference (July 10-11).

- Final congress dinner and farewell party (no speeches) at the spectacular Canadian Museum of Civilization (transportation included).

For more details, visit www.evolution2012.org. We look forward to seeing you in July.

Conference organizers:

Howard Rundle (uOttawa) Andrew Simons (Carleton University)

Howard D. Rundle, Associate Professor Department of Biology, 30 Marie-Curie Priv. University of Ottawa, Ottawa, ON, K1N 6N5, CANADA Ph: +1 613-562-5800 x2835; Fax: +1 613-562-5486 Skype: howarddrundle http://www.science.uottawa.ca/~hrund050 http://-www.evolution.uottawa.ca howard.rundle@uottawa.ca

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Ottawa iEvoBio Informatics Jul10-11

The Call for Abstracts for full talks is now open for the 2012 conference on Informatics for Phylogenetics, Evolution, and Biodiversity (iEvoBio), at http:/-/ievobio.org/ocs2/index.php/ievobio/2012. See below for instructions.

Accepted talks will be 15 minutes in length and will be presented during the full talk session of the conference. Because the number of program slots for full talks is limited, some talks may be moved to the Lightning Talk session (5 minutes in length).

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

Submissions should be 1 page long at most and include a title, a list of contributors, and an abstract. The abstract should provide an overview of the talk's subject, and give enough detail to allow reviewers to decide whether the submission merits a full talk, or whether it should be moved to a Lightning Talk session. If the subject of the talk is a specific software component for use by the research community, the abstract must state the license and give the URL where the source code is available so reviewers can verify that the open-source requirement(*) is met.

The deadline for submission is April 2, 2012. We intend to notify authors of accepted talks before early registration for iEvoBio (and Evolution) ends. Further instructions for submission are at the following URL: http://ievobio.org/ocs2/index.php/ievobio/-2012/schedConf/cfp Full talks are one of the five kinds of contributed content that feature in iEvoBio. The other four are: 1) Lightning talks (5 mins long), 2) Challenge entries, 3) Software bazaar demonstrations, and 4) Birds-of-a-Feather gatherings. The Call for Challenge entries is already open (see http://-ievobio.org/challenge.html). The calls for contribution to the other three sessions will open later, and will remain open until shortly before the conference or until the respective track fills up. In addition, 2012 iEvoBio sponsor Biomatters Ltd will be running the Geneious Challenge alongside this year's iEvoBio Challenge, see http://ievobio.org/geneious_challenge.html for more information.

More details about the 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 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 and Florida Museum of Natural History 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

(*) iEvoBio and its sponsors are dedicated to promoting the practice and philosophy of Open Source software development (see http://www.opensource.org/docs/definition.php) and reuse within the research community. For this reason, if a submitted talk concerns a specific software system for use by the research community, that software must be licensed with a recognized Open Source License (see http://www.opensource.org/licenses/), and be available for download, including source code, by a tar/zip file accessed through ftp/http or through a widely used version control system like cvs, Subversion, git, Bazaar, or Mercurial. Authors of full talks who cannot meet this requirement at the time of submission should state their intentions, and are advised that the requirement must be met by July 9, 2012, at the latest.

hlapp@nescent.org

Ottawa iEvoBio Informatics Jul10-11 CallForTalks

The Call for Lightning Talks is now open for the 2012 conference on Informatics for Phylogenetics, Evolution, and Biodiversity (iEvoBio), at http://ievobio.org/ocs2/index.php/ievobio/2012. See below for instructions.

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

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

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

Review and acceptance of lightning talks will be on a rolling basis. The deadline for submission is the morning of the first day of the conference (July 10), but see below. Further instructions for submission are at the following URL: http://ievobio.org/ocs2/index.php/ievobio/2012/schedConf/cfp Please make sure to choose the Lightning Talks track for your submission. Note that the number of lightning talk slots is finite and that therefore the track may fill up early. We cannot accept lightning talks until the open-source requirements are met, and so waiting with that until the deadline risks that the track is full by that time.

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

Lightning talks are only 1 of 5 kinds of contributed content that iEvoBio will feature. The other 4 are: 1) Full talks (open until April 2), 2) Challenge entries, 3) Software bazaar demonstrations, and 4) Birds-of-a-Feather gatherings. The Call for Challenge entries remains open (see http://ievobio.org/challenge.html). The calls for contribution to the other two sessions will open later, and will remain open until shortly before the conference or until the respective track fills up. In addition, 2012 iEvoBio sponsor Biomatters Ltd will be running the Geneious Challenge alongside this year's iEvoBio Challenge, see http://ievobio.org/geneious_challenge.html for more information.

More details about the 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 Systematic Biologists (SSB).

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

hlapp@nescent.org

Ottawa iEvoBio Informatics Jul10-11 ChallengeCall

Many trees enter. Fresh analysis ensues. New insights emerge.

The conference on Informatics for Phylogenetics, Evolution, and Biodiversity (iEvoBio) is again holding a Challenge competition in 2012, on the theme "Synthesizing Phylogenies". Somewhere, buried in large sets of trees, lies a stunning new revelation, a baffling discovery, the answer to a longstanding controversy, or simply something not obvious to the naked eye. The mission of the 2012 iEvoBio challenge is to find those revelations, discoveries and answers within your own data and/or within one of the datasets provided by the challenge. What new scientifically interesting results can you pull from these trees, using any combination of techniques at your disposal?

Further information on the nature of challenge entries and how to submit them can be found on the iEvoBio website at http://ievobio.org/challenge.html. Submissions are due by June 25, 2012. Selected candidates will make short oral presentations to demonstrate their work in a "Challenge session" at the conference, and if suitable will automatically be entered into the Software Bazaar track of the conference.

Cash prizes will be awarded for first place (USD 1,500) and runner-up entries. The winning entries will be selected by a vote of the iEvoBio meeting participants.

Alongside the iEvoBio Challenge, 2012 iEvoBio sponsor Biomatters Ltd is running the Geneious Challenge. The goal of this challenge is to develop a new plugin to Geneious Pro, using the public API, that enables a new and exciting visualization or analysis. The winning entry will receive a $1000 cash prize, and all entrants who submit by the deadline will receive a 12-month subscription license. The Geneious Challenge has the same open and closing dates as the iEvoBio Challenge. See http://ievobio.org/geneious_challenge.html for more information.

Separate from iEvoBio, the Encyclopedia of Life (EOL) is leading a Phylogenetic Tree challenge to encourage not only the development of large phylogenies, but their practical use. Together with the Global Names project they will choose two winning entries: one for the best large tree and one for the most promising but not necessarily large tree – both in Darwin Core Archive format suitable for use in major biodiversity websites such as EOL. The two winners will receive paid trips to the 2012 iEvoBio conference. See http://eol.org/info/-tree_challenge for more information.

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 Systematic Biologists (SSB).

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hlapp@nescent.org

Ottawa iEvoBio Informatics Jul10-11 TravelAwards

The 2012 conference on Informatics for Phylogenetics, Evolution, and Biodiversity (iEvoBio) is offering limited funds for travel expenses for the 2012 iEvoBio meeting in Ottawa, Canada. Preference will be given to participants lacking sources of funding for meeting attendance, such as graduate students, emerging professionals, and participants from underrepresented groups and countries. Please explain in an attached document the need for funding, the benefit that attending iEvoBio will afford you and how you will contribute to the meeting (max 350 words). We are looking for do-ers! A brief letter of support from your advisor, supervisor, or professional mentor should be submitted to the organizing committee (electronically), together with the application headed by the information below, to travelaward@ievobio.org by the deadline of 15 April 2012.

Participants are required to make all their own travel arrangements, including visas and lodging, if required.

Application format:

Name: Contact information (address/phone/email): Academic Institution: Role (student, researcher, etc.): Origination of travel (if different from home institution) and estimated travel expenses: Explain the benefit that attending iEvoBio will afford you and what you will bring to the meeting (350 words or less):

hlapp@nescent.org

Ottawa RoadmapMolecularEcology Jul6

Registration is now OPEN for the Molecular Ecology Symposium, to be held July 6th in Ottawa, Canada (the day before the Joint Evolution meetings).

Sign up is through the registration website for the main meeting: http://www.confersense.ca/Evolution2012/registration.htm The study of genes and their products in natural populations is now routine, and massive datasets will soon be available. What new questions should we be asking? Where is the field headed, and are we going in the right direction? Please join us for a combination of talks and panel discussions on July 6th in the Ottawa Convention Centre, from 8.30am to 6pm.

Topics and Speakers:

- Ecological Genomics / Molecular Adaptation: Jon Slate, Sean Rogers, Aurélie Bonin - Speciation and Hybridization: Alex Buerkle, Alex Widmer, Tatiana Giraud - Landscape Genetics, Phylogeography and Conservation: Francois Balloux, Bryan Carstens, Victoria Sork - Kinship, Parentage and Behaviour: Dave Coltman, Dany Garant - Ecological Interactions: Brent Emerson, Graham Stone

We hope to see you there!

Loren Rieseberg and Tim Vines

Tim Vines <managing.editor@molecol.com> Tim Vines <managing.editor@molecol.com>

Paris FrenchSocietySystematics Oct8-10

The French Society of Systematics (SFS) is pleased to announce its forthcoming annual meeting, which will convene on *8-10th October, 2012*, Paris, France.

This year, our annual meeting will address the issue of:

Systematics beyond phylogenetics

It will take place at the Institut Écologie et Environnement (InEE), 3 rue Michel-Ange, 75016 Paris.

Starting from today, submit your abstract online for talks and poster sessions to the Secretary of the SFS <jdubuiss@snv.jussieu.fr>

You can download the registration form at this address < http://sfs.snv.jussieu.fr/resources/Journees_automne/SFS%20annual%20meeting%202012,%20circular-7.doc > and take advantages of early discounted rates before the 15th of June.

– *Société Française de Systématique* Courriel : sfs.systematique@gmail.com Site web : http://sfs.snv.jussieu.fr sfs systematique <sfs.systematique@gmail.com>

Perth EvolPlantSignalling Sep16-21 Abst Mar20

Abstracts for the 1st Symposium on Plant Signalling & Behaviour are due by MARCH 20th.

We invite everyone conducting exciting research in the field of plant physiology, evolutionary biology and behavioural ecology - from the world of molecules to the broad processes underlying species interactions and co-evolution - to consider submitting an abstract to this inaugural meeting to be held in September 16th-21st 2012 in Perth, Western Australia.

The Symposium will cover themes such as Plant Cell Biology & Signalling, Plant Sensory & Behavioural Ecology, and Theoretical Botany.

Featured speakers (confirmed):

* Sonia Sultan (Evo-devo in plants - Wesleyan University, USA)

* Corne' Pieterse (Plant-microbe co-evolution - Utrecht University, Netherlands)

* Pamela Lyon (Evolution of embodied cognition in plants - University of Adelaide, Australia)

* Rick Karban (Plant behaviour ecology - University of California Davis, USA)

* Paul Paré (Plant chemical ecology - Texas Tech University, USA)

* Frantisek Baluska (Plant cell biology - University of Bonn, Germany)

* Stefano Mancuso (Plant electophysiology - University of Florence, Italy)

* Tracey Ann Cuin (Plant physiology - INRA-SupAgro, France)

* Rainer Hedrich (Plant biophysics - University of Wuerzburg, Germany)

Visit the website http://spsb2012.com/ and follow the instructions to submit your abstract... and keep checking the site as there is much more to come!!

Best regards

Monica Gagliano SPSB2012 Convenor

Dr Monica Gagliano Postdoctoral Research Fellow Centre for Evolutionary Biology | School of Animal Biology & Centre for Microscopy, Characterisation and Analysis The University of Western Australia | Crawley | WA 6009 | Australia ph: +61 8 6488 1361 website: http://www.uwa.edu.au/people/monica.gagliano ˜ CHECK OUT 1st SYMPOSIUM ON PLANT SIGNALLING & BEHAVIOUR in September 2012 at http://spsb2012.com/ ˜ ABSTRACTS SUBMISSION OPEN NOW!!

Monica Gagliano <monica.gagliano@uwa.edu.au>

Prague PolyploidyBiodiversity May7-10 program

Dear colleagues,

the conference program for the International Conference on Polyploidy, Hybridization and Biodiversity (ICPHB 2012), May 7-10, Pruhonice near Prague, is available here: http://icphb2012.ibot.cas.cz/-program.html Registration deadline is March 31.

With best wishes,

Judith

Dr. Judith Fehrer Institute of Botany Czech Academy of Sciences Zámek 1 25243 Pruhonice near Prague Czech Republic

phone +420 271015415 fax +420 267750031 fehrer@ibot.cas.cz

Judith Fehrer <Judith.Fehrer@ibot.cas.cz>

Tokyo ClimatePlantEvolution Aug23-30

International Palynological Conference (23-30th of August, 2012; Tokyo, Japan); http://www.psj3.org/ipc-iopc2012/Welcome.html Theme: Cenozoic plants and biosphere surrounding them

Symposium SS42: Neogene global tectonic and climatic change as drivers in plant evolution: linking the palynological, palaeobotanical and molecular records

The Neogene period represents the transition to our modern world, when crucial geographical features such as topographic relief, drainage patterns and oceanic currents were laid out. It also represents the run-up to the 'icehouse' world with final bleeps of a 'greenhouse' during the Middle Miocene (c. 15 Ma) and Middle Pliocene (c. 4 Ma). The combined effects of global tectonic and climatic change was critical for floral and faunal evolution, but also determined present biodiversity patterns, particularly this latter aspect was only identified by scientists in recent years. Interdisciplinary studies that include the geological history, palynology, palaeobotany and molecular phylogeny potentially can offer new insights into our understanding of plant evolution and diversification. In this session we encourage palynologists, palaeobotanists and molecular biologists who work at the interface of their disciplines to present their research on the Neogene evolution of plants and algae in geologically dynamic regions from all over the globe and from both marine and/or continental settings. The insights gained from this type of research are relevant when modeling the impact of future climatic change, but also where it concerns drafting guidelines for conservation policies in regions of high biodiversity.

Organizers:

Dr. Carina Hoorn Palaeo-ecology and Landscape Ecology, Institute for Biodiversity and Ecosystem Dynamics, University of Amsterdam, Science Park 904, 1098 XH Amsterdam, The Netherlands Email: M.C.Hoorn@uva.nl

Dr. Andre Pardo Universidad de Caldas, Facultad de Ciencias, Departamento de Ciencias Geológicas, Calle 65 No. 26-10, Manizales, Colombia Email: apardo66@yahoo.com

Dr. Alexandre Antonelli Gothenburg Botanical Garden, Carl Skottsbergs gata 22A, 413 19 Göteborg, Sweden & University of Gothenburg, Department of Biological and Environmental Sciences,Carl Skottsbergs gata 22B, 413 19 Göteborg, Sweden Email: alexandre.antonelli@dpes.gu.se

"Hoorn, Carina" <M.C.Hoorn@uva.nl>

UCalifornia LosAngeles FishFossilPhylogenetics

Dear colleagues,

I would like to bring to your attention the symposium on "Integration of fish fossil data into phylogenetic and comparative studies" that will take place on July 4 at the University of Liege during the upcoming European Congress of Ichthyology (http://www.eci-14.ulg.ac.be/-). I am hoping that this symposium will be a chance to bring together both neo- and paleo-ichthyologists that are integrating fossil data into systematic and macroevolutionary studies (e.g., phylogenetic inference using both extant and extinct taxa, dating of molecular trees, morphospace evolution across major clades, historical biogeography, mass extinctions, etc.) to discuss some of the advances in the field and some of the remaining challenges. Some financial support is available to help defray registration or travel costs for a few students and postdocs that plan to attend this symposium. Please note that the deadline for early registration for the congress and for submitting abstracts for the symposium is March 12th. Interested parties should feel free to email me with any questions.

Francesco Santini

– Francesco Santini Senior Research Associate Department of Ecology and Evolutionary Biology University of California at Los Angeles

610 Charles E. Young Drive South Room 2153, Terasaki Life Sciences Building Los Angeles, CA 90095, USA

Phone: 424-442-4348 (Office); 310-206-2240 (Lab) Fax: 310-206-3987 E-mail: santini@ucla.edu

santini@ucla.edu

UHawaii Hilo TropicalConservation

The Tropical Conservation Biology and Environmental Science Symposium Research è Networking è Community è Science

April 12-13, 2012 at University of Hawaii at Hilo

http://tcbes.uhh.hawaii.edu/symposium2012/-index.html Mark your calendars for the 4th Annual Research Symposium sponsored by the Tropical Conservation Biology & Environmental Science Program at UH Hilo! Over two engaging days of presentations about recent scientific research carried out in Hawaii, the public is invited to join us on April 12-13, 2012 (Thursday and Friday).

Our goal is to increase undergraduate and graduate student participation in both the oral and poster presentation sessions. To encourage widespread participation, we are offering this event free of charge, and will be awarding prizes for outstanding presentations in various categories.

Whether you are a graduate or undergraduate student, resident or visiting faculty, or agency personnel, we invite you to come and share and find out about the latest research in the community around you!

Keynote speaker - Dr. Alan Friedlander

We are pleased to welcome Alan Friedlander as our symposium's keynote speaker! Alan's work incorporates ecology, remote sensing and GIS technologies, along with traditional resource knowledge to better understand coral reef ecosystem function and how best to conserve and manage these resources for future generations. He is currently the assistant leader of the Hawaii Cooperative Fishery Research Unit and associate professor in the Department of Zoology at the University of Hawaii at Mnoa. Alan holds a Ph.D. from the University of Hawaii and was a National Research Council Postdoctoral Associate with the Pacific Fisheries Environmental Laboratory in Pacific Grove, California. Alan was as a fisheries extension officer in the Kingdom of Tonga in the early 1980s and for nearly 30 years he has conducted coral reef fisheries and ecosystem-based research throughout the Indo-Pacific and Caribbean regions.

Donald Price Director and Professor Tropical Conservation Biology and Environmental Science Graduate Program University of Hawaii at Hilo Hilo, HI 96720

808.974.7365 Fax: 808.974.7693 donaldp@hawaii.edu

http://tcbes.uhh.hawaii.edu/ http://www2.hawaii.edu/ ˜ donaldp/ Donald Price <donaldp@hawaii.edu>

UMichigan BiodiversityInformatics Mar25

We are pleased to announce this year's Early Career Scientist Symposium, to be held Sunday, March 25, 2012 at Palmer Commons in Forum Hall on the campus of the University of Michigan, Ann Arbor. The theme this year is "Biodiversity informatics."

We have an outstanding lineup of early career researchers who will discuss biodiversity informatics and its application to broad questions in ecology and evolutionary biology. The keynote address will be given by Dr. Robert Guralnick of the University of Colorado at Boulder, who will describe "Mapping life: challenges with overcoming the Wallacean shortfall and documenting global scale biodiversity change."

Registration is free of charge but we strongly encourage you to register so we may provide adequate food and refreshment. Graduate students from all universities and all disciplines are invited to present their work during a lunchtime poster session, and can indicate so when they register. For poster specifications, please refer to: http://sitemaker.umich.edu/ecss2012/posters. Lunch will be provided at the poster session and a dinner reception will follow the symposium.

Register to attend and obtain more information by going to http://sitemaker.umich.edu/ecss2012/home . On behalf of the 2012 ECSS organizing committee: Christopher Dick, Philip Myers, Stephen Smith, Evan Economo, Hayley Lanier, Ya Yang, Cindy Carl

http://sitemaker.umich.edu/ecss2012/home Christopher Dick <cwdick@umich.edu>

Virrat Finland PhDStudentsEvolBiol Sep25-30 Regst

Event: EMPSEB 18 (PhD Students in Evolutionary Biology) Date: 25-30 September, 2012 Location: Finland

REGISTRATION IS NOW OPEN for the 18th European Meeting of PhD Students in Evolutionary Biology (EMPSEB 18), which takes place from 25-30 September 2012 in Virrat, Finland. The event aims to bring together PhD students studying Evolutionary Biology to let them present their research, get feedback from top scientists in the field, and develop collaborations with their peers. There will also be a special symposium (speaker and discussion) about ethics in science.

Registration will close 30 April 2012. More information is available at www.empseb18.com. Students will be able to apply for travel grants.

Confirmed plenary speakers include:

Frank Ryan (University of Sheffield- United Kingdom) Martine Maan (University of Groningen- Netherlands) Mikael Fortelius (University of Helsinki- Finland) Hanna Kokko (Australia National University- Australia) Marc Johnson (University of Toronto at Mississauga- Canada) Thomas Flatt (University of

Veterinary Medicine Vienna- Austria) Craig Primmer (University of Turku- Finland) Leena Lindström (University of Jyväskylä- Finland) Naomi Pierce (Harvard University- United States)

Organization committee: Robert Hegna, Ossi Nokelainen, Philipp Lehmann, Venera Tyukmaeva, Gaia Francini, Janne Valkonen, Veronica Chevasco, Aapo Kahilainen and Anni-Maria Örmälä

Robert Hegna EMPSEB 18 University of Jyväskylä Dept. of Biology & Env. Science FINLAND
www.empseb18.com president@empseb18.com

GradStudentPositions

Berlin 5 SpeciationGenomics

Job offer

The newly formed research network "GENART-Functional Genomics of Speciation" investigates the genetic and molecular mechanisms leading to speciation by premating reproductive isolation. In depth behavioural analysis of male courtship signals and female preferences will be linked with genomic data on DNA sequence polymorphisms and gene expression levels by association studies in three animal taxa (acoustically communicating grasshoppers and crickets as well as weakly electric fish). The network GENART announces six open positions:

one POSTDOCTORAL RESEARCHER IN GE-

NOMICS/BIOINFORMATICS (code 08/2012), one PhD POSITION IN GENOMICS/BIOINFORMATICS (code 09/2012), three PhD POSITIONS IN THE FIELD OF ANIMAL BEHAVIOR (code 10/2012) and one LABORATORY TECHNICIAN IN MOLECULAR GENETICS/GENOMICS (code 11/2012)

All six positions are funded for three years and are available from July 1st, 2012.

We are looking for highly motivated candidates that preferably have a solid background in the specific duties of the different positions such as animal behaviour, evolutionary biology and genetics/genomics/bioinformatics. For the successful applicant in the fish project (one PhD position), proven expertise in breeding of electric fish is desired.

The network's principal investigators have a strong research backgrounds in behavioural physiology, evolutionary biology, genomics and bioinformatics and are affiliated with the Museum für Naturkunde - Leibniz Institute for Research on Evolution and Biodiversity at the Humboldt University Berlin (PD Dr. Frieder Mayer), the Institute of Biology of the Humboldt University Berlin (Professor Bernd Ronacher, Professor Matthias Hennig), the University of Potsdam (Professor Ralph Tiedemann), the Berlin Center for Genomics in Biodiversity Research (Dr. Camila Mazzoni) and the Max Delbrück Center for Molecular Medicine (Dr. Christoph Dieterich). All institutions are equal opportunity employers.

The network is located in the national capital area of Germany comprising the cities of Berlin and Potsdam, which provide a unique scientifically and culturally vivid environment at moderate living costs.

For further information about the positions, please contact the project coordinator Dr. Frieder Mayer: phone +49 (0)30 2093 8702, e-mail frieder.mayer@mfn-berlin.de.

Applications should include a cover letter, a curriculum vitae including a list of publications and a short description of past research accomplishments and future research ambitions. Please provide names and e-mail addresses of two referees and specify the date you will be available to start the position. Please specify the position (code) you apply for.

Applications (preferably as a single pdf-file) should be sent to recruiting@mfn-berlin.de or to Kaufmännischer Geschäftsführer, Museum für Naturkunde Berlin, Invalidenstrasse 43, D-10115 Berlin, Germany. The review process will start on April 15th, 2012. It cannot be guaranteed that applications received thereafter are considered. Printed applications are not sent back. Therefore, only copies should be submitted.

PD Dr. Frieder Mayer Museum für Naturkunde Leibniz-Institut für Evolutions- und Biodiversitätsforschung Invalidenstraße 43 D-10115 Berlin Tel. +49 (0)30 2093 8702 Fax +49 (0)30 2093 8868

Frieder.Mayer@mfn-berlin.de

CzechRepublic AntEvolution

PHD POSITION IN ANT ECOLOGY

Laboratory of Ecology and Evolution of Social Insects Biology Center, Czech Academy of Sciences is looking for a PhD student for project:

MECHANISMS STRUCTURING ARBOREAL ANT COMMUNITIES IN TROPICAL FORESTS

We are looking for a motivated student to join our research team focused on ecology of tropical insects and plants (V. Novotn. Basset group). The PhD candidate will study ecology and diversity of ants of New Guinea. He/she will participate on processing of unique material and datasets from one of the last unknown frontiers rain forest canopies. She/he will combine traditional taxonomic methods with molecular tools (barcoding, species phylogeny) and analyse ecological community data. He/she will work on available material and have opportunity to conduct research at our field stations in Papua New Guinea.

We offer 4 years scholarship at PhD program at Faculty of Science, University of South Bohemia (http://www.prf.jcu.cz/en/) and grant contract (50% position) at Biology Center, Czech Academy of Sciences (http://www.entu.cas.cz/en/). All research costs are fully covered. The scholarship including salary (~7000 annually) is highly sufficient to cover all living expenses in the Czech Republic.

Starting date for the position is flexible between April and September 2012.

Requirements:

Master degree (or equivalent) in biology & environmental sciences enthusiasm for the topic and motivation to learn new things analytical experience with R and/or other statistical packages fluent English and ability to communicate within an international team

We offer:

participation in cuttingedge tropical ecology research access to unique ecological and biological data and original research topics opportunity to learn novel methods combination of lab and field work

Candidates should send a statement of interest, a CV, and support letters from two referees to Dr. PETR KLIMEÅ: peta.klimes@gmail.com. Deadline for applications is 1st April.

For further information do not hesitate to contact:

Petr KlimeÅ, Biology Center, Czech Academy of Sciences Branisovska 31, 370 05, Ceske Budejovice, Czech Republic, Ph.N. + 420 387 775 332 Information sources: www.newguineants.org, www.entu.cas.cz/png/research.htm

– Tom Fayle

Laboratory of Tropical Ecology University of South Bohemia Branisovka 31 370 05 Ceske Budejovice Czech Republic

Forest Ecology and Conservation Group Imperial College London Silwood Park Campus Buckhurst Road, Ascot Berkshire SL5 7PY, UK

Tel: +44 (0)7816 092365 / +420 777083800 Email: t.fayle@imperial.ac.uk Web: www.tomfayle.com Recent publication: Optimising diversity assessment protocols for high canopy ants in tropical rain forest (2012). Biotropica 44: 73-81.

Key to the ant genera of Borneo in Malay and English: http://www.tomfayle.com/research%20link.htm Tom Fayle <tom_fayle@hotmail.com>

EasternKentuckyU InvertDiversity

MS Opportunity, Freshwater Invertebrate Diversity, Eastern Kentucky University

I am seeking one or two MS degree seeking students to join my lab at Eastern Kentucky University, Department of Biological Sciences in the Fall of 2012. Specific project topic is flexible but will focus on exploring ecology and conservation of freshwater invertebrates using next generation sequencing techniques. Opportunities for some field and lab work exist but the main focus will be in bioinformatics.

Required qualifications: Bachelor's degree in biology or related field. Some computer programming experience (e.g. Perl) or other bioinformatics experience.

Desired (but not required) qualifications: Experience with molecular techniques such as DNA extraction, PCR, or next generation sequencing.

Interested candidates should contact Dr. David M. Hayes (david.hayes@eku.edu) with a CV/resume including relevant experience, GPA, and GRE scores. Information about our program may be found on the Department of Biological Science's website (http://www.biology.eku.edu/master-science-biology). Applications are due by March 15 to be considered for a departmental assistantship.

"Hayes, David" <David.Hayes@eku.edu>

ETH Zurich TrypanosomeEvolDynamics

The Institute of Integrative Biology at ETH Zurich - Experimental Ecology Group - is offering a PhD position

"Trypanosome parasitism: ecology and evolutionary dynamics"

The project is flexible but a first aim is to use current methods study the genetic epidemiology and effect of host defences. Our study system involves Bombus spp. on the host side and the trypanosome, Crithidia, as the infectious disease. We seek to understand some principles that govern the dynamics and adaptive processes in this model host-parasite system. The anticipated project is part of an ERC Advanced Grant on alternative host resistance systems and the population structure of parasites. We look for candidates that are interested in challenging ecological and evolutionary questions and who are willing to explore new methodical tools for this purpose. A successful candidate may have some experience, for example, in molecular or population genetics, the use of gene data banks, or be familiar with the analysis of adaptation. The project will be embedded in a small, active research group with long-term experience of the system.

Starting date is negotiable, but ideally no later than autumn 2012. Please send applications (CV, Publication list, Names and emails of referees) by email to Prof. Paul Schmid-Hempel (psh@env.ethz.ch), ETH Zurich, Institute of Integrative Biology, ETH-Zentrum CHN, CH- 8092 Zurich (review of application starts 15 April 2012 until filled). Further information on ETH, the group, or life in Zurich can, for example, be obtained from www.eco.ethz.ch paul.schmid-hempel@env.ethz.ch

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Frankfurt InvertebrateEvolution

The Department of Phylogeny and Systematics (Institute for Ecology, Evolution and Diversity) at Goethe-University Frankfurt am Main, Germany, invites applications for a

PhD position (EG 13 TV-G-U, 50%, ˜ £á 12.000 V 13.000 netto per annum).

The position is limited to three years and will start as soon as possible.

Our group focuses on molecular systematics, phylogenetics and evolution of invertebrates. Recently strong emphasis is laid upon questions relating to the correlation between past climate changes and diversification. We are part of the Biodiversity and Climate Research Centre and in close collaboration with various researchers in this centre.

We are looking for a highly motivated biologist with a strong research focus in phylogenetics and/or evolutionary biology of invertebrates. An MSc. degree in Biology is required. The successful applicant will work on gastropod phylogeny and evolution with special emphasis on Pulmonata. Evolutionary questions like the transition from marine to terrestrial habitats shall be addressed. Solid methodological expertise in molecular phylogenetic techniques (including lab work and phylogenetic inference methods) is required. Knowledge of genomics is advantageous. Additionally taxonomic knowledge of Gastropoda is desirable.

The candidate will be involved in teaching activities of the Department of Phylogeny and Systematics at bachelors and masters degree. Therefore a solid knowledge of the German language is required (fluency in German, writing and speaking).

Please send your applications until April 11th 2012 to Klussmann-Kolb@bio.uni-frankfurt.de. The application should include a CV, a summary of the master thesis, an outline of the planned PhD project as well as two references of academic supervisors.

Alexander M. Weigand Goethe-University (Biologicum) Institute for Ecology, Evolution and Diversity Dep. Phylogeny and Systematics Max-von-Laue-Str. 13 60438 Frankfurt am Main, Germany

http://www.bio.uni-frankfurt.de/klussmann-kolb/index.htm Member of the Biodiversity and Climate Research Center (BiK-F) http://www.bik-f.de/root/index.php?page_id=285 Empfehlen Sie GMX DSL Ihren Freunden und Bekannten und wir belohnen Sie mit bis zu 50,- Euro! https://freundschaftswerbung.gmx.de WeigandA@gmx.net

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GroningenU MarineMammalGenomics

PhD position in Marine Mammal Evolutionary genomics (1.0 fte) (Reference number 212075)

Organisation

The PhD position is with the Marine Evolution and Conservation (MarECon) group at the Centre for Ecological and Evolutionary Studies (CEES) which is placed with the Faculty of Mathematics and Natural Sciences at the University of Groningen in the Netherlands. The research conducted by the members of MarECon is aimed at the evolution and conservation of pelagic marine organisms, in particular marine mammals. We are interested in those processes that partition genetic variation within those species that inhabit this comparatively open environment. Our primary research approach is population genetics and genomics. The research is conducted with a global network of collaborators who collect data and tissue samples in the field.

Job description

The pinnipeds and cetaceans represent some of the most derived mammal groups. The many convergent features in these two groups provide clear evidence of the strong natural selection the mammal “bauplan” is subjected to when transitioning to a marine existence. The combination of strong convergent evolution in different lineages of mammals constitutes an excellent opportunity to gain insights into the genomic underpinnings of the evolution and adaptation in pinnipeds and cetaceans and the subsequent radiations into different distinct marine habitats.

The objective of this PhD project is to utilize genome enabled methods to identify those traits under past and recent selection in pinnipeds and cetaceans. The research will mainly consist of genome wide-scans in select population samples and subsequent bioinformatics and population genomic analyses of those data. The newly fitted laboratory is situated in the new green building Linneausborg on the Zernike Campus with excellent facilities for this kind of work.

The PhD student will be supervised by Dr. Martine Bérubé and Prof. Per Palsbøll.

Qualifications

We are looking for a highly motivated person with a master's degree in biology or equivalent discipline, with a strong background in empirical and theoretical population genetics. The ideal candidate for this position has good quantitative skills and the ability to conduct bioinformatics analyses of the large amounts of short-read sequence data. Programming skills (or the interest and ability to acquire such) is a necessity. The candidate should be able to work and solve problems independently. Some knowledge of marine mammals is beneficial, but not a prerequisite. It should be noted that the opportunities for fieldwork will be few and brief. A good command of English is required. The candidate will be enrolled in Groningen Graduate School of Science, attend graduate courses within the Research School Ecology and Evolution and participate in our teaching program (10% of time).

Conditions of employment

The University of Groningen offers a salary of EUR 2,042 gross per month in the first year up to a maximum of EUR 2,612 gross per month in the final year. The employment is initially in a temporary position of 1.5 years with possible extension with another 2.5 years provided satisfactory performance during the first year. The PhD candidate will be evaluated after the first year in order to determine the likelihood of the successful completion of the PhD thesis within the following three years. If a successful completion is deemed unlikely, the employment will not be extended. The main objective of the position is to publish research articles in peer-reviewed scientific journals. These publications will form the basis of the doctoral thesis and obtaining the PhD degree (Dr) at the University of Groningen.

Application A full complete application in English consists of a letter describing your personal motivation for applying for this position outlining which skills pertinent to the position you have, past experience as well as a brief explanation what you think the main research questions in evolution and conservation are today for marine mammals. Also make sure to add a complete curriculum vitae along with names and addresses, including telephone/fax and e-mail addresses for three referees.

We would like to receive applications until 15 May 2012, 24:00 CET by means of the application form.

Start date before 1 September 2012.

Information

For information you can contact: Dr. Per Palsboll, p.j.palsboll@rug.nl palsboll@gmail.com

CEES< http://www.rug.nl/fmns-research/cees/index >

Applications should be submitted on-line at http://www.rug.nl/corporate/vacatures/vacaturesRUG(the reference number for this position is 212075) before May 15^th 2012.//

– Per J. Palsboll, Professor

Marine Evolution and Conservation Centre for Ecological and Evolutionary Studies University of Groningen Nijenborgh 7 9747 AG Groningen

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LeidenU FungalBiodiversity

The National Herbarium of the Netherlands at Leiden University in cooperation with the Netherlands Centre for Biodiversity Naturalis (NCB Naturalis) is offering a position for a:

PhD Student on the subject mycology (38 hours per week) Vacancy number: 12-054

Tasks: The diversity and ecology of fungi is one of the foci of the botany department of NCB Naturalis. The arctic tundra, which is on the brink of significant changes due to the climatic changes and growing human impact. Despite their critical roles, fungi are still understudied in arctic ecosystems. The aim of the current PhD project, funded by the Netherlands Organization for Scientific Research (NWO), is to better understand how fungal community composition correlates with vegetation and soil characteristics, and what fungal taxa are expected to play roles in vegetation change and/or the resilience of plant communities to climatic stress.

To achieve this aim the candidate will: * Assess taxonomic and phylogenetic diversity of arctic fungi; * Compare species composition of fungal communities among vegetation types along soil moisture and pH gradients;

* Determine the influence of elevated air and soil temperature on fungal diversity and species composition.

In the current project, the taxonomic focus will be on root-associated fungi, e.g. root endophytes and various mycorrhizal fungi. The envisaged PhD candidate will closely collaborate with another PhD student who is working on the ectomycorrhizal basidiomycetes in the same area.

More information: http://vacatures.leidenuniv.nl/-wetenschappelijk/12-054-phd-mycology.html József Geml, PhD. Assistant Professor National Herbarium of the Netherlands Netherlands Centre for Biodiversity Naturalis Leiden University P.O. Box 9514 2300 RA Leiden The Netherlands

"Geml, J. (József)" <geml@nhn.leidenuniv.nl>

LinkopingU BehaviourVariation

PhD student position in Ethology: Causes and consequences of variation in animal personality

At the Department of Physics, Chemistry and Biology (IFM), Division of Biology. Linköping University, Linköping, Sweden.

Job description A 4-year PhD position is offered in the subject of ethology, to conduct research on the causes and consequences of variation in animal personality. Animal personality is defined as behavioural responses that differ among individuals, but are consistent within individuals across context and/or time. While variation in personality was previously largely ignored, the field has recently experienced considerable attention. We are now aware that, among a diversity of species from insects to humans, individuals show personalities. As a consequence, research on animal personality has become a highly popular research area within animal behaviour. However, the fundamental questions in animal personality remain unanswered, and these are often relevant to key questions in evolutionary biology more generally. For example, what limits behavioural plasticity, why does variation in personality arise, and how is polymorphism maintained?

The aim of the proposed project is to improve our understanding of the evolution of personality using the red junglefowl and domestic chickens as models, by investigating both proximate mechanisms and ultimate consequences of variation. The fowl is a particularly suitable species for research on personality due to the possibility of combining our extensive understanding of behaviour, physiology and genetics in chickens, to apply a strong experimental design while examining natural behaviours. The advertised position can be combined with a teaching assistantship of up to 20% within the biology undergraduate program, which will extend the position accordingly.

Requirements The successful applicant will be a highly motivated and talented candidate with a Masters degree in biology (or equivalent), with a specialization in ethology, behavioural ecology, evolutionary biology or similar. Research experience in experimental animal behaviour, sound statistical knowledge and analytical abilities are merits, as is experience in scientific writing. Good knowledge of written and oral English is required. Both good cooperation skills and the ability to work independently are emphasised. The successful candidate should be enthusiastic about animal behaviour and handling birds.

What we offer Linköping University is a modern, innovative university with over 27000 students and 3900 employees. Biology at Linköping University offers excellent molecular facilities and exceptional avian housing facilities. The successful candidate will be part of the behavioural genomics and physiology group (AVIAN, which currently has around 20 group members, including 9 PhD students), which is a part of the Centre of Excellence for Animal Welfare Science (in collaboration with SLU Uppsala).

Linköping is a popular university city, and is the fifth largest city in Sweden. It is located in central Sweden, just two hours by train from Stockholm, and offers proximity to the beautiful nature of Östergötland, including the great lake Vättern, as well as both recent and pre-historic history, and cultural attractions.

Equal opportunity Linköping University continues to develop as an attractive and creative work place characterized by equal opportunities, which works actively to promote diversity and gender equality.

Starting date 1st of June 2012 or according to agreement.

Salary According to present rates at the university (starting at 24000 SEK per month), including health insurance and other benefits, for 4 full years.

More information Contact Hanne Løvlie (hanne.lovlie@liu.se), tel +46 (0) 13-286681. The trade union representatives are Örjan Lönnevik (SACO), (orjlo@ifm.liu.se), phone +46 (0) 13 286634 and Gabriel Thott (OFR/S), (gabriel.thott@isak.liu.se), tel +46 (0) 11 363171.

Application procedure All applications must be sent directly to Mikael Sundqvist. Material sent to anyone else will not be evaluated. All applications must be clearly marked Dnr IFM-2012-00053. The application should include a 1-2 page cover letter describing your research experience and interests, and your interest in this project, and a full CV (including name and contact details of 2 references who are willing to provide letters of support). Transcript of grades and copy of a relevant publication (e.g. BSc, MSc thesis or article) may be required at a later stage.

The application should be received at the latest 11th of April, 2012:

By e-mail to: work@ifm.liu.se Documents that are sent electronically must be in MS Word (.doc) or Adobe Acrobat (.pdf) format.

Or by mail to: Linköping University IFM Mikael Sundqvist SE-581 83 Linköping SWEDEN

Hanne Løvlie, Assistant professor IFM, Biology AVIAN Behavioural Genomics and Physiology Group Linköping University 58183 Linköping

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Liverpool RIKEN BacterialGenomics

Funded PhD: Single cell bacterial genomics to improve biomass engineering

*Prof. Moriya Ohkuma, RIKEN BioResource Center Dr Toshiya Iida, RIKEN BioResource Center *Dr Alistair Darby, University of Liverpool Prof. Neil Hall, University of Liverpool

* Primary supervisors

There is a need for new sustainable technologies that utilize the biomass of plants to replace the use of petrochemicals and creating new fuels.

Termite guts could hold the key as they are highly efficient 'bioreactors', the symbiotic bacteria harbored in the insects intestine are capable of digesting lignocellulose to short-chain fatty acids. The symbiont community of the termite gut cannot be cultured by conventional methods and are phylogenetic diversity with a complex community structure. Therefore the aim of this project is to apply the rapidly developing techniques of single cell genomics to sequence small groups of bacteria and unlock the enzymatic potential of the termite gut symbiosis for industrial biomass conversion.

Training: This project is funded in partnership with RIKEN, Japan (www.riken.jp/engn/) and the University of Liverpool providing a 4-year PhD studentship to commence from October 2012. The studentship is part of the Liverpool International Graduate Programme and provides an opportunity for the student to spend up to 2 years in the lab of Dr Moriya Ohkuma Wako, Japan. The candidate will receive specific training in molecular biology, developing expertise in using techniques of single cell genomics and a broad training in bioinformatics, including the handling of large data sets and their computational interrogation. The candidate will also get bespoke training from the instrument providers. A broad generic training program is also in place for postgraduate students ranging from Bioinformatics through to intellectual property and business.

Funding Notes:

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Dr Alistair C. Darby

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Marseille DrosophilaEvolutionOdours

PhD Fellowship for a Neurobiology project in Marseille (France): Gompel/Prud'homme lab

In the context of the Initial training Network, FliACT (www.fliact.eu), we are hiring a PhD student to work on the the following project:

Neuronal basis of the evolution of sensitivity to specific odours in Drosophila

Goal: Identifying genetic and neuronal differences underlying variations in olfactory behaviours

Methodology: Different species respond differently to similar sensory stimuli. Variations in the sensory response could be encoded in the sensory neurons and in the sensory receptors expressed in these neurons. In a screen for variations in olfactory receptor (OR) expression between Drosophila species, some species were found to depart from the rest of the survey for expression of given ORs. Preliminary data indicate that these changes in expression are associated with altered sensitivity to the corresponding odour. The project aims at characterizing and quantifying these differences in the neural response and behaviour, and identifying their cellular bases. To this end, the fellow will first make use of classical genetics in D. melanogaster to demonstrate the link between a given OR and a specific odorant compound. Then, to tackle the evolution of olfaction between species with different levels in OR expression, s/he will make reporter constructs with the regulatory regions of such ORs, then test them in different species. This is meant to reveal the molecular origin of the differences in gene expression, and look for possible changes in neuronal anatomy between species. Once the genetics and neuroanatomy of the system are clarified, the next step will be to characterize the functional changes between species. To test for causality between changes in OR expression and changed sensitivity to an odour, s/he will make use of transgenesis in different species, testing OR alleles of one species into the other, and assessing the consequences on neural activity and behavior. S/he will also take advantage of the possibility to make hybrids between some species with different levels of expression in specific ORs. Altogether, the results should identify the molecular and functional changes responsible for the evolution of sensitivity to particular odours.

Nicolas Gompel Institut de Biologie du Développement de Marseille-Luminy CNRS UMR 7288, case 907, Parc scientifique de Luminy 13288 Marseille cedex 9, France Office: + 33 4 91 26 92 06 Fax + 33 4 91 26 97 26 LAB WEBSITE

PLEASE NOTE NEW ADDRESS: nicolas.gompel@univ-amu.fr

Nicolas Gompel <nicolas.gompel@univ-amu.fr>

MaxPlanckInst RavenEvolution

Master thesis: Object exploration and object play in ravens (Corvus corax) We are looking for an enthusiastic student who is interested in investigating object exploration and object play in ravens (Corvus corax) to enable a better understanding of raven's physical and social cognitive skills. Interestingly, especially young individuals show a predisposition to explore and manipulate almost every kind of object they encounter. In addition, ravens often use non-food items in social interactions to attract the attention of recipients. The present study aims to investigate object exploration and object play during ontogeny in six hand-raised ravens by carrying out observations in combination with controlled behavioural experiments. The study will start in June 2012.

We seek a highly motivated person with organizational skills, able and willing to work independently. You will learn to work with six hand-raised ravens, set up the observation schedule, film the behavior and experiments, design and develop a coding scheme and analyze the behavioral interactions.

We offer the opportunity to work at one of the leading institutes for bird research in Germany and Europe and to learn methods in comparative research and behavioural biology.

For further information please contact:

Dr. Simone Pika Max-Planck-Institut für Ornithologie Humboldt Research Group "Comparative Gestural Signalling" Max-Planck-Institut für Ornithologie Eberhard-Gwinner-Str. Gänsehaus D-82319 Seewiesen E-mail: spika@orn.mpg.de Webpage: www.orn.mpg.de/cgs Simone Pika <spika@orn.mpg.de>

MaxPlanck Kiel 10 EvolBiol

The *International**Max-Planck Research School**for Evolutionary Biology* is offering *up to**10 PhD fellowships*.

The graduate school is dedicated to highest level of research and training in all areas of contemporary Evolutionary Biology. It is a joint initiative of the Max Planck Institute for Evolutionary Biology, the University of Kiel and the Helmholtz Center for Ocean Research Kiel (GEOMAR). The school offers an internationally competitive research environment with state of art facilities. The participating groups are working on a broad variety of scientific topics including molecular, behavioral, theoretical and organismal approaches.

The graduate program starts with a rotation period of three months followed by a PhD project of three years including seminars, courses and workshops. The language of the graduate school is English. Financial support is provided throughout the program.

To obtain further information about our PhD program and application details please visit our website at http://imprs.evolbio.mpg.de . Well-motivated and highly-qualified students from all countries are welcome to apply. A Master of Science degree or a Diploma as well as a strong interest in Evolutionary Biology and flexibility in the research project are prerequisites for application. We are looking forward to your application for a PhD fellowship in the beautiful landscape of Northern Germany.

The deadline for applications is April 15, 2012.

The start of the program will be September 17, 2012.

Contact: Dr. Kerstin Mehnert,

August-Thienemann-Str. 2, 24306 Plön, Germany

email: imprs@evolbio.mpg.de +49(0)4522 763 233

The coordinator

Kerstin Mehnert

The steering committee

Diethard Tautz, Hinrich Schulenburg, Manfred Milinski and Thorsten Reusch

Kerstin Mehnert <mehnert@evolbio.mpg.de>

MNH Bergen BeetlePhylogenomics

PhD fellowship in molecular systematics (http://www.jobbnorge.no/job.aspx?jobid=81963)

At the Museum of Natural History, University Museum of Bergen, a position as PhD fellow is available for 3 years in the NFR funded project <A phylogenomic approach to understand the diversification of bark beetles and associated microbes>. The fellow will be associated with the research group Phylogenetic Systematics and Evolution at the museum (http://www.uib.no/rg/fse).

The research will focus on screening new molecular markers for the phylogenetic analysis of weevils, with particular focus on large scale molecular phylogenetics of bark and ambrosia beetles. Phylogenies will be used for comparative analyses of host plant preferences, fungus symbiosis, and the evolution of reproductive systems in these beetles. In this work, the PhD fellow will work in team together with project advisor, project partners at Michigan State University and University of Florida, during the project, and one postdoctoral fellow in the second half of the project.

Applicants must hold a master- / cand.scient.-degree in evolutionary biology, with relevance to biosystematics. The master's degree must be completed by the application deadline. It is preferable with experience in molecular methods applied to biosystematics. Further criteria in the evaluation process included the applicant's ability to work independently and in team, study progression, grades from MSc thesis work and other relevant evolutionary biology subjects, and scientific authorship.

The research fellows must take part in the University's approved PhD program leading to the degree within a time limit of 3 years. Hence, applicants must meet the formal admission requirements for the PhD program. Application for admission to the PhD study, including progress plan for education and research will be made together with the project advisor. The PhD fellow will become a member of the Norwegian-Swedish research school in Biosystematics (http://www.forbio.uio.no). Expected starting date is July 2012.

Starting salaries at salary level 48 (code 1017) on the government salary scale (corresponding to NOK 383.900 per year, following ordinary meriting regulations.

Additional information on the position is obtainable from associate professor Bjarte Jordal (PI), phone +47 55 58 2233, e-mail: bjarte.jordal@um.uib.no

State employment shall reflect the multiplicity of the population at large to the highest possible degree. The University of Bergen has therefore adopted a personnel policy objective to ensure that we achieve a balanced age and sex composition and recruitment of persons of various ethnic backgrounds. Persons of different ethnic backgrounds are therefore encouraged to apply for the position.

The University of Bergen applies the principle of enhanced access to information when hiring for academic positions.

The successful applicant must comply with the guidelines that apply to the position at any time.

The application must include a complete review of education and professional experience with copies of exams and certificates and scientific works including a list of publications (All in three copies, sorted in three identical bundles).

The application should be sent to: The University Museum of Bergen, Post Box 7800, N-5020 Bergen, Norway, latest by 11.April

In addition an application including an application letter and CV must be sent electronically to the University of Bergen using www.jobbnorge.no . Application deadline: 11th of April 2012

The application must be marked: 12/2632

Bjarte Henry Jordal <Bjarte.Jordal@um.uib.no>

MNHN Paris AdaptiveVariation

PhD proposal in Paris on the Origin and persistence of adaptive variation in heterogeneous environment.

We just obtained a grant from the LABEX BCDiv to finance a PhD at the National Museum of Natural History in Paris (France) on the topic ≪ Origin and persistence of adaptive variation in heterogeneous environment ≫. This PhD thesis will be supervised by Violaine Llaurens (junior CNRS researcher in the unit 7205 entitled Origin, Structure and Evolution of Biodiversity) and Marc Théry (senior CNRS researcher in the unit 7179 entitled Adaptive Mechanisms: from Organisms to Communities).

The starting date will be October 1st, 2012. The PhD consists in a 3- years fixed term contract with the CNRS with 21 000 per annum gross salary. The shortlisted candidates will be interviewed in May 2012.

We are looking for a dynamic and motivated student to perform this PhD. Fluency in French is not requested. If you wish to apply, please send us the following documents before April, 18th 2012 by email (llaurens@mnhn.fr and thery@mnhn.fr):

- A detailed CV, including your previous research experience and the marks or ranking obtained for your Master's degree (or equivalent diploma),

- A cover letter, stating in particular the match between your profile and the PhD project,

- Two reference letters to be sent directly to us by email.

Abstract of the PhD project:

Understanding the origin and persistence of diversity within and among species in a central question in evolutionary biology. Genetic dominance among variants in a population plays a key role in the invasion success of new adaptive traits.

This Phd project focuses on the distribution of morphological and genetic variation of mimic patterns in neotropical butterflies from the genus Heliconius. In these species, many species exhibit a mutual adaptive resemblance. This convergence so called mimicry constitutes an aposematic signal of their unpalatability, which can be learned by predators. Several mimicry rings coexist in a given habitat and some polymorphic species are involved in few distinct mimicry rings. These polymorphic species constitute an ideal model to understand how new adaptive traits can be established and can be favored by selection.

In this context, since the level of dominance is modifying the expression of different variants, it had an influence on their resemblance to the mimic patterns. Hence the origin and persistence of new variants depends both on dominance and discrimination capacities of predators. We thus aimed at jointly investigating how the variation is genetically controlled in the polymorphic species Heliconius numata and how predators can perceive this variation.

Few selected publications of the supervisors linked to this PhD project:

- Théry M., Gomez D. 2010 Insect colors and visual appearance in the eyes of their predators. Advances in Insect Physiology. 38: 267-353.

- Gomez D., Richardson C., Lengagne T., Plenet S., Joly P., Léna J.-P., Théry M. 2009 The role of nocturnal vision in mate choice: females prefer conspicuous males in the European tree frog (Hyla arborea). Proceedings of the Royal Society B, 276: 2351-2358.

- Llaurens V., Billiard S., Castric V., Vekemans X., 2009. Evolution of dominance in sporophytic self-incompatibility systems: I. Genetic load and coevolution of levels of dominance in pollen and pistil. Evolution, 63: 2427-2437.

- Llaurens V., Leducq J.-B., Billiard S., Castric V., Klein E.K., Vekemans X., 2008. Does frequency-dependent selection with complex dominance interactions accurately predict allelic frequencies at the self-incompatibility locus in Arabidopsis halleri? Evolution, 62: 2545-2557.

WEB pages :

http://www.mnhn.fr/oseb/Violaine-LLAURENS http://www.mabiodiv.cnrs.fr/RubriquesEnAnglais/-IndividualFiles/Thery_File.html Violaine Llaurens (CR2 CNRS) Museum National d'Histoire Naturelle Laboratoire OSEB UMR7205 Batiment d'entomologie CP50 45, rue Buffon 75005 PARIS France

Phone : 00 33 (0)1 40 79 38 61 Fax : 00 33 (0)1 40 79 33 42

WebPage: http://www.mnhn.fr/oseb/Nouvelle-traduction-Violaine Violaine Llaurens <llaurens@mnhn.fr>

MonashU BirdAdaptation

PhD studentship available at Monash University, Melbourne, Australia Project title: Are human-induced changes in visual environment affecting bird signaling and camouflage? Supervised by Dr. Kaspar Delhey, as part of a DECRA project (DE120102323) awarded by the Australian Research Council (ARC). The project will assess the effect of habitat degradation due to human disturbances of the visual environment on signalling and camouflage of Australian woodland birds. This project will combine work from museum collections with field-work in the box-ironbark woodlands of Victoria, south-east Australia. The candidate will measure coloration of bird specimens and their natural backgrounds using a combination of UV/VIS digital photography and spectrometry, and analyse these data in the context of current psychophysical models of avian colour vision. Strong quantitative skills are highly desirable and familiarity with the methods of colour measurement and the R statistical environment would be very advantageous. Starting date: Mid 2012 Duration: three years

Send inquiries and applications (consisting of expressions of interest and a CV detailing relevant experience, publication list, academic grades and names and contact details of two-three referees) to Kaspar Delhey (E-mail: kaspar.delhey@monash.edu , web: https://-sites.google.com/site/kaspardelhey/). Applications

will be reviewed from March 2012 until the position is filled.

– Kaspar Delhey e-mail: kaspar.delhey@monash.edu https://sites.google.com/site/kaspardelhey/ Tel:+61-(0)3-99020377 Bldg.18 School of Biological Sciences Monash University Clayton, 3800 Victoria Australia

Montpellier EvolutionOfRecombination

Dear members,

May I draw your attention on the URGENT possibility of applying an international call for PhD fellowships launched by the EpiGenMed Labex (Laboratory of Excellence) in Montpellier, France:

http://www.epigenmed.fr/ Although the Labex is molecular biology oriented, interdisciplinarity is strongly encouraged and at least one of the subjects in competition is at the interface between molecular biology, evolution and bioinformatics, as described here:

http://sympasrv.univ-montp2.fr/sympa/-d_read/evolfrance/offres_emplois/-BdMEpiGenMed_PhD_2012.pdf

The application procedure is very simple, but the DEADLINE IS MARCH 30!

See the Labex site to apply. Contact me concerning the subject, <pierre.boursot@univ-montp2.fr>

Best,

Dr. Pierre BOURSOT Institut des Sciences de l'Evolution (UM2-CNRS UMR 5554) Universite Montpellier 2 Case Courrier 063 34095 Montpellier cedex 5 FRANCE tel: +33 (0)4 67 14 46 86 fax: +33 (0)4 67 14 45 54 Email: Pierre.Boursot@univ-montp2.fr

Pierre Boursot <Pierre.Boursot@univ-montp2.fr>

MPI CE Germany PlantComparativeGenomics

Department of Molecular Ecology in Max Plank Institute for Chemical Ecology is offering a PhD position on comparative genomics.

The department information can be found here:

http://www.ice.mpg.de/ext/molecular-ecology.html?&L=

The research in our department focuses on the ecological function and their molecular mechanisms of ecologically important traits in /Nicotiana attenuata/, a diploid annual tobacco plant (2n=2x$) native to Western North America. This plant initiates growth in a post-fire environment in response to water-soluble chemical cues in wood smoke, and evolved sophisticated herbivore induced defense strategies and remarkable phenotypic plasticity, which have been intensively investigated in our department during the last twenty years by elegant integrative approaches of reverse genetics, molecular biology, chemical ecology and field work. In this project we will take the advantages of next generation sequencing technology and comparative genomic approaches to study genome evolution and genetic basis of ecologically important traits in plant.

Max Plank Institute for Chemical Ecology is one of the world's leading research institutes in chemical ecology, providing excellent research atmosphere and PhD training programs. In addition, the institute is situated at the Beutenberg Campus in Jena Germany, which guarantees close proximity to other biological, medical, physical and chemical institutes and offers an excellent base for scientific co-operations and the establishment of several networks across Europe and the world.

We are looking for a highly motivated candidate with a solid background in bioinformatics, genomics, and genetics. A master degree and computer programming skills are required for this position. Interests in evolutionary biology and / or plant biology will be considered as a plus.

Closing date for application: 1^st May 2012.

If you are interested in this position, please send us a CV and an application letter that explains your research interests and scientific experience to Dr. Shuqing Xu (sxu@ice.mpg.de).

Further information of our institute and department can be found in our institute website, http://www.ice.mpg.de/ext/.If you have any questions, please feel free to contact Dr. Shuqing Xu sxu@ice.mpg.de

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Department of Molecular Ecology Max Planck Institute for Chemical Ecology Hans-Knöll-Straße 8 D-07745 Jena Germany E-mail: sxu@ice.mpg.de Phone:+49 (0)3641 57 1121

sxu@ice.mpg.de

NewZealand Insect Genomics

Genome evolution, speciation and molecular population genetics of stick insects

Supervisor: Associate Professor Thomas Buckley Co-supervisors: Associate Professor Richard Newcomb, Dr Howard Ross

Next generation DNA sequencing and analysis of whole genomes has opened new possibilities for testing fundamental questions in speciation and adaptation. The successful candidate for this PhD project will generate a draft genome sequence for a New Zealand stick insect (Clitarchus hookeri) and use this as a tool for exploring detailed questions on adaptation within a species and between closely related species. The common stick insect (Clitarchus hookeri) is widespread through much of New Zealand. This species is particularly interesting at it is a geographic parthenogen and has hybridized with closely related species. The successful candidate will perform Illumina sequencing and assemble and annotate a draft genome. This draft genome will be used as a scaffold for RAD-tag studies of SNP variation within C. hookeri and among closely related species. Transcriptome data will also be collected and mapped to the draft genome to obtain candidate genes underlying phenotypic traits for further studies on selection and adaptation. Variation at candidate genes will be measured and compared within and among populations of C. hookeri and among related species. The successful candidate should have experience in molecular evolution and genomics with an interest in developing skills in the assembly and analysis of Next Generation DNA sequence data. This project is funded by the Allan Wilson Centre for Molecular Ecology and Evolution and includes a $25,000 NZD per year scholarship, $5,000 for tuition fees, and funding for international travel.

For more information and host institutions and supervisors' research interests see the following links:

Associate Professor Thomas Buckley http://www.landcareresearch.co.nz/research/staff_page.asp?staff_num=1110 http://www.bioscienceresearch.co.nz/staff/thomas_buckley/ Associate Professor Richard Newcomb http://www.bioscienceresearch.co.nz/staff/richard-newcomb/ Dr Howard Ross http://www.bioscienceresearch.co.nz/staff/howard-ross/ To apply for this position please contact Thomas

Buckley at the email address below. Potential candidates should submit a CV, two references, and a short statement of research interests to:

Thomas Buckley (buckleyt@landcareresearch.co.nz)

Thomas Buckley Research Group Leader, Landcare Research Associate Professor, University of Auckland Principal Investigator, Allan Wilson Centre for Molecular Ecology & Evolution

Tel: (+64 9) 574 4116 | Fax: (+64 9) 574 4101 | Email: buckleyt@landcareresearch.co.nz

Post: Private Bag 92170, Auckland, New Zealand | Web: http://www.landcareresearch.co.nz/-research/staff_page.asp?staff_num=1110 BuckleyT@landcareresearch.co.nz

NHM Denmark SystematicBotany

PhD Fellowship in Systematic Botany at the Natural History Museum of Denmark

A fully funded PhD fellowship on phylogenetics of tribe Cinchoneae (Rubiaceae) is available from 01-05-2012 or soon thereafter in the Botany group at the Natural History Museum of Denmark, Faculty of Science, University of Copenhagen, Denmark.

The fellowship will be an integral part of an interdisciplinary 3-year research project entitled: “The quest for Cinchona - a phylogenetic tale” co-financed by the Faculty of Science, University of Copenhagen and the Carlsbergfoundation. The research project is international and includes several collaborators in Denmark, Sweden and Latin America.

Project area The PhD student will be conducting extensive fieldwork with local collaborators in Latin America (e.g. Peru, Ecuador, Colombia) to collect material of Rubiaceae tribe Cinchoneae. The project will include DNA-sequencing and phylogenetic analyses of tribe Cinchoneae. The phylogeny of tribe Cinchoneae will be used to address various questions within the larger project exploring the quest for Cinchona such as diversification, correlation with plant defensive chemistry, biogeography of the Andes, population genetics, taxonomy etc. depending on the development of the project and the student’s background and interests.

Primary supervisor is Associate Professor Nina Rønsted, The Natural History Museum of Denmark. Co-supervisors are Alexandre Antonelli, Gothenburg Botanical Garden, and Claes Persson, Gothenburg University (Sweden).

The applicant must be prepared for extensive periods of fieldwork in Latin America (e.g. Peru, Ecuador, Colombia) and research exchange at Gothenburg Botanical Garden and Gothenburg University (Sweden) is envisioned.

Qualifications a) MSc in biology or related area, preferably with a strong background in systematic botany. b) Tropical field experience (botanical collection) is an advantage. c) Experience with molecular techniques (DNA sequencing) and phylogenetic analysis is an advantage. e) Ability to independently run research projects, in particular in the field away from day-to-day supervision. f) Excellent English speaking, reading and writing skills are required. g) Spanish speaking and reading is an advantage due to extensive fieldwork in Latin America.

Place of employment and principal place of work Botanic Garden and Museum, Natural History Museum of Denmark, Sølvgade 83, Opg. S, DK-1307 Copenhagen.

Terms of employment The successful PhD candidate will be offered a full-time Ph.D. position for a period of three years, contingent on a satisfactory performance, with the specific intent that it results in a Ph.D. degree and scientific publications. It is a prerequisite for the appointment as a Ph.D.-fellow, that the person concerned can be registered as a Ph.D. fellow according to the Ministry of Science, Technology and Innovation Executive Order no 18 of 14. January 2008. Information about the Ph.D. programs at the Faculty of Science can be found at http://www.science.ku.dk/phd/ . The salary depends on seniority, as agreed between the Ministry of Finance and the Danish Confederation of Professional Associations within the range of 23,000-30,000 DKK/month (approximately 3,100-4,000 Euro/month).

Further information can be obtained from Associate Professor Nina Rønsted (e-mail: nronsted@snm.ku.dk). General information on the botany group and the Natural History Museum of Denmark can be found at www.snm.ku.dk . How to apply Applications must include (i) a motivation for the application with statement of your research interests (0.5 A4 page), (ii) curriculum vitae (maximum 2 pages), (iii) list of publications, (iv) a copy of MSc diploma and grade transcript, (v) a short abstract of the M.Sc. thesis or equivalent, and (vi) the names, e-mails, telephone numbers and addresses of 2-3 referees.

The main criterion for selection will be the research potential of the applicant and match with the project. In addition, fulfillment of the above mentioned qualifications will be an advantage.

Applications should be sent electronically by using the link below.

Deadline for applications is 01-04-2012. Applications received after the deadline will not be considered.

The University of Copenhagen wishes to reflect the diversity of society and welcomes applications from all qualified candidates regardless of personal background.

Apply online at http://www.ku.dk/english/-available_positions/vip/ Nina Rønsted <NRonsted@snm.ku.dk>

NottinghamTrentU YersiniaEvolution

Vice Chancellor's PhD Studentships - School of Science and Technology

PhD Studentship in Determining the impact of recombination on Yersinia enterocolitica evolution

A previously funded Vice Chancellor studentship has led to the creation of a comprehensive genome data set for Y. enterocolitica, from which the evolution of this pathogen has been extensively characterised. However, the role of recombination in this evolutionary process is still unclear. This project will utilise novel phylogenetic methods developed by Professor Mark Achtman to unravel recombination signatures in the phylogeny, and assist in a clearer picture of the molecular epidemiology of Y. enterocolitica human infection.

Entry requirement The minimum qualification for entry is a First or Upper Second Class Honours degree (or equivalent) or an MSc / MRes with merit or distinction in a biological discipline with heavy bioinformatics or computational biology content or a related discipline.

Award The studentships will pay UK / EU fees and provide a maintenance stipend linked to the RCUK rate (currently £13,590 per annum) for up to three years. Applications from non-EU students are welcome, but a successful candidate would be responsible for paying the difference between non-EU and UK / EU fees. (Fees for 2011 / 12 are £10,950 for non-EU students and £3,732 for UK / EU students.)

Eligibility Applications can be accepted from UK / EU and also International students. The minimum English language proficiency requirement for candidates who have not undertaken a higher degree at a UK HE institution is IELTS 6.5 or TOEFL 560 / iBT 94 - 95.

Applying For informal enquiries about the studentship, please email Dr Alan McNally <alan.mcnally@ntu.ac.uk>.

Get more information and download an application pack < http://www.ntu.ac.uk/apps/ResearchForms/-UI/pages/researchdegreeenquiry.aspx?syssection=1 > or telephone +44 (0)115 848 6321.

Please return completed application forms, with copies of academic certificates, via email to the School <gradschool@ntu.ac.uk>.

The closing date for receipt of completed application forms is Friday 23 March 2012 at 9 am. Application by CV only will not be accepted.

Dr Alan McNally Senior lecturer molecular microbiology Nottingham Trent University Clifton Lane Nottingham NG11 8NS 0115 8483324

"Mcnally, Alan" <alan.mcnally@ntu.ac.uk>

OxfordBrookesU HybridZones

Applications are invited for the following PhD project:

Genetic and geographical characterisation of the Ceratophyllus styx styx and C.s. jordani (sand martin flea) hybrid zone.

A hybrid zone between subspecies of the sand martin flea Ceratophyllus styx was mapped previously across central England but since the 1990s the sand martin host has arrived significantly earlier in the spring. The flea subspecies differ in morphology of the external mating structures in males and females and overwinter as pupae in nest holes, emerging when disturbed by returning birds, suggesting possible mechanisms for maintaining the hybrid zone. Using combined approaches of morphology and molecular genetics this project will investigate whether the location and structure of hybrid zone has been influenced by changes in host phenology and behaviour. Specifically the project will use the following strategies: 1. Extensive field sampling and precision mapping of the hybrid zone of the sand martin flea using morphological criteria and comparison of the subspecies' ranges for fleas from recent and long-established sand martin colonies. 2. DNA sequencing to genotype populations of sand martin fleas from recent and long-established sand martin colonies along a north-south transect including single subspecies populations and putative mixed/hybrid populations allowing a genetic characterisation of the two subspecies and estimating levels of divergence versus introgression along the transect. 3. DNA sequencing of sand martins to ascertain if there is a genetic population structure that parallels the distributions of the flea subspecies and sand martin breeding records. In addition to these core aims we would allow the student some license to roam, which may include some of the following: 4. Comparative study of the hybrid zone between the Scandinavian subspecies C.s.freyi and C.s.styx. 5.Behavioural/ecological studies of flea mating within and between subspecies and sand martin movement patterns.

The student will be based in the Department of Biological and Medical Sciences, Oxford Brookes University and supervised by Dr Bruce Riddoch, Dr Casper Breuker and Dr Alistair McGregor.

We are looking for a student who is robust and adaptable, with a full driving license and good interpersonal skills (required for access to sand martin colonies), a sound knowledge of evolutionary biology and competence in both lab and field. We will provide specialist training.

Further information on the project please e-mail: Dr Bruce J Riddoch - e-mail briddoch@brookes.ac.uk

Further details can also be viewed through findaphd

The official stuff:

Eligibility: Applicants require a good Honours degree (minimum 2.1 or equivalent) and have been educated to degree level equivalent to a UK degree which was taught in English in a majority English speaking country or a valid IELTS Test certificate minimum score level 6 in each of the four areas of reading, writing, listening and speaking with overall minimum score 7.0 or equivalent. Home, EU and international students are eligible

Start date week beginning 17th September 2012

Value p.a.: Bursary of £13,590 for 2012/13 & fees

Closing Date: 30th March 2012 with interviews in April Applications will only be accepted by post and not by email Please complete the Faculty of Health and Life Sciences PhD Research Studentship Application Form which you should download from the following site;- http://www.hls.brookes.ac.uk/images/docs/research/-studentship-application-form.doc You will also need to ask for references from two academic Referees. Please download form from http://bms.brookes.ac.uk/-research/studentships/docs/referee-form.doc Please post to Mr Phil Voysey Research Administrator Faculty of Health and Life Sciences Oxford Brookes University Headington Oxford OX3 0BP UK Please email Phil Voysey pjvoysey@brookes.ac.uk or telephone +44 (0)1865 482904 with any administrative queries.

p0075759@brookes.ac.uk

TexasStateU SanMarcos PlantEvolution

PhD and Masters Student Positions Available, beginning Spring 2012:

A PhD and/or Masters (Thesis) student position is available for a full-time student interested in studying the evolutionary and ecological processes that lead to speciation in plants. The candidate will work with Dr. Noland Martin on National Science Foundation - funded projects examining the genetic architecture of speciation / reproductive isolation in Louisiana Iris, as well as conservation-oriented projects examining the origin (and continued persistence) of the endangered homoploid hybrid species Iris nelsonii (funded by the Louisiana Dept. of Wildlife and Fisheries). Research areas may include QTL mapping projects that examine the genetic architecture of reproductive barriers in Louisiana Iris. In addition, the student will be required to develop and execute independent research projects (with guidance / assistance from Dr. Martin) to complete the thesis/dissertation requirements. The position starts as early as June 2012. Funding for this project is provided by a renewable 9-month teaching assistantship at $10,000 +/- plus benefits for Masters-level students, and ~ $30,000 +/- plus benefits for PhD-level students with the potential for an augmented 3-month summer salary should the student be performing satisfactory work and external funds remain available.

Texas State University - Dept. of Biology offers a strong environment in population ecology, population biology, wildlife, and conservation biology. Candidates are invited to apply to a variety of MS programs (http://www.bio.txstate.edu/graduate.html) including a MS in Biology and a MS in Population and Conservation Biology, or the PhD program (http://-www.aquaticresources.bio.txstate.edu/) in Aquatic Resources.

Qualifications: Requirements for MS and PhD candidates include an interest in evolutionary biology, a valid drivers license, and the physical ability to traverse rugged swamp terrain. PhD candidates must have completed a Masters degree in Biology (or a closely related field) or have a demonstrated academic writing ability.

Preference will be given to candidates with laboratory and/or field experience. Interested persons should contact Noland Martin by e-mail (nm14@txstate.edu). To apply, please send a statement of interest, a CV, relevant coursework, GPA, and GRE scores to nm14@txstate.edu. Reference letters will be solicited at a later date. Deadline: May 15 or until position(s) filled. Applications will be reviewed as they come in. A more detailed description of the research program and further information about our team's research are available by e-mailing Noland Martin as well.

Noland H. Martin Texas State University - San Marcos

nm14@txstate.edu

TrentinoItaly GrapevineDiversity

Deadline for applications is March 23, 2012.

GENOMIC DISSECTION OF DOMESTICATION TRAITS IN GRAPEVINE

This position is offered by Edmund Mach Foundation (Italy) within the International PhD Program in Genomics and Molecular Physiology of Fruits (GMPF). The fellow will receive a salary of 20000 Euro per year (taxable). The funding is provided for 3 years with the possibility of a one-year extension.

The PhD student involved in this project will exploit the diversity of agronomically important traits in domesticated and wild grapes (Vitis vinifera subsp. sativa and Vitis vinifera subsp. sylvestris) to accelerate the development of new varieties through marker-assisted breeding. The Eurasian grape is the most widely cultivated and economically important fruit crop in the world, but it takes three years to grow this woody perennial from seed to fruit, making traditional breeding long and expensive. Recent studies have shown that although grapes were domesticated up to eight thousand years ago in the Near East, they still have enough genetic diversity to offer potential for developing desirable traits. The domestication of grapevine involved a selection of suitable genotypes producing larger and sweeter berries of attractive colors, followed by their vegetative propagation. Wild sylvestris significantly contributed to the generation of grape cultivars, possibly through multiple introgression events from local populations. A common feature of the cultivated species is the differentiation of genetic diversity relative to the wild species. Such patterns of polymorphism can be investigated by high-throughput sequencing and genomic scans for selection. We propose to study the spread of domestication alleles by collecting genetic information from a diverse sampling of both cultivated and wild grapes. Using these methods the PhD student will hunt for and then characterize the set of candidate genes likely to have experienced selective pressures in the recent past. Understanding this mechanism of accelerated evolution is essential, because of the rising demand for speeding up the development of grape varieties that have the right combination of aroma and taste, and are able to resist diseases, cold and drought.

Applicants holding or expecting a Master degree (or an equivalent degree) in a field relevant to the research undertaken within the GMPF program are invited to submit their application on-line:

http://www.gmpf.eu/eng/Applications/Application-form-GMPF-2012 For further information about the project and selection procedure, please visit the website at http://www.gmpf.eu/eng/PhD-Fellowships/Call grzeskowiak@zi.biologie.uni-muenchen.de

UAdelaide AncientDNA

Adaptation to Climate change/ Genomics/ Ancient DNA

3 year PhD project in Australia and the Yukon Territory, Canada:

A 3 year, ARC funded project is available at the Australian Centre for Ancient DNA, University of Adelaide, Australia. The project will analyse genomic DNA extracted from frozen seeds and bones preserved in Arctic permafrost for over 120,000 years to perform a detailed genomic analysis of how plants and animals respond to pronounced periods of climate change over evolutionary time scales. The project will examine the extent to which, and how, genetic adaptation occurs at a genomic level - and contrast this with the impact and utilisation of range shifts - which is commonly accepted as the primary means of adaptation to climate change. We will use NGS technology to build largescale genome sequences from ancient plants and animals, and apply advanced population genetics analyses to neutral and coding data to perform detailed analyses of how species adapt across time and space. This project promises to provide unique views of the potential of plants and animals to adapt to climate change, and the use of ancient samples to provide detailed views of genomic evolution.

The project will primarily be housed within the Australian Centre for Ancient DNA (http://www.adelaide.edu.au/acad/), located in the School of Earth and Environmental Sciences, University of Adelaide. There will also be an opportunity for fieldwork in permafrost areas of the Yukon Territory. We are looking for a highly motivated individual with wide interests who enjoys challenging and unusual research, and has the ability to work closely with a wide range of researchers, including bioinformaticists, climate change researchers, museum personnel and evolutionary biologists. A strong interest or (preferably) experience with genomics, Next Gen sequencing, or bioinformatics is important. Evidence of independent research and writing/publishing skills would also be essential.

Project partners include Dr Grant Zazula (Yukon Paleontologist), Prof Joe Cook (UNM), and Prof. Charles Davis (Harvard).

Interested Australian and New Zealand residents are encouraged to apply as soon as possible, and competitive international students will also be considered until the end of August.

Contacts:

Project PI: Prof. Eric Dechaine, Western Washington University, http://myweb.facstaff.wwu.edu/~dechaie/, dechainelab@gmail.com

Co-PI: Prof. Alan Cooper, ACAD (http://www.adelaide.edu.au/acad/), University of Adelaide, South Australia, alan.cooper@adelaide.edu.au

alan.cooper@adelaide.edu.au

UCanterbury RNA Bioinformatics

PhD position in evolution and bioinformatics of RNA

University of Canterbury, New Zealand.

There is an open PhD position in bioinformatics, comparative genomics and evolution of noncoding RNAs at the University of Canterbury in New Zealand.

The Bioinformatics and Molecular Evolution team at the School of Biological Sciences (http://www.biol.canterbury.ac.nz/) is a new and dynamic group with a broad range of interests including, bioinformatic characterisation of novel RNA families and RNA pseudogenes, genome annotation and comparative genomics of ncRNAs, RNA evolution, and the analysis of gene expression data.

The University of Canterbury provides a strong interdisciplinary research environment in computational and molecular biology. The successful candidate will be associated with the Biomolecular Interaction Centre (http://www.bic.canterbury.ac.nz/) and the BlueFern supercomputing facility (http://www.bluefern.canterbury.ac.nz/), and we also interact closely with the Biomathematics Research Centre (http://www.math.canterbury.ac.nz/bio/).

Required background: An honours or masters degree in a biological or mathematical discipline such as biochemistry, genetics, molecular biology or evolution, maths, statistics, physics, computer science or equivalent and a demonstrated interest in using computational tools to test biological hypotheses.

Funding: The PhD is jointly funded by the Biomolecular Interaction Centre and BlueFern up to NZ$30,000 (inclusive of fees) per annum for 3 years, depending on the candidate. International PhD students pay tuition fees at the New Zealand domestic rate, provided that the students reside in New Zealand and study under a New Zealand student visa.

Information for international students can be found at: http://www.canterbury.ac.nz/international/ Application procedure: Please email a CV, cover letter and the names of at least two referees to: Dr. Anthony Poole (anthony.poole@canterbury.ac.nz) and Dr. Paul Gardner (paul.gardner@canterbury.ac.nz)

Closing date for applications: 30 March, 2012.

– Dr. Anthony M. Poole RSNZ Rutherford Discovery Fellow & Senior Lecturer School of Biological Sciences University of Canterbury Private Bag 4800, Christchurch 8140, New Zealand

tel. +64 3 364 2987 extn 3863 fax. +64 3 364 2590 http://www.biol.canterbury.ac.nz/people/poole.shtml anthony.poole@canterbury.ac.nz

UCollegeLondon EvolutionaryGenomics

NERC-funded PhD studentship with Professor Francois Balloux in Computational Systems Biology

The effect of population size fluctuations on the rate of evolution

One of the central dogmas of evolutionary genetics states that the rate of evolution at neutral genes (substitution rate) is unaffected by population size fluctuations. However, we have recently shown that this result does not hold in populations with overlapping generations (i.e. populations comprising individuals from different age classes). This result may have important implications for our understanding of the fate of natural populations given that overlapping generations and population size fluctuations are typical in most organisms. Moreover, all - mutations - be they selected or not - are affected by population demography. As such, any regime of population fluctuations could have a dramatic, currently unrecognised, additional genetic impact on the ability of populations to respond to environmental change. It is vitally important to establish the generality of our previous findings and to increase our understanding of the accumulation of resistance in organisms with large amplitude in population fluctuations. Also it is critical to refine our understanding of the ability of declining populations to adapt to changing environmental conditions.

The student will first characterise the effect of demography on substitution rates in realistic population models using analytical approaches in combination with stochastic simulations. The second step of the project will allow the student to test the theoretical predictions using computational analyses of genomic data. We have already in our possession several suitable genomic datasets from species comprising clades/lineages with documented differences in past demography. The final step of the project will be an experimental validation of the effect of population fluctuations on the rate of evolution. Various demographic regimes will be imposed upon lineages of bacteria in an experimental setup of “microchemostats” developed by our collaborator from Biological Engineering at UCL. The genomes of the various lineages having experienced various treatments will be sequenced at the end of the experiment, thus allowing for a direct quantification of the number and nature of the mutations accumulated in the various treatments.

While focused on a well-defined question, the project offers exposure to theoretical, computational and experimental biology and thus represents an ideal training for a student to become a well-rounded biologist. The ideal student would have already acquired a decent quantitative background. However, the most sought-after qualities are enthusiasm, curiosity, creativity and dedication to the project. The project will be supervised by Professor Francois Balloux (Professor of Computational Systems Biology, Dept. of GEE, UCL).

Applicants need to satisfy UK/EU eligibility requirements and have a minimum 2.1 Hons. undergraduate degree. Current annual studentship stipend is £15,590 per annum. Please apply to Prof Balloux by email (Francois Balloux f.balloux@ucl.ac.uk) by the 30 March. Applications should include a CV and the names, contact details and email addresses of two academic referees.

Selection of some recent publications by the Balloux lab

Balloux F, Lehmann L 2012 Substitution rates at neutral genes depend on population size under fluctuating demography and overlapping generations. Evolution 66: 605-611.

Farrer RA, Weinert LA, Bielby J, Garner TWJ, Balloux F, et al. 2011 Multiple emergences of genetically diverse amphibian-infecting chytrids include a globalized hypervirulent recombinant lineage. Proceedings of the National Academy of Sciences of the United States of America 108: 18732-18736.

Rasmussen M, Guo X, Wang Y, (.) Balloux F , et al. 2011 An Aboriginal Australian Genome Reveals Separate Human Dispersals into Asia Science 333: 94-98.

Tanabe K, Mita T, Jombart T, (.) and Balloux F 2010 Plasmodium falciparum accompanied the human expansion out of Africa. Current Biology 14: 1283-1289.

Morelli G, Song Y, Mazzoni CJ, Eppinger M, (.) Balloux F , et al. 2010 Yersinia pestis genome sequencing identifies patterns of global phylogenetic diversity. Nat Genet 42: 1140-1143.

Jombart T, Devillard S and Balloux F 2010 Discriminant analysis of principal components: a new method for the analysis of genetically structured populations BMC Genetics 11: 94.

Balloux F, Lawson-Handley LJ, Jombart T, Liu H and Manica A 2009 Climate shaped the worldwide distribution of human mitochondrial DNA sequence variation. Proceedings B 276: 3447-3455.

f.balloux@ucl.ac.uk

UCollegeLondon NHM 2 EvolBiol

University College London & the Natural History Museum (London)

PhD opportunities in Biodiversity, Ecology & Evolution

Two studentships available to start September 2012 arising from new strategic research collaborations between The Natural History Museum, London & the Department of Genetics, Evolution and Enviroment (UCL). Applications are invited for the following projects:

1. Squamate richness through time: disentangling macroevolutionary signals from sampling biases. Supervisors: Dr P Barratt (NHM), Prof S Evans (UCL).

2. We are how we eat: evolution of trophic mechanism at the dawn of multicellularity. Supervisors: Dr Tom Richards (NHM), Dr Nick Lane (UCL) & Prof Andrew Pomiankowski (UCL).

3. Maximum likelihood supertrees. Supervisors: Dr M Wilkinson (NHM), Dr P Foster (NHM) & Prof Ziheng Yang (UCL).

4. De novo evolution of segmentation in flatworms. Supervisors: Dr P Olson (NHM) & Prof Max Telford (UCL).

5. Predator control of biodiversity: case studies using microbial microcosms. Supervisors: Dr David Bass (NHM) & Dr David Murrell (UCL).

Further details: www.ucl.ac.uk/gee/-phd_and_mres_research/phd_projects www.findaphd.com (search term - Biodiversity, Ecology & Evolution)

Studentships are funded for 3 years and are open to UK/EU nationals. Applicants need a minimum 2.1 BSc Hons degree. Students will be registered at UCL. Applications to be sent to (including full academic CV with the names and email addresses of two referees and covering letter) to the indicated supervisor (see web links for more details) no later than Wednesday 4 April 2012.

Andrew Pomiankowski Department of Genetics, Evolution and Environment University College London +44 20 7679 7697

ucbhpom@ucl.ac.uk ucbhpom@ucl.ac.uk

UExeter BumblebeeViruses Mar18

As advertised on findaphd.com, we would like to advertise a NERC-funded PhD project on the virulence and host-specificity of bumblebee viruses at the Cornwall Campus of the University of Exeter, supervised by Dr. Lena Wilfert and Prof. Mike Boots. The deadline for application is March 18 2012.

We are inviting applications for this NERC funded PhD studentship to commence October 2012. For eligible students the award will cover UK/EU tuition fees and an annual stipend (in 2011/12 this was £13,590 for full-time students, pro rata for part-time students) for at least three years. This project is one of a number that are in competition for funding. Studentships will be awarded on the basis of merit.

Successful applicants will benefit from working within a lively research environment within the Centre for Ecology and Conservation, Biosciences, Cornwall Campus, near Falmouth at the College of Life and Environmental Sciences, University of Exeter.

Bumblebees are among the most important pollinating insects. Many species and populations have recently suffered drastic declines, with impacts on plant biodiversity and agriculture. Next to habitat loss, parasite pressure is one of the potential causes of these species declines. In particular rapidly adapting viral diseases, which might readily jump between host species, may drive host population dynamics. Viruses are important parasites of honeybees, but have so far been little studied in bumblebees. The aim of this project is to investigate the virulence and host specificity of newly identified bumblebee viruses. The project will combine fieldwork with experimental infection experiments to determine the effects of viral infections on bee health. From this starting point, the degree of host-specificity - and thus the risk for disease emergence - may be assayed directly through experimental evolution. Using phylogenetic methods, experimental results can be compared to the demographic history of viruses in the field to test whether experimental evolution recapitulates natural evolution.

This project will combine fieldwork in the UK with experimental infection assays in the lab. The work will heavily rely on molecular techniques, such as quantitative PCR and sequencing, for quantifying infections and for studying viral sequence evolution. The student will be trained in these methods and will be closely involved with the disease group at Tremough, including Prof. Mike Boots, Prof. Angus Buckling, Dr. Britt Koskella and Dr. Michiel Vos. Please contact Dr. Lena Wilfert (lena.wilfert@ed.ac.uk) for informal enquiries. More information can be found at http://www.biology.ed.ac.uk/research/groups/wilfert Please note that Dr Wilfert will be relocating to the Centre for Ecology and Conservation, Biosciences, Cornwall Campus, near Falmouth at the University of Exeter in May 2012.

Funding Notes:

You must have obtained, or be about to obtain, a First or Upper Second Class UK Honours degree, or the equivalent qualifications gained outside the UK, in a relevant subject. The studentship is only available to UK and other EU nationals (due to funding criteria, EU nationals who have not been resident in the UK for the three years prior to the start of their studentship will be restricted to a fees-only award). If you have not always lived in the UK refer to the NERC Studentships Handbook, section B for more information (http://www.nerc.ac.uk/funding/application/studentships/).

Dr. Lena Bayer-Wilfert Royal Society Research Fellow

Institute of Evolutionary Biology University of Edinburgh King's Buildings Ashworth Laboratories West Mains Road Edinburgh EH9 3JT

lena.wilfert@ed.ac.uk Tel: +44 (0)131 6507335 Ash 2, room 126 http://www.biology.ed.ac.uk/research/groups/wilfert v1lbwilf@staffmail.ed.ac.uk

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UExeter InsectFitnessMaximization

A fully funded NERC PhD position is available from October 2012 at the Centre for Ecology and Conservation at the University of Exeter's Cornwall Campus.

Social networks in wild insects

This project will investigate the possibility that wild insects have networks of places and/or other individuals that they interact with in a non-random fashion. An important issue in animal reproduction is to identify a mate that will maximise the fitness of the searching individual or their offspring. Many different cues have been identified that are used for both mate finding and mate choice, but we have no idea whether non-social invertebrates may preferentially interact with a group of preferred conspecifics rather than simply encountering other individuals at random. This study will be integrated with a project we have to record the lives of every individual in a natural population of field crickets (Gryllus campestris) in a field in Northern Spain. All individuals are tagged and DNA fingerprinted and a network of video cameras records their movements and interactions (see www.wildcrickets.org). The studentship will test hypotheses about movement, social interactions and behaviour in this unique study system. It requires a highly self motivated, resourceful and ambitious student with a strong interest in evolution and behaviour, prepared to work in Spain for several weeks a year and not afraid of using quantitative techniques to analyse data.

Supervisors: Professor Tom Tregenza Dr Rolando Rodríguez-Muñoz http://www.selfishgene.org/Tom/Opportunities.htm Available now, will close when an offer is made, get in touch now!

Tom Tregenza Professor of Evolutionary Ecology Centre for Ecology & Conservation School of Biosciences University of Exeter Cornwall Campus Penryn TR10 9EZ

T.Tregenza@Exeter.ac.uk Tel: (+44) 1326 371862 Fax: (+44) 871 528 2950

Reprints of publications can be downloaded from my website: http://www.selfishgene.org/Tom/ "Tregenza, Tom" <T.Tregenza@exeter.ac.uk>

UExeter JackdawCognition

PhD STUDENTSHIP: COMMUNICATION AND COGNITION IN WILD JACKDAWS

University of Exeter, Centre for Ecology & Conservation, Cornwall Supervisor: Dr Alex Thornton Studentship available for 2012 start Application deadline April 30th 2012

This project will use observations, playback experiments and acoustic analyses to investigate the development and function of vocal communication, and explore the cognitive challenges of social life in a large-brained bird, the jackdaw. The student will join the dynamic Centre for Ecology & Conservation at the University of Exeter's Cornwall campus and conduct fieldwork on wild jackdaws in the beautiful Cornish countryside.

Corvids (members of the crow family) are renowned for their cognitive sophistication, but the selective pressures driving corvid cognitive evolution are not understood. This project will explore an important potential driving force, the need to navigate the challenges of life in complex and dynamic societies. Working with a nest-box population of wild jackdaws, the project will examine how jackdaws' communicative abilities develop and investigate the socio-cognitive skills involved in recognising group members and tracking the relationships between them.

The candidate will join a growing research group working on the evolution and development of cognition and culture and will be supervised by Dr Alex Thornton, a specialist in behaviour and cognition in wild animals. Please note that Alex Thornton is currently based in Cambridge but will be relocating to the CEC in September 2012.

Entry requirements:

You must have obtained, or be about to obtain, a First or Upper Second Class UK Honours degree, or the equivalent qualifications gained outside the UK, in a relevant subject. The studentship is only available to UK and other EU nationals (due to funding criteria, EU nationals who have not been resident in the UK for the three years prior to the start of their studentship will be restricted to a fees-only award).

For more information on the research group see: www.wildcognitionresearch.com Informal enquiries can be addressed to Dr Alex Thornton: jant2@cam.ac.uk

To apply, visit: http://www.exeter.ac.uk/-studying/funding/award/?id=968 – www.wildcognitionresearch.com Dr Alex Thornton BBSRC David Phillips Research Fellow Department of Experimental Psychology University of Cambridge Cambridge CB2 3EB

Sub-Department of Animal Behaviour High Street, Madingley Cambridge CB23 8AA

Alex Thornton <jant2@cam.ac.uk>

UGroningen Evolutionary Theory

PhD (4 years) or Post-doc (3 years) position in Theoretical Evolutionary Ecology

"Causes and consequences of variation in dispersal behaviour"

Organization

This research project 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 University of Groningen (The Netherlands). The research is funded by a TopGrant (ALW-TOP/11.017) allocated to Prof. Jan Komdeur from the Netherlands Science Foundation (NWO).

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 post-doctoral 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.

Qualifications

- 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

For the PhD

The University of Groningen offers a salary of 2042 (scale 50, number 0) gross per month in the first year, up to a maximum of 2612 (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.

For the Post-Doc

The university offers a gross salary depending on qualifications and experience, ranging between 2744 gross (scale 10, number 3) per month and a maximum of 3755 (scale 10, number 12) gross per month for a full-time post-doctoral 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 June 1, 2012. The position will be filled as soon as suitable candidates have been found.

Additional information

Information about the University of Groningen can be found at the website www.rug.nl. Detailed information about the Theoretical Biology and the

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UKonstanz PlantCompetition

Graduate position- Testing the relative roles of competition and plant-soil feedbacks in explaining commonness and rarity of alien and native plants

PhD in plant ecology, University of Konstanz, Germany

Project supervisors- Prof. Mark van Kleunen, Dr. Wayne Dawson

Stabilising mechanisms, such as resource-partitioning and density-dependent soil pests and pathogens, are considered to be crucial for species coexistence. The role of these stabilising mechanisms in explaining variation in abundance of species has received recent attention, as common species may suffer less from negative intraspecific interactions, or less from soil pests and pathogens at high density, compared to rare species. This PhD position will involve conducting field and greenhouse experiments, to tease apart the relative roles of plant-soil feedbacks and competitive ability in explaining commonness of both native and alien plant species occurring in Germany. The position will start from the 1st May.

The successful candidate should ideally have some experimental experience working with plants, as well as experience in analysing ecological data. Applicants should send a letter of application, explaining your motivation, research interests and relevant experience as well as a CV and contact details of at least two references, to Wayne Dawson (wayne.dawson@uni-konstanz.de) by 31st March.

wayne.dawson@uni-konstanz.de Tel +497531882116
http://cms.uni-konstanz.de/vkleunen/
Wayne.Dawson@uni-konstanz.de

ULeicester InsectGeneticLoad

NERC PhD Studentship:

Genome-wide genetic load in a social insect

University of Leicester

About the award We are inviting applications for this NERC funded PhD studentship to commence October 2012. For eligible students the award will cover UK/EU tuition fees and an annual stipend (in 2011/12 this was

Â£13,590 net for full-time students) for at least three years. Studentships will be awarded on the basis of merit.

The successful applicant will benefit from working within a lively research environment in the Department of Biology, within the larger School of Biological Science and will also fit into the College of Biology, Medicine and Psychology's research theme Genome Science.

Background selection - selection that purges deleterious mutations - is an important mechanism shaping genomic variation. The efficacy of background selection, however, depends upon mutations being âvisible' to selection. For example, recessive deleterious mutations can be purged when homozygous because they express the deleterious phenotype, but ineffectively purged when heterozygous because the deleterious allele is sheltered by the expressed allele.

We are looking for a PhD student to investigate the effect of gene expression and ploidy on the visibility of genetic variation to selection and the resultant genome-wide genetic load. Hymenoptera are haplo-diploid: males haploid and females diploid, and these ploidy differences, coupled with sex-specific expression, will alter the relative visibility of genes to selection. The male-only expressed genome is continuously exposed to selection because of haploidy. Conversely, female-only expressed deleterious genes will be sheltered from selection when heterozygous. We wish to test two explicit predictions of this reasoning. First, that the distribution of genetic load (the proportion of deleterious mutations at a locus in a population) across the genome should be âlumpy' with lower genetic load at male-only expressed genes compared to female-only expressed genes. Second, that, on average, overall load is lower than that found in diplo-diploid species.

This studentship requires a highly motivated and ambitious student with a strong interest in evolution, genomics and the use of next generation sequencing. The experiments will mostly be lab based (little fieldwork). This studentship is timely, as more than ten Hymenoptera genomes have been sequenced in the past year, and developments in next generation sequencing make tractable genomic re-sequencing studies on non model species with interesting biology. The successful student will get excellent training in these influential and important techniques.

Supervisors: Dr Robert Hammond and Dr. Eamonn Mallon

Entry requirements: Applicants must have obtained, or be about to obtain, a First or Upper Second Class UK Honours degree, or the equivalent qualification gained outside the UK, in a relevant subject. The studentship is only available to UK and other EU nationals (due to funding criteria, EU nationals who have not been resident in the UK for the three years prior to the start of their studentship will be restricted to a fees-only award). The award provides funding for tuition fees and stipend, subject to eligibility. If you have not always lived in the UK refer to the NERC Studentships Handbook, section B for more information.

Application procedures: Informal enquiries to Dr Hammond (rh225@le.ac.uk) or Dr. Mallon (ebm3@le.ac.uk). For formal applications please email Dr. Hammond electronic copies of the following:

- CV (detailing your education, training and experience) - Personal Statement (clearly outlining why you are applying for this project) - Names and contact details of two academic referees

Application deadline: 30th March 2012

"Mallon, Eamonn B. (Dr.)" <ebm3@leicester.ac.uk>

ULeuven EvolutionaryEcophysiology Daphnia

UNIVERSITY OF LEUVEN

DEPARTMENT OF BIOLOGY

"Evolutionary ecophysiological study of synergisms between UV stress and heavy metals"

We offer a four year fully funded PhD student fellowship (+ 1 predoctoral year depending on the candidate's level) within the research groups of Robby Stoks and Luc De Meester at the Laboratory of Aquatic Ecology, Evolution and Conservation at the University of Leuven, Belgium (http://bio.kuleuven.be/de/dea/).

BACKGROUND

The candidate will carry out a coordinated project (together with toxicologist Erik Smolders of the department of Earth and Environmental Sciences) to study the synergism between UV stress and heavy metals focusing on (i) the physiological-mechanistic underpinnings and (ii) micro-evolutionary changes of vulnerability of Daphnia to these stressors and (iii) resulting eco-evolutionary dynamics with regard to vulnerability to predation. The PhD project will therefore combine different approaches: physiological assays of defense mechanisms, candidate gene expression analysis, resurrection ecology and experimental evolution, and predation experiments. There will be strong international collaboration with (i) the group of Prof. Ruben Sommaruga (Laboratory of Aquatic Photobiology and Plankton Ecology, Univ. Innsbruck) and (ii) the group of Prof. Susana Agusti (Department of Global Change Research, Mediterranean Institute for Advanced Studies) for the experimental work on UV stress and the resurrection ecology study.

ESSENTIAL SELECTION CRITERIA

Candidates should have: - Obtained their Master Degree outside (!) the EER. [EER students willing to apply for a national grant are encouraged to contact us as well.] - Solid knowledge of evolutionary ecology.

- Previous experience in (or at least a strong willingness to learn) ecophysiology and molecular ecology (qPCR). - Strong language skills: high level of written and spoken English absolutely required. - Full time dedication to pursuing PhD studies.

APPLICATION

Applications should consist of a curriculum vitae, a one-page cover letter explaining your scientific background and experience, as well as your interests, and the email address of 2 academic references who can supply letters of recommendation upon our request.

Applications and informal requests for additional information should be sent to: Robby Stoks (robby.stoks@bio.kuleuven.be) and Luc De Meester (Luc.demeester@bio.kuleuven.be).

APPLICATION DEADLINE: May 1, 2012

Leuven (http://www.leuven.be) is a pretty, historical university city with a very high and pleasant standard of living. The historic university, founded in 1425, has a top research and teaching standard (http://www.kuleuven.be/english).

robby.stoks@bio.kuleuven.be

ULondon VirulenceEvolution

Modelling the evolution of virulence in a bacterial pest control agent

Supervisors: Prof. Vincent Jansen and Dr Ben Raymond

School of Biological Sciences, Royal Holloway, University of London

Fully funded PhD position to start September 2012:

Bacteria and bacterial toxins are widely used in the control of insect pests. The most successful of these is the bacterium Bacillus thuringiensis which accounts for most of the world's production of organic microbial formulations and which provides the toxin genes for the vast majority of the world's insect resistant genetically modified crops.

As a natural agent the capacity for bacteria to kill their hosts is subject to selection, and bacterial virulence (i.e. the capacity to kill the host) will adapt and evolve. Two major selective forces that will act on such bacteria are the competition for host resources that will take place between bacteria, and on the other hand the amount of spores that will be produced from a host. Often increased ability to compete trades off against spore production, and therefore the evolution of the bacteria will have to strike a balance between these two forces. As both the magnitude of the effect of production and competition depend on the presence of other strains, the evolution of virulence is similar to the evolution of social traits such as cooperation and altruistic behaviour.

This project aims to understand the evolution of virulence through the development of mathematical models, and will build on previous work by the Jansen research group in this area (see e.g Gandon et al. 2002, Bryden and Jansen 2010, Lion et al. 2011). The research will be informed by empirical work on the role of competition, virulence and reproductive success of B. thuringinsis in the insect Plutella xylostella (Raymond et al 2007, Garbutt et al 2011). An aspect of particular interest is the presence of population structure of a bacterial population within the insect host, which emerges through spatial structure within the host and the occurrence of and co-infection of a host by multiple strains of bacteria. This work will seek to understand on the one hand the factors that control the virulence of the pathogen, which is important for practical application of the bacteria as a pest control agent. On the other hand the research will aim to understand the theoretical connections between the frameworks used for the evolution of virulence and the evolution of social behaviour. The details of the project will be finalised taking the interests and capabilities of the candidates into account. Although the project is intended to be mainly theoretical, depending on whether this in the interest of the development of the candidate and the science, practical elements could be included. This project is suitable for candidates with a proven record in mathematical modelling. We are looking for candidates, either with a background in the life sciences, and experience in mathematical or simulation modelling, or for candidates with a background in a quantitative subject (e.g. mathematics, computer science, physics, economics) and an affinity for research in ecology and evolution. We expect a 2.1 or first class degree (or equivalent if not a UK degree).

This studentship will be part of the BBSRC doctoral training partnership that Royal Holloway has together with Imperial College London. Therefore the conditions and eligibility rules of the BBSRC apply, of which the main condition is residency in the UK for the last 3 years (see http://www.bbsrc.ac.uk/web/FILES/Guidelines/studentship_eligibility.pdf). In case you are not eligible but can (at least in part) find funding for the studentship, please contact me (Vincent.jansen@rhul.ac.uk) to discuss the options.

For more information about the department see http://www.rhul.ac.uk/biosci Or about my research: http://personal.rhul.ac.uk/ujba/115/ To apply the application form http://www.rhul.ac.uk/biologicalsciences/documents/doc/sbsstudentshipapplication2012.doc should be submitted with a CV and followed by 2 references to tracey.jeffries@rhul.ac.uk by 11th April 2012.

References:

Bryden, J. and Jansen, V.A.A. (2010). The impact of clonal mixing on the evolution of social behaviour in aphids Proceedings of the Royal Society B 277, 1651-1657.

S. Gandon, V.A.A. Jansen and M. van Baalen (2001) Host life-history and the evolution of parasite virulence. Evolution 55, 1056-1062

J. Garbutt, M. B. Bonsall, D.J. Wright, and Raymond B. (2011). Antagonistic competition moderates virulence in Bacillus thuringiensis. Ecology Letters 14, 765-772.

Lion, S, Jansen VAA and Day, T. (2011) Evolution in structured

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UNeuchatel EvolutionaryEcology Sparrows

PhD Position in evolutionary ecology, University of NeuchÃtel, Switzerland

A fully-funded 3-year PhD position is available in Fabrice Helfenstein's lab 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 more information, please do not hesitate to contact me!

Fabrice Helfenstein, Assistant Professor SNF Please note that Fabrice Helfenstein is currently based at the University of Berne, but, from september 1, 2012, will be based at the 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 fabrice.helfenstein@free.fr

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UNevada Reno TrophicEvolution

We are seeking to recruit a highly motivated student to become part of an NSF-funded team of researchers working on tri-trophic evolution and ecology in tropical forests. The project involves molecular phylogenetics and population genetics of a complex and diverse lineage of moths in the family Geometridae. The successful applicant for this position should have a Master's degree in molecular ecology or evolution, and experience generating sequence data from non-model organisms. Experience with next-generation sequencing is a plus, but not essential.

The Research Assistantship would be part of the Ecology, Evolution, and Conservation Biology graduate program at the University of Nevada, Reno (links below). Work would be conducted in the Forister lab, working closely with the Dyer and Smilanich labs. We are hoping to fill the position this coming Fall of 2012; but we are also open to a starting date in the subsequent Spring semester (start of 2013). We can offer 2 years of RA support, followed by TA positions; additional RA support pending availability of funds.

To apply, please send the following: (1) CV including names and contact info for 3 references; (2) GRE scores and GPA from Master's program; (3) cover letter stating your interest in pursuing a PhD and stating your ability to start in either Fall (2012) or Spring (2013). Send materials to: forister@gmail.com.

Relevant links: University of Nevada, Reno: http://www.unr.edu/ Graduate Program in EECB: http://environment.unr.edu/eecb/ Forister lab: https://sites.google.com/site/greatbasinbuglab/ Smilanich lab: http://www.angelasmilanich.com/ Dyer lab: http://wolfweb.unr.edu/~ldyer/ The University of Nevada, Reno is located in the western Great Basin, close to the east side of the Sierra Nevada mountains. Reno is a small and very livable city, with opportunities for dining and community events along the scenic Truckee River that runs through town. We find that quality of life here is high, particularly if you are interested in outdoor activities: with a 30-minute drive from town you can be hiking or skiing in the alpine overlooking Lake Tahoe.

Position will be open until filled. Matt Forister

forister@gmail.com

UNottingham SticklebackAdaptation

Dear Colleagues

A NERC funded studentship is available on "The mechanistic basis of parasite resistance in three-spined sticklebacks", co-supervised by myself, Jan Bradley and Sara Goodacre at the University of Nottingham. The project will use genomic data and qPCR to examine the evolution of immune genes and quantify variation in immune profiles among and within Scottish populations of three-spined sticklebacks. Further analyses and experiments will examine the ecological and evolutionary relevance of this variation (e.g. for parasite resistance, life-history traits and fitness).

Please bring this advert to the attention of any high quality UK undergraduate or Masters students, especially those with a background in evolutionary biology, ecology, parasitology or immunology.

The studentship will be awarded to the best applicant, following a limited intradepartmental competition.

In the first instance students should contact me with a CV and a one page description of how they would tackle the project.

Best wishes

Andrew MacColl

Lecturer in Evolutionary Ecology School of Biology University of Nottingham University Park Nottingham

NG7 2RD Tel: +44 115 951 3410 Fax: +44 115 951 3251 Email: andrew.maccoll@nottingham.ac.uk http://www.nottingham.ac.uk/biology/research/animal-behaviour-and-ecology/andrew.maccoll http://ecology.nottingham.ac.uk/maccoll.html Andrew.Maccoll@nottingham.ac.uk

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UOttawa FungalComparativeGenomics

One position for a graduate student (at the PhD or MSc level) is currently available in the Corradi lab; with the starting date being either early September 2012, or early January 2013. The lab is a recently established, CIFAR (Canadian Institute for Advanced Research) affiliated, laboratory of fungal comparative genomics located at the University of Ottawa.

The lab website can be found here: http://mysite.science.uottawa.ca/ncorradi/index.html . The research in the Corradi lab focuses on the comparative genomics of two evolutionary unrelated groups of fungi, the Arbuscular Mycorrhizal Fungi (AMF) and the Microsporidia. The research performed by the MSc student will involve the study of AMF genomics in a broad sense.

Applicants for the position should have a strong background in one of more of the following: in-vitro culturing of AMF and conventional molecular biology (PCR, Sanger sequencing, RT-PCR, qPCR) and inverted microscopy. Previous experience with bioinformatics software (e.g. Consed, Augustus, Artemis), in programming (Perl) or with high-throughput DNA sequencing technologies will represent a strong asset in the final selection of the candidate.

Enquiries about specific projects can be sent to Nicolas Corradi (ncorradi@uottawa.ca).

A complete application package including a CV, a brief (1-page) statement of research interests, and the names and e-mail addresses of at least 2 referees should be sent to ncorradi@uottawa.ca. Evaluation of applications will start immediately, and continue until a suitable candidate is found.

Relevant papers:

Pelin A., Pombert J.F., Salvioli A., Bonen L., Bonfante P. and N.Corradi. 2012.The mitochondrial genome of the arbuscular mycorrhizal fungus Gigaspora margarita reveals two unsuspected trans-splicing events of group I introns. New Phytologist.

Riley R. and N. Corradi. 2012. Searching for clues of sexual reproduction in the genomes of arbuscular mycorrhizal fungi. Fungal Ecology.

Halary S., Malik S.B., Lildhar L., Slamovits C.H., Hijri M.and N. Corradi. 2011. Conserved meiotic machinery in Glomus spp., a putatively ancient asexual fungal lineage. Genome Biology and Evolution. 3: 950-958

Corradi N. and C. Charest. 2011. Some like it Toxic. Molecular Ecology. 20: 3289-3290

Selman M., Pombert J.F., Solter L., Farinelli L., Weiss L.M., Keeling P.J. and N. Corradi. 2011. Acquisition of an animal gene by microsporidian intracellular parasites. Current Biology. 21, Issue 15, R576-R577.

Nicolas Corradi <ncorradi@uottawa.ca>

UStAndrews NewCaledonianCrows

UNIVERSITY OF ST ANDREWS SCHOOL OF BIOLOGY

4-year fully funded PhD studentship “Tool use and culture in wild New Caledonian crows”

BACKGROUND

The New Caledonian crow Corvus moneduloides is endemic to a remote, tropical island in the South Pacific, where it habitually uses tools for extracting invertebrate prey from deadwood and vegetation. New Caledonian crows exhibit a remarkable degree of behavioural sophistication: they manufacture at least three different tool types (including the most sophisticated animal tool yet discovered); they can modify and combine tools to achieve a goal; and they have even been observed inventing new tool designs to solve novel problems.

Perhaps most intriguingly, it has been suggested that wild New Caledonian crows may progressively refine their tool technology through culturally accumulating innovations – a phenomenon hitherto believed to be uniquely human. Most research to date has focused on the species cognitive abilities and on mapping natural variation in tool morphology, but the evolutionary, ecological and social context of these birds unusual tool-use behaviour remains poorly understood.

This PhD project will chart the ecology and behaviour of wild, free-ranging crows, using detailed field observations, systematic surveys, and a suite of novel biologging technologies, including animal-borne video cameras. In addition, specific hypotheses will be examined in controlled experiments with wild and captive crows (the latter will be kept for brief periods of time in field aviaries). Taken together, this observational and experimental research will produce a much clearer picture of the ecological significance of crow tool use, and its possible cultural underpinnings.

This fully-funded PhD project offers exciting opportunities for a keen field biologist: to conduct topical research on animal tool use and culture in a high-profile study system; to join an established, well-funded field research project; to receive training in state-of-the-art ecological research techniques; and to join a dynamic, expanding research group (Head: Dr Christian Rutz) at an internationally recognised centre of excellence – the School of Biology, University of St Andrews.

KEYWORDS: animal, behaviour, behavioural ecology, bird, cognition, culture, ecology, evolution, field biology, intelligence, ornithology, tool use.

APPLICATION DEADLINE: 30 April 2012

START DATE: 27 May 2012 (or as soon as possible thereafter)

CONTACT: Dr Christian Rutz (c.rutz@gmx.net)

FURTHER DETAILS: www.findaphd.com RESTRICTIONS: Home or EU students only

ESSENTIAL SELECTION CRITERIA

V excellent academic track record V demonstrable skill and enthusiasm for fieldwork V ability and willingness to live and work for extended time periods under challenging field conditions (e.g., lone work, research in remote rainforest sites, difficult weather conditions) V conversational knowledge of French, or willingness to learn the language V clean driving licence, and good driving skills V ability to obtain a visa for research in New Caledonia (French overseas territory)

REFERENCES

Bluff, L.A., Kacelnik, A. and C. Rutz (2010). Vocal culture in New Caledonian crows Corvus moneduloides. Biol. J. Linn. Soc. 101, 767–776.

Bluff, L.A., Troscianko, J., Weir, A.A.S., Kacelnik, A. and C. Rutz (2010). Tool use by wild New Caledonian crows Corvus moneduloides at natural foraging sites. Proc. R. Soc. B 277, 1377–1385.

Hunt, G.R. (1996). Manufacture and use of hook-tools by New Caledonian crows. Nature 379, 249–251.

Hunt, G.R. and R.D. Gray (2003). Diversification and cumulative evolution in New Caledonian crow tool manufacture. Proc. R. Soc. B 270, 867–874.

Kenward, B., Weir, A.A.S., Rutz, C. and A. Kacelnik (2005). Tool manufacture by naive juvenile crows. Nature 433, 121.

Rutz, C., Bluff, L.A., Weir, A.A.S. and A. Kacelnik (2007). Video cameras on wild birds. Science 318, 765.

Rutz, C., Bluff, L.A., Reed, N., Troscianko, J., Newton, J., Inger, R., Kacelnik, A. and S. Bearhop (2010). The ecological significance of tool use in New Caledonian crows. Science 329, 1523–1526.

Rutz, C. and J.J.H. St Clair (2012). The evolutionary origins and ecological context of tool use in New Caledonian crows. Behav. Processes 89, 153–165.

Christian Rutz <christian.rutz@zoo.ox.ac.uk>

UWesternSydney LifeHistory

PhD Scholarship: Using telomere dynamics to detect a physiological constraint on the pace of life-histories.

The Hawkesbury Institute for the Environment at the University of Western Sydney, Australia, is seeking a PhD candidate to work on a project in the field of physiological and evolutionary ecology. The PhD candidate is anticipated to commence in first semester 2012.

The project broadly seeks to understand the physiological basis of trade-offs in life history ecology and evolution. In particular, it will test the hypothesis that oxidative stress is a cost associated with increased investment in current production relative to future survival. The candidate will design and conduct a series of hypothesis-driven experiments to determine how variation in the pace of key life-history traits affect rates of telomere shortening and other molecular indices of oxidative stress. These experiments will shed light on the potential for individual mice to make physiological adjustments in response to perceived environmental conditions that maximise lifetime fitness but are associated with variation in rates of decline in physiological function.

The student will be advised by Dr Christopher Turbill (Hawkesbury Institute for the Environment) and work in collaboration with Professor Rob Brooks, Director of the Evolution and Ecology Research Centre at the University of New South Wales.

CRITERIA

The successful applicant should: demonstrate excellent academic performance related to the research proposed; hold qualifications and experience equal to an Australian First Class Bachelor Honours degree; be highly motivated to undertake further study at an advanced level; preferably have a background that includes the fields of comparative animal physiology, metabolism and ageing, free radical biology, and the evolution of variation in life history traits. Knowledge and experience of experimental design and statistical data analysis would be an advantage.

International applicants must also demonstrate a high level of proficiency in the English language. Please refer to the University's web site for information about English language requirements at www.uws.edu.au/international/admissions/-english_language_requirement WHAT DOES THE SCHOLARSHIP PROVIDE?

Tax free stipend of $33,728 per annum and a funded place in the doctoral degree. International candidates with a strong track record will receive a fee waiver. Funding is also available for project costs and conference travel.

NEED MORE INFORMATION?

Applicants should discuss their research aspirations and eligibility with Dr Christopher Turbill: c.turbill@uws.edu.au. Contact the Research Training, Policy and Programs Officer to discuss enrolment and scholarships: Ms Natalie McLaughlin: n.mclaughlin@uws.edu.au. To find out more about the Hawkesbury Institute for the Environment: www.uws.edu.au/hie HOW TO APPLY

Submit an application form and CV (including two referees) by the closing date. The application form can be downloaded from the web: www.uws.edu.au/-research/scholarships APPLICATIONS CLOSE: 30 APRIL 2012

C.Turbill@uws.edu.au

UWyoming ConservationGenetics

Graduate Assistantships available in Restoration Ecology and Genetics at the University of Wyoming

We are seeking to recruit two highly motivated graduate students (one M.S. and the other Ph.D.) to study ecological genetic and landscape approaches to plant community restoration at the University of Wyoming in Laramie. Research will investigate genotype-environment interactions relevant for plant establishment at restoration sites in high elevation ecosystems. Prospective students with a background in natural resources, ecology, and/or population genetics are encouraged to apply.

Qualifications include a strong academic record and interest in evolutionary ecology. Evidence of excellent written and analytical skills, as well as enthusiasm for field and laboratory research will be a plus. Applicants for the Ph.D. assistantship should have completed a Master's degree by summer 2012.

Each graduate assistantship includes a generous annual stipend, tuition and fees, health insurance and research support for either two years (M.S.) or three years (Ph.D.). To apply, please send application materials, including a cover letter and copies of transcripts, GRE scores, resume and contact information for 3 references to Kristina Hufford: khufford@uwyo.edu

Review of applications will begin immediately and continue until each position is filled.

The University of Wyoming is located in Laramie, a town of 30,000 in the heart of the Rocky Mountain West. Located on a high plain between the Laramie and Snowy Range mountains, Laramie has more than 200 days of sunshine a year and near year-round outdoor activities that include skiing, hiking, camping, bicycling, fishing and climbing. The community provides the advantages of a major university and a distinctive identity as an important city in a frontier state. Laramie is near many of Colorado's major cities and university communities (Fort Collins: 1 hour; Boulder: 1.5 hours; Denver: 2 hours). More information about the University and its regional setting is available on the University's website: (www.uwyo.edu). More information regarding ongoing research projects can be found at: http://www.uwyo.edu/esm/faculty-and-staff/kristina-hufford.html khufford@uwyo.edu

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Vienna PopGenetics DeadlineMay15

The 2012 call for PhD applications at *The Vienna Graduate School of Population Genetics* has been reopened. The new deadline is *May 15, 2012*.

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

Applications from highly motivated and outstanding students with a background in one of the following disciplines will be considered: bioinformatics, statistics, evolutionary genetics, functional genetics, theoretical and experimental population genetics. Students from related disciplines, such as physics or mathematics are also welcome to apply. Applicants with a genuine interest for interdisciplinary PhD education will be preferred.

All information about the about the PhD program, the projects and the application procedure can be found at www.popgen-vienna.at Only full applications (CV, motivation letter, university certificates, indication of the two preferred topics in a single pdf) received by *May 15, 2012* will be considered. Two letters of recommendation need to be sent directly by the referees.

Available topics include:

- Inferring selection using *Drosophila* whole genome sequence data - New algorithm and models to analyze population genetic massive parallel sequence data - Experimental evolution in *Drosophila* - Evolution of gene expression in *Drosophila* - Evolution of transposable elements in *Drosophila* - Natural variation in transposable element defense systems - Tracing the genomic signature of hybridization between *D. mauritiana*and *D. simulans* - The nature of differentiation between two closely related species of oak - The genetics of two closely related species of *Aquilegia* - Functionally important variation in lifespan and other life history traits in natural and experimental evolution populations - Mathematical models of spatially varying selection in subdivided populations - Statistical methods for detecting selective sweeps using genome- wide data - Population genetic estimators from NGS data: assessing the power for methods for genome scans of selection - The footprint of adaptive gene introgression after secondary contact - Probabilistic models for the population genetics of molecular evolution

Dr. Julia Hosp Vienna Graduate School of Population Genetics Coordinator www.popgen-vienna.at c/o Institut für Populationsgenetik Vetmeduni Vienna Veterinärplatz 1 A-1210 Vienna

Tel: +43 1 25077 4338 Fax: +43 1 25077 4390

julia.hosp@gmail.com

Zurich Strasbourg SA EvolutionaryPhysiology

PhD position in evolutionary physiology: Zurich (Switzerland), Strasbourg (France) and South Africa

Physiological flexibility as an evolved trait to adapt to changing environments

Position available immediately for 2.5 years, with the option to extend for one year. Deadline for application is the 2nd of April and interviews will take place in April.

Key words: respirometry; animal handling; blood sampling; AVP; hormone assays; physiological adaptation; social flexibility; ecology and evolution

I am looking for a PhD candidate to study physiological flexibility as an evolved trait. Changes in physiology enable adaptation to changing environments (physiological adaptation) and regulate behavioral adaptation. The main aim of our research group is to understand the evolved physiological mechanisms that allow animals to behave adaptively in a changing environment. (See full project summary at end of email).

The student will be supervised by Dr. Carsten Schradin and be part of the research group studying African striped mice (Rhabdomys pumilio; see www.stripedmouse.com and www.ieu.uzh.ch/-research/behaviour/endocrinology.html).

I am seeking a highly-motivated, independent candidate with excellent organizational skills. Strong intellectual skills are desired. Technical skills are mandatory to run the respirometry field laboratory.

The ideal candidate has a background in ecophysiology, behavioral endocrinology or behavioral ecology. Of advantage is experience with animal handling, with respirometry, with hormone analyses, in experimental design and statistical analysis of data. The working language in my group is English.

The student will be based at the Department of Animal Behavior, Institute of Evolutionary Biology and Environmental Studies at the University of Zurich. In Zurich the PhD student has to visit courses (12 ECS) and give lectures to fulfill the conditions of the PhD program in evolutionary biology: http://-www.evobio.uzh.ch/index.html. Zurich is a highly attractive city in beautiful surroundings, with a multinational population, and many educational and recreational opportunities (http://www.zuerich.com).

Laboratory work will be done at the CNRS in Strasbourg (France) where I will be positioned from October 2012 onwards.

Data will be collected in the field in South Africa, where the PhD student has to spend two field seasons of approx. 9 months each. In the field, the candidate has to run independently the respirometry laboratory and conduct field experiments with the help of field assistants.

The student will be supervised by me during my stays in Zurich (twice a year) and in the field (twice a year) as well as during the stay of the student in Strasbourg, which is only 2 hs from Zurich.

The first 6 months will be a trial period during which time the student has to visit courses in Zurich, develop a research proposal and spend 2 months in the field. After the trial period the position can be extended for another 2 years. The student can apply for funding another year from the University of Zurich.

The salary follows the Swiss National Science Foundation scale and is very competitive, especially for somebody spending significant time in South Africa (CHF 41 000 for the first year, CH 44 400 for the second year; this is 34 000 Euro during the first and 37 000 Euro during the second year). The student is expected to apply for funding for an additional year, for example from the Forschungskredit in Zurich (http://www.researchers.uzh.ch/promotion/forschungskredit_en.html).

The position can be filled immediately.

Deadline for application is the 2nd of April and interviews will take place in April.

Please send your application by email and as PDF to carsten.schradin@ieu.uzh.ch. Your application should include: * a letter outlining your past research and particular motivation for this position, information on when you could start and contact details of two referees (max. 2 pages) * your CV * PDFs of publications (published, in press or in preparation) * PDF of your master thesis (if not published yet)

PD Dr. Carsten Schradin Group Leader Behavioral Endocrinology and Eco-Physiology

Institute of Evolutionary Biology and Environmental Studies Department of Animal Behavior University of Zurich, Winterthurerstrasse 190, 8057 Zurich, Switzerland. Tel: +41 - (0)44 635 5486

Tel. secretary: +41 - (0)44 635 5271 Fax: +41 - (0)44 635 5490

Honorary Associate Professor

School of Animal, Plant and Environmental Sciences

University of the Witwatersrand, Johannesburg, South Africa

Head

Succulent Karoo Research Station, Goegap Nature Reserve, Private Bag X1,

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Jobs

BiKF Germany ComputBiology

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

Postdoctoral Researcher “Bioinformatician/Computational Biologist” for project D2.3 / Prof. Janke Project area D [Ref. #D18b]

We are looking for a research-oriented person for the primary analysis of conventional DNA-sequence and NGS data (454/Illumina). The task profile includes genome assembly and annotation, NGS transcriptome analysis for adaptive traits, developing new genetics marker (SNP, VNTR) and retroposon characterization. This will be done in close cooperation with an international team of population geneticists and retroposon biologists.

We are working on the genomic basis of adaptation to climatic conditions in arctic vertebrates, phylogenomic analysis of mammalian radiation, and characterization of genomic signatures of retroposon activity.

The successful candidate has experience with the analysis of conventional and NGS DNA data, has the appropriate IT skills (experience with various operating systems and expertise in at least one scripting language) and may have already developed own methods in this field. Scientific cooperation with the bioinformatics professorship at the University of Frankfurt in the field of NGS and data mining is possible. A basic understanding and interest in the underlying biological processes is an advantage. In addition, own research interest in this field and own grant applications are expected, and the position will give the opportunity for habilitation, if desired.

The successful candidate must have a PhD in bioinformatics, genetics, evolutionary biology, molecular biology, molecular ecology or related fields and a strong, independent research record.

Salary and benefits are according to a public service position in Germany (TV-H E13).The Research Centre BiK-F advocates gender equality. Women and other underrepresented groups are therefore strongly encouraged to apply. Equally qualified severely handicapped applicants will be given preference.

The contract shall start as soon as possible and will be offered until 30.06.2014, with the possibility of an extension pending performance and future of the research centre. The workplace will be Frankfurt am Main, Germany. The employer is the Senckenberg Gesellschaft fuer Naturforschung.

Please send your application by mail or (preferably) by e-mail attachment, mentioning the reference of this position (#D18b) and including a letter outlining your suitability for the post, a detailed CV, contact details of 2 referees and a copy of your PhD thesis and/or other exams before April 15th 2012 to: Prof. Dr. Dr. h.c. V. Mosbrugger, Scientific Coordinator Biodiversity and Climate Research Centre, Senckenberganlage 25, D-60325 Frankfurt am Main, Germany. E-mail to Service and Administration: recruiting@senckenberg.de .

For enquiries about the position and the contract conditions please write to Prof. Dr. A. Janke (e-mail: axel.janke@senckenberg.de).

recruiting <recruiting@senckenberg.de>

Bonn BarcodeOfLife

Entomologist position open for 3 years at the Museum Koenig, Bonn GBOL (German Barcode of Life, see http://www.bolgermany.de/) is a project funded by the German Federal Ministry of Education and Research (BMBF) and is dedicated to catalog and characterize the fauna and flora in Germany. We seek an entomologist to coordinate the inventory at the Zoologisches Forschungsmuseum A. Koenig in Bonn (www.zfmk.de).

The tasks include managing taxon lists (for dipterans, beetles, hemipterans, spiders, etc.), maintaining contacts with taxon experts and support of the collectors, coordinating the sample income pipeline (incl. photography and preparation by designated personnel), and validating of species-determinations as well as results from tree reconstructions. We expect very good, broad entomological knowledge, outstanding organizational and negotiating skills and intimate knowledge of the German entomological scene. GERMAN language skills ON A NATIVE LEVEL are a necessary prerequisite. Basic knowledge in DNA barcoding is beneficial. A number of domestic travels will be expected (entomologists' meetings, workshops, etc.)

The position will be paid to grade TV-L E 13 in the German Public Service scheme and will be available for three years during the first funding period. It should be filled as soon as possible.

The ZFMK is an equal opportunity employer. Women are therefore strongly encouraged to apply. Equally qualified handicapped applicants will be given preference. Please send your application until March 25th 2012 to Zoologisches Forschungsmuseum Alexander Koenig, z. Hd. Frau Heike Lenz, Adenauerallee 160, D-53113 Bonn, Germany h.lenz.zfmk@uni-bonn.de

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

w.waegele@zfmk.de (NEW !!!!) Tel.: 0049 (0) 228 9122 200 Fax: 0049 (0) 2289122 202 http://www.zfmk.de Werden Sie Mitglied der Alexander Koenig Gesellschaft! (http://www.zfmk.de/web/Foerderer/Freunde/index.de.html)

"Wägele J. Wolfgang" <W.Waegele@zfmk.de>

CambridgeU EvolutionaryGenetics

Applications are invited for a five year University Lectureship in the Department of Genetics, from scientists with the potential to become leaders in their field of research. The Department wishes to attract candidates with interests in the areas of quantitative, population or evolutionary genetics or genomics, and who could contribute to teaching of genetics in these areas. With the academic status of a University Lecturer you will be expected to play a full role in the teaching and research activities of the Department, including the training of postgraduate students and postdoctoral Fellows, and undergraduate teaching in the Faculty of Biology. You should be able to start on 1 October 2012 or as soon as possible thereafter.

The Department expects to recruit a highly active researcher. The duties of the post will be comparable to those of permanent lecturers and the post holder will have equal scope to pursue their research projects.

Informal enquiries may be made to the Head of Department, Dr. Cahir O'Kane (Email: head@gen.cam.ac.uk, Tel +44 1223 333998).

Further particulars and an application form may be requested by email from jobs@gen.cam.ac.uk or downloaded from http://www.gen.cam.ac.uk/department/vacancies/vacancies.html Applications, to include a CV, CHRIS/6 application form (Parts I and III only including the names and addresses of three referees), a brief statement (two sides maximum) of future research plans and a list of publications, should be submitted to the Departmental Administrator, Mrs Tracy Oakley, Dept. of Genetics, Downing Street, Cambridge, CB2 3EH, e-mail: jobs@gen.cam.ac.uk

* Limit of tenure: Five years from 01 October 2012

Quote Reference: PC15072,Closing Date: 27 April 2012

Interview Date(s): Mid to late May

fmj1001@cam.ac.uk

ClarksonU EvolBiol

The advertisement below is open to all biologists, including Evolutionary Biologists of all flavors. I would appreciate you posting this to the Jobs list at Evoldir.

Kind regards, Jim

Please note that the disciplinary focus is actually open to all fields of biology and a strong record of teaching and research.

Endowed Chair in Biology at Clarkson University

The Biology Department at Clarkson University invites applicants for the Bayard and Virginia Clarkson Endowed Chair of Biology. Candidates should have a Ph.D. in the biological sciences with demonstration of outstanding research, current external funding, and experience mentoring students. We are particularly interested in applicants who have expertise in medical microbiology / immunology or environmental microbiology. However, candidates who have a strong background in other areas of the biological sciences will be fully considered. The position requires limited teaching (upper level courses in the candidates area of expertise) in support of the Biology Departments undergraduate program and Ph.D. Program in Bioscience and Biotechnology. Clarkson offers a highly interdisciplinary environment and opportunities for collaboration with faculty in areas of Cell & Developmental Biology, Bioinformatics, Environmental Biology, Nanotechnology, Biomedical Engineering, and Biomaterials Science. A description of research interests of current Biology faculty can be found online at http://www.clarkson.edu/biology/-faculty_pages/index.html . All inquiries regarding this position are welcome and will be treated confidentially.

Clarkson University is a nationally ranked research university with a tradition of exceptional degree programs in science and engineering. Clarkson has 221 full-time teacher-scholars engaged in world-class research. The student body consists of over 3,000 undergraduate and 480 graduate students. Clarkson is located in the rural village of Potsdam on the Raquette River in northern New York State. The village is within easy driving distance of Ottawa and Montreal, Canada, the Adirondack Park, and Lake Placid. Potsdam is a college town with nearly ten thousand students within a ten-mile radius. The community offers a stimulating social and intellectual environment, thanks largely to the presence of Clarkson and three nearby colleges: St. Lawrence University, SUNY Potsdam, and SUNY Canton.

For more information about the Endowed Chair in Biology please contact: Craig D. Woodworth, Professor & Chair Department of Biology, Clarkson University, CU Box 5805 Potsdam, NY 13699 Tel: 315-268-2391 Email: woodworth@clarkson.edu

Applications for this position may be submitted at: https://clarkson.peopleadmin.com/postings/941

James Schulte <jschulte@clarkson.edu>

CollegeWooster Tech MosquitoEvolution

A part time (with benefits) research technician position is available in the Sirot lab at the College of Wooster in Wooster, OH, beginning in June 2012 (with the possibility to start in May). Support is available for one year (with possible continuation for up to three additional years) to participate in an NIH-funded project, in which we seek to identify and functionally characterize seminal fluid proteins in two species of mosquitoes. Seminal fluid proteins are produced by males and transferred to females during mating and affect both the physiology and behavior of mated females.

The responsibilities of the technician will include: supporting all aspects of research on mosquito reproductive biology; conducting experiments including those related to behavior, biochemistry, bioinformatics, and molecular biology; maintaining mosquito colonies, equipment, and lab safety; and training and supervising undergraduate researchers.

Motivated applicants with experience working with insects and in molecular biology are especially encouraged to apply, but training can be provided in these areas to motivated applicants who lack experience in these areas. Applicants should be proficient in the use of word processing, spreadsheet, and statistical programs. Applicants with an MSc in a relevant field are preferred but Bachelors applicants will be considered.

The College of Wooster is located in northeast Ohio and is very close to the Ohio State University's Agricultural Research and Development Center (OARDC), which has many research entomologists and sequencing facilities. Applications will be reviewed as received and the position will remain open until filled. Applications should include a statement that describes research experience and relevant skills for the project (1 page), curriculum vitae or resume, and contact information for three references (including emails and phone numbers). Materials should be sent to humanresources@wooster.edu

Department of Biology College of Wooster Mateer Hall 931 College Mall Wooster, OH 44691 Phone: 330-263-2341

lsirot@wooster.edu

DukeU ResTech EvolutionaryGenetics

Research Technician, Biology Department, Duke University:

DukeU.EvolutionaryGenetics

Duke University, Biology Department, Research Technician (Associate in Research)

A research technician is wanted to participate in research in evolutionary ecology and genetics of plants. Recent university graduates looking for additional research experience before entering graduate school are especially encouraged to apply. Research in this lab combines work in the field, laboratory, and greenhouse to study genotype-environment interactions. This position requires a bachelors degree in Biology or related field, experience in plant care, impeccable organizational skills, and familiarity with basic molecular biology procedures. Duties include plant care, molecular and biochemical work; maintenance of field/greenhouse experiments, data management, general lab and clerical tasks. Available 15 May, 2012. Currently for one year. Competitive salary and full Duke benefits. Duke University is an Equal Opportunity/Affirmative Action employer.

Please send CV and names of 3 references to Kathleen Donohue: k.donohue@duke.edu

DEADLINE FOR CONSIDERATION: APRIL 15, 2012

Kathleen Donohue Associate Professor Department of Biology Duke University Box 90338 Durham, NC 27708 USA

Office: 919 613-7467 Lab: 919 613-7468 Fax: 919-660-7293 k.donohue@duke.edu

Kathleen Donohue <k.donohue@duke.edu>

DukeU TeachingEvolution

Full-time teaching/prep positions in Biology 102L "Genetics and Evolution," Duke University

Position description: Work full time (40 hours/week) as a teaching assistant and laboratory prep assistant in the introductory biology program for the 2012-2013 academic year. The position has two main components, teaching and behind-the-scenes laboratory preparation.

Teaching component: The primary teaching responsibility of the position is to lead laboratory sections of up to 16 students in the Biology Department's new genetics and evolution Gateway course, Biology102L. Each Biology 102L section meets weekly for 2.5 hours for a combined hands-on laboratory/problem-based learning session. Additional teaching responsibilities include (a) attending and taking notes at all course lectures including the weekly large discussion section, (b) grading weekly student written assignments and occasional oral presentations, (c) helping with the preparation and grading of mid-semester hourly and final exams, and (d) assisting students during office hours and otherwise mentoring students as beginning biologists.

Teaching assistants should plan to be in Durham early the week of August 20, 2012, and are expected to participate in a teacher-training workshop before the fall semester begins. TAs also attend weekly prep sessions during the semester on Mondays.

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

Salary: The projected salary for the position is $17,500 or commensurate with experience. Employment begins on August 20, 2012 and ends May 10, 2013, with most of the winter and spring breaks off, with payment made in 9 equal amounts on the 25th of each month starting in

September and ending in May. Full-time teaching/prep employees are eligible for health plans made available by the University.

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

Interviews and Application Process: Formal interviews are planned to begin after March 25, 2012. Hiring decisions will be made on a rolling basis thereafter, continuing as necessary.

Interested applicants should provide (a) a cover letter, (b) a transcript, and (c) a resume with the names of two references (preferably at Duke for Duke students or alumni) to Julie Noor. These may be emailed to jkfnoor@duke.edu, or mailed to her at the Department of Biology, Box 90338, Duke University, Durham, NC 27708- 0338. To be assured of consideration, applications should be submitted by March 25, 2012.

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

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

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EvolutionInst ExecDirector

Executive Director of the Evolution Institute

The Institute has operated without a staff since its inception as a 'proof of concept' in 2009 under the auspices of the Humanists of Florida Association. It incorporated in Florida, 2010 and received 501c-3 status from the IRS in March, 2011. The Institute has functioned as a result of the volunteer efforts of its board of directors and part-time graduate students. Funding until now has limited the activities of the Institute to employ full-time professional personnel and maintain a core organizational infrastructure. Yet much has been accomplished and the reputation of it has grown considerably along with increased financial support.

The Institute is now in a position to appoint a full-time executive director to assist it in transitioning to a viable and sustainable internationally recognized evolutionary science based research and policy institute. However, funding and commitment has still not reached the level needed to ensure a long-term commitment to support an executive director or build an infrastructure that can function effectively in the long-term. This necessitates appointing an executive director for at least a year that has the ability and experience to work closely with the board to implement the approved business/strategic plan that will result in a successful transition from a cyberspace organization to one that will seriously consider a strategic location and presence to advance its mission and goals.

Therefore, the recruitment of the first executive director will require someone with considerable talent willing to take some risk, but not expected to relocate initially.

Responsibilities:

- Overall management and the implementation and achievement of the approved board of directors' business/strategic plan - Direction, supervision and evaluation of all employees directly in the chain of command to the office as determined by the board - Maintaining effective communication with the board of directors, including organizing and preparing for its meeting and providing informed reports and recommendations - Ensuring the science and executive advisory councils are functioning effectively in achieving their mission and responsibilities - Coordinating and fully participating in fundraising efforts (including grant writing) that enables the organization to achieve its annual objectives and grow - Timely submission of all reports required by state and federal agencies to maintain non-profit status - Building a database that includes information to submit and file reports and policies and procedures to properly operate the organization and maximize transparency and accountability - Serves as central staff person for timely and effective communication between EI its external partners, organizations it is cooperating with and interested parties. - Reports to the board of directors

Qualifications: An excellent documented track record in serving as a top or senior level non-profit organization is highly desirable. Preference will be given to someone that combines a background in science and/or technology and is an accomplished manager. Special consideration will be given to a prospect who is presently or recently employed in an important professional position with an organization that has strong scientific credentials and considerable accomplishments. A person who has raised substantial money from individuals and foundations will be given additional weight. Prior successful relations with representatives of the media/press and governmental officials are important. A Ph.D. or its equivalent is preferred. A M.A. or M.S. is required.

Salary: Commensurate with experience, credentials, past performance and recommendations.

Starting: $45,000-$60,000

*How to Apply: *Send your resume or vitae and cover letter to ei@evolution-institute.org < http://evolution-institute.org/job-opportunities/-ei@evolution-institute.org >. Those we identify as the most qualified candidates for this position will be contacted for further consideration. We anticipate announcing our decision sometime in June, 2012. It is strongly recommended that you submit your application by May 1.

Robert M. Kadar Evolution: This View of Life < http://www.thisviewoflife.com > Founder

Evolution Institute < http://www.evolution-institute.org/ > Executive Assistant

Robert M Kadar <rkadar1@binghamton.edu>

Evry France Genomics

Environment: The LABGeM team located at the Institute of Genomics of the French Atomic Energy Commission (CEA- Genoscope, Evry - FRANCE) is essentially composed of bio-IT specialists. The current fields of research revolve around two main scopes, namely expert annotation of procaryotic genomes and comparative genomics of prokaryotes in the broadest sense of the term. Due to its recognized expertise in the world of bacterial genomics, our laboratory establishes numerous collaborations especially within the framework of ANR calls (The French National Research Agency). To complete successfully one of our projects (ANR ReplicolScope), we are currently seeking for an engineer in bio-computing.

Project scope: Constant increase in acquired resistance to antibiotics is a major problem of public health. In the case of Escherichia coli species, one of the ubiquitous opportunistic pathogen of Man and Animals, we are currently facing the emergence of Extended Spectrum Beta-lactamases (ESBL) capable of hydrolyzing all Beta-lactams but carbapenems and cephamycins. The goal of the *ReplicolScope* project is to better understand the interactions between plasmids harboring ESBL genes and various populations of E. coli in order to explain the evolutionary success of ESBL.

Missions: The successful candidate will participate in *missions* assigned to the laboratory within the framework of the *Replicolscope* project: - setting up of a relational database containing sequences and other MetaData related to plasmids of Enterobacteria (public and locally sequenced). - performing syntactic and functional annotations of plasmidic sequences based on original strategies for the construction of gene models and on the protein families characterization. - integrating and performing comparative analyses of the data in order to target genomic regions for which expert annotation is required. - training of the partners of the project on the use of the platform MicroScope / ReplicoScope.

The whole work will rely on the use and the extension of the MicroScope platform developed in our laboratory (further details at http://www.genoscope.cns.fr/agc/-microscope).

Required skills and experiences: The successful applicant will have: - a Master degree in computer science, computational biology, or related field - good knowledge of Prokaryote genomics - experience in tools devoted to genome analyses (comparative genomics, statistics). - experience in oriented bioinformatics programming languages in UNIX environment (Bash, Perl, SQL, Java) and compiled languages (C/C++), relational databases and construction of computational pipelines.

Position: Minimum one year fixed-term contract. Effective start date ASAP. Salary will depend on the candidate's experience (minimum gross salary: 2200 euros/month).

Closing Date: *April 11 2012* Send detailed CV and a cover letter along with names of 3 references to Claudine Médigue and Stéphane Cruveiller (cmedigue@genoscope.cns.fr) & Stéphane Cruveiller (scruveil@genoscope.cns.fr)

– “La science a certes quelques magnifiques réussites à son actif mais à tout prendre, je préfère de loin être heureux plutôt qu'avoir raison.” D. Adams

Stéphane CRUVEILLER Ph. D. CEA -Institut de

Génomique - Genoscope Laboratoire de Génomique Comparative 2, Rue Gaston Cremieux CP 5706 91057 Evry Cedex - France Phone: +33 (0)1 60 87 84 58 Fax: +33 (0)1 60 87 25 14 scruveil_NOSP@M_genoscope.cns.fr

scruveil@genoscope.cns.fr

Fairbanks GenomicsCollectionManager

Genomic Resources Collection Manager *University of Alaskas Museum* *Fairbanks, Alaska*

The University of Alaska Museum (UAM) is seeking qualified applicants for a position as Collection Manager of Genomic Resources. UAM houses one of the largest museum frozen tissue collections in the world, with samples from over 85,000 mammal, bird, fish, amphibian, insect, marine invertebrate, and plant specimens. Recent rapid growth is expected to accelerate in the near future with expanded collecting efforts in all six of UAM's biological departments (Mammalogy, Ornithology, Ichthyology, Entomology, Earth Sciences, and the Herbarium).

Primary responsibilities include the daily management and organization of frozen samples (including databasing and barcoding); maintenance of the cryogenic facilities (including liquid nitrogen and ultracold freezers); loan reviews, correspondence, and processing; management of UAM's separate Ancient DNA and Molecular Research Laboratories; and active engagement in outreach, proposal preparation, and development. The successful applicant will also be encouraged to actively contribute to the growth of the Genomics Resources collection through field collecting efforts.

Minimum qualifications include a bachelor's degree in an appropriate scientific discipline, experience in modern genetic or genomic applications, and familiarity with specimen-based science and relational databases and/or bioinformatics. Preference will be given to applicants with a graduate degree and collections management experience.

The UA Museum is housed in a newly expanded and renovated building on the campus of the University of Alaska Fairbanks, in interior Alaska. More information can be found at www.uaf.edu/museum/ and www.uaf.edu/museum/collections/af/. Fairbanks has ready access to spectacular outdoor opportunities, and as the second-largest population center in Alaska, offers diverse cultural, artistic, and recreational opportunities.

Salary starts at $36,070 plus benefits for an annual 10-month contract, with additional salary contingent on extramural funding.

To apply, please submit (1) an application and curriculum vitae, (2) a collections management statement describing your experience, interests, and vision of your role at UAM, and (3) the names and contact information of three references to the URL below. Review of applications will begin on 18 March. For more information contact Link Olson (link.olson@alaska.edu).

Job URL: http://www.uakjobs.com/applicants/-Central?quickFind=75778 – Link Olson < http:/-/linkolson.org/ > Curator of Mammals, University of Alaska Museum< http://www.uaf.edu/museum/-collections/mammal/ > Associate Professor, Department of Biology and Wildlife University of Alaska Fairbanks 907 Yukon Drive Fairbanks, AK 99775-6960 tel: (907) 474-5998 link.olson@alaska.edu

See the UAM Mammal Collection database: http:/-/arctos.database.museum/uam_mamm/ Link Olson <leolson@alaska.edu>

LMU Munich EvolutionaryGenomics

Group Leader, Evolutionary and Functional Genomics, LMU-Munich

A group leader position in evolutionary and functional genomics is available at the University of Munich (LMU). Requirements are a Ph.D. in biology and a proven track record in molecular evolution, functional genomics, and/or population genetics. Preference will be given to candidates whose research interests are compatible with current projects in the department (e.g., gene expression variation in natural populations, functional analysis of gene regulation, evolution of sex-biased genes and sex-biased gene expression, sex chromosome evolution).

The position is intended for a recent Ph.D. or early postdoc and is best described as something between a senior postdoc and an assistant professor position. There is the opportunity to conduct independent research, apply for external funding, and supervise graduate students, however the position is not tenure-track

("Akademisher Rat auf Zeit" under the German employment system). There is a teaching requirement of roughly one course per semester (teaching may be in German or English).

The position is available beginning September 1, 2012 and has an initial appointment of 3 years, with the possibility of renewal for an additional 3 years. The University of Munich has a strong, interactive group in evolutionary biology, including theoreticians and experimentalists working on both plant and animal systems. We have an very international group and the everyday working language is English. The department is housed in a new, state-of-the-art BioCenter on the University of Munich High-Tech campus. More information is available on the web at:

http://evol.bio.lmu.de To apply, please send a PDF including your CV, list of publications, statement of research interests, and the contact information of 2-3 referees to:

parsch@zi.biologie.uni-muenchen.de

Application review will begin April 15 and continue until the position is filled.

The LMU-Munich is an equal opportunity employer with an affirmative action program for the handicapped. Applications from women are encouraged.

John Parsch Department of Biology II University of Munich Grosshaderner Str. 2 82152 Planegg-Martinsried Germany

parsch@zi.biologie.uni-muenchen.de

MasseyU 2 Bioinformatics

Dear EvolDir,

We have two Bioinformatics/Genomics Lecturer (Group Leader) positions available at Massey University in New Zealand. One is available at the Auckland campus and one at the Palmerston North campus.

These positions would suit candidates who are enthusiastic about bioinformatics/genomics, and who are highly motivated to build successful research careers and contribute to undergraduate and postgraduate teaching. They will also contribute time to providing bioinformatics service through Massey University to the bioinformatics arm of the newly-established New Zealand Genomics Ltd (http://www.nzgenomics.co.nz/), and will be responsible for managing a technician to provide this service.

The successful candidates will have a PhD and postdoctoral experience, a demonstrated track record in research, and must have experience in bioinformatics analysis of next-generation sequencing data. They will be expected to lead their own research groups, establish collaborations both within Massey University and externally, and be engaged in the wider New Zealand bioinformatics/genomics community. One position will be based in the Institute of Molecular BioSciences in Palmerston North (http://imbs.massey.ac.nz), and the other will be in the Institute of Natural Sciences in Auckland (http://ins.massey.ac.nz).

For more information about the Palmerston North position, please contact Prof. Barry Scott (d.b.scott@massey.ac.nz). For more information about the Auckland position, please contact Dr. Austen Ganley (a.r.ganley@massey.ac.nz).

For salary range information and to apply, please follow this link for the Palmerston North position (vacancy number A047-12): http://massey-careers.massey.ac.nz/PositionDetail.aspx?p=7312, or this link for the Auckland position (vacancy number A042-12): http://massey-careers.massey.ac.nz/PositionDetail.aspx?p=7300 . Closing date: 11 April 2012

A.R.Ganley@massey.ac.nz

Montpellier Bioinformatics NGS

2-years post in Bioinformatics at CNRS, Montpellier, France.

We are seeking a bioinformatician to join our team to conduct computational biology work on high throughput sequencing data. The successful applicant will contribute computational and bioinformatics expertise to an ANR and EU-funded project devoted to characterise the genomics of speciation in the house mouse. Work will include the development of bioinformatics pipelines in Perl and/or Python to automate the analysis of NGS data sets (assembly of genome resequencing and RNAseq data, SNP and structural variant detection, epigenomics and transcriptomics analysis). The successful applicant will be expected to work as part of a team and to train biologist colleagues to NGS data analysis.

Candidates will hold a Master or PhD degree in any relevant area of expertise (bioinformatics, computer sciences, genomics) with some working experience in bioinformatics or life science research IT. Extensive knowledge of bioinformatics tools and NGS applications as well as a proven background in analysing Next Generation Sequencing data is required. Strong programming skills in Perl/Python is expected, and knowledge in R and C ++ programming would be a plus.

This post will be based in Montpellier (South of France), European centre of excellence in biodiversity research and known for its quality of life in the Mediterranean region. The Institute for Evolutionary Biology has a long lasting history of research excellence in genetics and evolution and the successful applicant will directly benefit from this outstanding scientific environment while building a strong and valuable experience in biodiversity informatics. Candidates will not need to speak French and the working language will be English.

This post is fixed term for 2 years and net monthly salary will be 2100-2500 Euros depending on experience.

Applications should be sent to carole.smadja@univ-montp2.fr AND Pierre.boursot@univ-montp2.fr by ***10 April 2012*** and should include a detailed CV, names and contact details of 3 referees and a 1-page statement which will detail your bioinformatics experience (programming languages, research projects, training workshops, development of software, pipelines or tutorials).

Dr. Carole Smadja CNRS research scientist Chargée de recherches CNRS http://www.carole-smadja.staff.shef.ac.uk/ Institut des Sciences de l'Evolution cc065, Université Montpellier 2 34095 Montpellier France Phone: +33 (0)4 67 14 92 70

carole.smadja@univ-montp2.fr

NewZealand Bioinformtics 2

Dear EvolDir,

My apologies for re-posting, but it has come to my attention that somehow the links for the two bioinformatics/genomics lecturer positions and the two bioinformatics technician positions that I previously posted become corrupted. Therefore I would like to repost these links for your information:

Lecturer positions: http://jobs.massey.ac.nz/PositionDetail.aspx?p=7300 http://jobs.massey.ac.nz/PositionDetail.aspx?p=7312 Technician positions: http://jobs.massey.ac.nz/PositionDetail.aspx?p=7311 http://jobs.massey.ac.nz/PositionDetail.aspx?p=7301 Best regards,

Austen

We have two Bioinformatics/Genomics Lecturer (Group Leader) positions available at Massey University in New Zealand. One is available at the Auckland campus and one at the Palmerston North campus.

These positions would suit candidates who are enthusiastic about bioinformatics/genomics, and who are highly motivated to build successful research careers and contribute to undergraduate and postgraduate teaching. They will also contribute time to providing bioinformatics service through Massey University to the bioinformatics arm of the newly-established New Zealand Genomics Ltd (http://www.nzgenomics.co.nz/), and will be responsible for managing a technician to provide this service.

The successful candidates will have a PhD and postdoctoral experience, a demonstrated track record in research, and must have experience in bioinformatics analysis of next-generation sequencing data. They will be expected to lead their own research groups, establish collaborations both within Massey University and externally, and be engaged in the wider New Zealand bioinformatics/genomics community. One position will be based in the Institute of Molecular BioSciences in Palmerston North (http://imbs.massey.ac.nz), and the other will be in the Institute of Natural Sciences in Auckland (http://ins.massey.ac.nz).

For more information about the Palmerston North position, please contact Prof. Barry Scott (d.b.scott@massey.ac.nz). For more information about the Auckland position, please contact Dr. Austen Ganley (a.r.ganley@massey.ac.nz).

For salary range information and to apply, please follow this link for the Palmerston North position (vacancy number A047-12): http://massey-careers.massey.ac.nz/PositionDetail.aspx?p=7312, or this link for the Auckland position (vacancy number A042-12): http://massey-careers.massey.ac.nz/PositionDetail.aspx?p=7300 . Closing date: 11 April 2012

A.R.Ganley@massey.ac.nz

NewZealand Tech Bioinformatics

Dear EvolDir,

We have two technician positions in bioinformatics available at Massey University in New Zealand. One is available at the Auckland campus and one at the Palmerston North campus. These are in parallel to the two Lecturer positions in Bioinformatics that we recently advertised.

The successful candidates will provide bioinformatics expertise to the newly-established New Zealand Genomics Ltd (NZGL; http://www.nzgenomics.co.nz/) through Massey University. They will provide services in experimental design, and statistical and bioinformatics analyses, with an emphasis on next-generation DNA sequencing data. They will deploy and maintain analytic and data management pipelines as well as generating custom bioinformatic solutions. The successful candidates will be key members of the distributed NZGLbioinformatics team, and will also have a small component of their time dedicated to research.

The successful candidates will have a BSc (or equivalent) and a post-graduate qualification in molecular biology and/or computing. Applicants must have experience working in a UNIX environment and should be familiar with at least one of Perl, Java, Python, C or C++. Experience in the analysis of next-generation sequencing data is preferred. Good communication and writing skills are essential. One position will be based in the Institute of Molecular BioSciences in Palmerston North (http://imbs.massey.ac.nz), and the other will be in the Institute of Natural Sciences in Auckland (http://ins.massey.ac.nz).

For more information about the Palmerston North position, please contact Dr. Patrick Biggs (p.biggs@massey.ac.nz). For more information about the Auckland position, please contact Dr. Austen Ganley (a.r.ganley@massey.ac.nz).

For salary range information and to apply, please follow this link for the Palmerston North position (vacancy number G046-12ZZ): http://jobs.massey.ac.nz/-PositionDetail.aspx?p=7311 or this link for the Auckland position (vacancy number G043-12ZZ): http:/-/jobs.massey.ac.nz/PositionDetail.aspx?p=7301 Closing date: 15 April 2012

A.R.Ganley@massey.ac.nz

PennState SoftwareEngineers GalaxyProject

Want to work on a rapidly growing open source bioinformatics project? The Galaxy Project (http://-galaxyproject.org/) is a highly successful high throughput data analysis platform for Life Sciences, with over 15,000 users worldwide. We are hiring post-docs and software engineers in multiple locations.

The Taylor Lab in the Biology and Mathematics & Computer Science at Emory University (http://-bx.mathcs.emory.edu/) is looking for software engineers and Postdoctoral Scholars to work on the Galaxy Project.

We are seeking Software Engineers with expertise in * distributed computing and systems programming, * web-based visualization and visual analytics, * informatics and data analysis and integration, and * bioinformatics application areas such as re-sequencing, de novo assembly, metagenomics, transcriptome analysis and epigenetics. These are full time positions located in Atlanta, GA. See the official posting for full details. (http://bx.mathcs.emory.edu/joining/sw/)

Postdoctoral applicants should have expertise in Bioinformatics and Computational Biology and research interests that complement but extend the lab's current interests: * the Galaxy project, * distributed and high-performance computing for data intensive science; * vertebrate functional genomics, and * genomics and epigenomic mechanisms of gene regulation, * the role of transcription factors and chromatin structure in global gene expression, development, and differentiation. See the announcement for full details. (http://-bx.mathcs.emory.edu/joining/postdocs/)

The Nekrutenko Lab at the Huck Institutes of Life Sciences at Penn State (http://www.bx.psu.edu/~anton/) is seeking highly opinionated and biologically inclined Postdoctoral researchers within the Galaxy Project to develop best practices for analysis of next-generation sequencing data in all areas of Life Sciences where NGS is used. Successful candidates will join a vibrant research group at the Center for Comparative Genomics and Bioinformatics at Penn State University. Please send your CV to jobs@galaxyproject.org.

Dave Clements

http://galaxyproject.org/GCC2012 http://-

galaxyproject.org/ http://getgalaxy.org/ http://usegalaxy.org/ http://galaxyproject.org/wiki/ clementsgalaxy@gmail.com

Smithsonian 2 SystematicEntomology

SMITHSONIAN INSTITUTION SYSTEMATIC ENTOMOLOGIST

The Smithsonians National Museum of Natural History seeks two systematic entomologists to conduct integrative, collections-based research programs focused on terrestrial arthropods or aquatic insects. Each successful candidate is expected to develop an internationally recognized research program utilizing modern methods, which may include bioinformatics, in pursuing systematic research on Diptera, Heteroptera, Coleoptera, or another terrestrial arthropod or aquatic insect group, with relevance to phylogenetics, genetics, evolution, morphology, behavior, biogeography, biodiversity, ecology, or related fields. Frequent publication of highly regarded papers in competitive, peer-reviewed journals, curation of collections in specialty area, service to the scientific community in leadership capacities, acquisition of external funding, engagement in outreach activities, and mentorship of students are expected.

There are two positions: (i) Federal Civil Service (U.S. citizenship required) and (ii) Trust (private sector, U.S. citizenship not required, proof of eligibility to work in the U.S. required). Both will be filled at the GS-12 level ($74,872-$79,864 per year). Applicants who are U.S. citizens are encouraged to apply for both the Federal and Trust Funded positions (two applications required). For application procedures go to www.sihr.si.edu and refer to Announcements 12A-RB-297507-DEU-NMNH (Federal) or 12A-RB-297508-TRF-NMNH (Trust), or contact Robinette Burrell, 202-633-6318, burrellro@si.edu. Applications must be received online by April 11, 2012 and must reference the announcement number. Applicants will be notified by email when their applications are received.

We encourage all qualified candidates to apply for both positions.

The Smithsonian Institution is an Equal Opportunity Employer.

Sen Brady Research Entomologist Curator of Hymenoptera National Museum of Natural History Smithsonian Institution email: bradys@si.edu phone: 202-633-0997 website: http://entomology.si.edu/StaffPages/BradyS.htm "Brady, Sean" <BRADYS@si.edu>

Smithsonian ComputGenomics

Computational Genomics Specialists

The Biodiversity Genomics Initiative, Smithsonian Institution (SI) is seeking skilled professionals with bioinformatics and computational expertise in genomics. Successful applicants will be part of a bioinformatics group working as an integrated team with Smithsonian scientists and computer support professionals. Incumbents will interact with scientists in all participating SI units including the National Museum of Natural History, National Zoological Park, Smithsonian Tropical Research Institute and Smithsonian Environmental Research Center, and may have his/her duty station located within any one of these units.

Responsibilities of these positions include: 1) Developing or implementing data analysis pipelines for Next Generation DNA Sequence (NGS) or other genome scale datasets 2) Working closely with SI scientists on the experimental design of NGS and other genome scale projects 3) Making high performance computational resources accessible to SI researchers involved in genome scale research via consultation, training, and web site development 4) Developing new experimental protocols for NGS data production in the laboratory and new procedures for computational analysis of the data produced 5) Consulting and collaborating with Biodiversity Genomics scientists, postdocs and students on research grant proposals and publication of results 6) Coordinating bioinformatics activities of the Biodiversity Genomics Initiative 7) Keeping abreast of new developments and related research conducted elsewhere in order to improve genome scale research at SI.

Knowledge, skills and experience desirable for these positions include: -Relevant scripting and/or programming skills and experience

-Expertise with NGS workbench environments (e.g., Galaxy, Biolinux, Genious, Qiime)

-Experience with NGS data analysis from multiple platforms (e.g., Illumina and 454)

-Expertise in computational aspects of one or more of the following research areas: phylogenetics, population genetics, metagenomics, gene expression, evolutionary genomics.

These positions will begin as two-year contracts, with the possibility of extension. Salaries will be commensurate with experience. To apply, submit resumé, statement of relevant experience, and names and contact information of 3 references via e-mail to Michael Braun, Chair, Biodiversity Genomics Steering Committee (braunm@si.edu). Review of applications will begin on April 1 and continue until the positions are filled.

“Fleischer, Robert” <FleischerR@si.edu>

SmithsonianInst Tech GeneticAnalysis

Technician/Pathogen Genetic Analyses Center for Conservation and Evolutionary Genetics Smithsonian Institution

We are recruiting a technician to conduct laboratory diagnoses and genetic analyses of pathogens (bacteria, fungi, parasites), including ancient DNA methods. The position will involve microscopy, DNA extraction, PCR and standard DNA sequencing, next-generation (454) sequencing, and other molecular methods as required. The position is available initially for one year and will begin as soon as possible following the deadline, but no later than May 2012. Minimum qualification is a bachelor’s degree in biology or similar field, or an equivalent combination of education or experience. Demonstrated laboratory experience is required.

To apply, email (1) a brief letter of application detailing your experience in molecular genetics, ancient DNA and diagnosis of pathogens, (2) a current curriculum vitae or resume, and (3) names, addresses and phone numbers of at least three references to Robert Fleischer (fleischerr@si.edu). Deadline for applications is 9 March 2012. Please contact Dr. Fleischer if you have any questions concerning the position.

Center for Conservation and Evolutionary Genetics Smithsonian Conservation Biology Institute National Zoological Park PO BOX 37012 MRC 5503 Washington, DC 20013-7012 USA

“Fleischer, Robert” <FleischerR@si.edu>

Tours EvolutionInsectInteractions

Dear Colleagues,

A permanent Associate professor position is available at the Institute of Research on Insect Biology (Tours, France) http://irbi.univ-tours.fr/ Title: Evolution and Chemical Ecology of multitrophic systems.

The deadline for application is 27th of March 2012.

The candidate will be involved in teaching Population Genetics, Evolutionary Genetics and Molecular Evolution at the B.Sc (3rd year) and M.Sc levels.

Research: The candidate will study signaling molecules involved in plant-insect-endosymbiont interactions, their metabolic consequences and the evolution of underlying biochemical pathways. The applicant will join a research group working on nutritional ecology of insects and on the evolution of nutrient acquisition and allocation strategies. He/She is expected to develop an integrative approach using fine chemical/biochemical techniques but candidates using other methodologies such as metabolomics, proteomics or stable isotopes are also expected to apply. Keywords: Chemical Ecology, Evolution, Metabolism, Biochemical Pathways, Nutrition, Plant-insect-endosymbiont interactions, Metabolomic, Proteomic, Stable istotopes

For more information: http://casas-lab.irbi.univ-tours.fr/giron.html http://irbi.univ-tours.fr/-index.php?page=giron contact: david.giron@univ-tours.fr

sincerely

david

Dr. GIRON David CR1 CNRS - Directeur Adjoint Institut de Recherche sur la Biologie de l’Insecte Faculté des Sciences et Techniques Parc Grandmont 37200 Tours, FRANCE david.giron@univ-tours.fr

Tel +33 (0)2 47 36 73 49 Fax +33 (0)2 47 36 69 66

En Français: http://irbi.univ-tours.fr/-index.php?page=giron In English: http://casas-lab.irbi.univ-tours.fr/giron.html http://irbi.univ-tours.fr/index.php?page=giron-uk Institut de Recherche sur la Biologie de l’Insecte Institute of Research on Insect Biology http://www.irbi.univ-tours.fr Equipe Ecologie Physique et Interactions Multitrophiques Physical Ecology and Multitrophic

Interactions group http://casas-lab.irbi.univ-tours.fr UFR Sciences et Techniques http://www.sciences.univ-tours.fr http://www.petit-pausailleur.fr/ David Giron <david.giron@univ-tours.fr>

UAlberta Tech GroundSquirrelPops

Head Field Technician Required-Columbian ground squirrels

Sheep River Provincial Park, Alberta, Canada

We are looking for a head field technician to assist with, and coordinate, fieldwork on the ecology of a wild population of Columbian ground squirrels. The head tech will supervise 4-5 volunteers for the period of May 1 to Aug 31, 2012. Duties will include monitoring the phenology (when animals emerge from hibernation), reproduction and survival of individuals, data entry and data verification. Fieldwork will involve live-trapping and handling of animals, behavioural observation, radio-telemetry (to locate natal burrows) and assistance with the measurement of physiological (metabolism) traits on free-ranging animals. The successful candidate will have previous fieldwork experience, ideally in a field camp/station setting, have experience in data entry and management and show a high level of responsibility. Additionally, you should have an interest in a number of the following (the more the better!): ecology, evolutionary biology, wildlife, field biology, and animal behaviour. Periods of time will be spent camping and, as such, successful applicants need to enjoy the outdoors, be up-beat, positive, responsible and work well as a member of a team.

All fieldwork is carried out in the spectacular Rocky Mountains of southwestern Alberta, Canada, home to some of the most majestic wildlife in North America. We will be staying at the University of Calgary's R.B. Miller research station in Sheep River Provincial Park, Alberta (http://bgs.ucalgary.ca/facilities/-facilities). You will interact with other researchers working with ground squirrels on a diversity of projects in behavioural and population ecology. Additionally, the field station is home to a number of other researchers working on a variety of projects, ranging from insects to large mammals.

Salary is $1800/month. Food, accommodation and travel within western Canada are provided. Applicants from further afield are encouraged to apply. In this case the equivalent of travel within western Canada will be reimbursed. If you wish to apply for this position, please send a CV with a cover letter and contact details of three references (with e-mail address), by email to Jeff Lane (contact info below), by April 07, 2012. Note that due to Canadian immigration laws, Canadian citizens and permanent residents will be given priority.

Contact:

Dr. Jeff Lane u.columbianus@hotmail.com Department of Biological Sciences University of Alberta Edmonton, AB Canada T6G 2E9

u.columbianus@hotmail.com

UBath MolEcology

The Department of Biology & Biochemistry at the University of Bath has just opened a search for a Lecturer in Molecular Ecology.

We seek an outstanding scientist with an established track record of independent research in molecular ecology, and in particular in ecological and environmental genomics. The person appointed will be expected to establish and sustain a rigorous externally funded research programme and to have a commitment to excellent teaching. Applications are particularly welcome from candidates who have the potential to develop and sustain collaborations with academics in our Department research themes and to foster collaboration across the University and beyond. The intention is to search broadly, so we encourage applications from people working on a diversity of topics.

Informal enquiries may be made to the Head of Department, Dr. Richard Hooley (r.a.hooley@bath.ac.uk), but please ensure that applications are submitted through the University of Bath Website.

Closing Date: Monday 30 April 2012

Further details are available online:

http://www.bath.ac.uk/jobs/Vacancy.aspx?ref=JK984 jason@evolutionarygenetics.org

UBern FieldAssist AvianEvolution

Job: UBern.FieldAssist.AvianEvolution

Field assistants in evolutionary ecology of Great tits (Parus major), Switzerland

I am looking for two enthusiastic field assistants for the upcoming field season (1st of April until end of June 2012) to join my project investigating the relationship between begging behavior and oxidative stress in great tits. The fieldwork will take place in a forest near Bern.

I will require field assistants to help with all aspects of the work, including nest checks, ringing and taking body measures of the birds, recording the nests and some smaller amount of lab work. Experience in fieldwork and bird handling would be an advantage. Since we will work many hours in the forest in all weather conditions, motivation is very important.

Applicants should speak English fluently and have a driving license.

Travel expenses and accommodation will be paid, additionally; the field assistants will receive approximately 900 Swiss Francs per month to cover their expenses.

Applications should include a CV and a short letter of motivation.

Please send your application to: Lea Maronde (Evolutionary Ecology, University of Bern) E-mail: lea.maronde@iee.unibe.ch

“Maronde, Lea (IEE)” <lea.maronde@iee.unibe.ch>

UBern FieldAssist SwedishLapland

Expenses paid field assistant positions to study life-history evolution in Siberian Jays in Swedish Lapland (May-July 2012) We are looking for a highly motivated expenses paid field volunteer to join our field project investigating life-history evolution in Siberian jays (Perisoreus infaustus). The study population is located near Arvidsjaur, Swedish Lapland. Our current project investigates the influence of dispersal timing and female quality on the evolution of life-history strategies.

The work of the field volunteer will be to help in field experiments, behavioral observations, following radio-tagged birds, and data management. This work will give insight into exciting experimental fieldwork and will be carried out partly in managed forests and partly in scenic pristine boreal habitats. We will work 5-7 days per week in the field depending on the workload of the experiments. Days in the field can be long in particular around midsummer when following dispersing individuals. Observe that temperatures in the beginning of the season can be below 0C. The work is physically strenuous at times.

Qualifications: (1) BSc/MSc in Biology, Ecology or similar qualification (2) Previous field experience (3) Ability to work in small teams and sociable personality (4) Knowledge in observing & handling birds is a plus (5) Driving license required (6) Fluent in English (7) Physically able to cope with at times strenuous fieldwork We will cover for the accommodation, travel expenses from and to the study site (up to 300 Euros) as well as the living expenses.

Applications - including a CV, a letter of motivation (1 page) and the name of two referees - should be send as soon as possible to: michael.griesser@iee.unibe.ch

Michael Griesser Institute for Ecology and Evolution University Bern Baltzerstrasse 6 3012 Bern Switzerland

Tel +41 (0)31 631 3010 michael.griesser@iee.unibe.ch michael.griesser@slu.se

http://www.iee.unibe.ch/content/staff/griesser/index_eng.html Michael.Griesser@slu.se

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UChicago TheoreticalEvolution

The Department of Ecology & Evolution at The University of Chicago is seeking to fill a tenure track position at the level of ASSISTANT PROFESSOR with an individual applying theoretical approaches to understand ecological and evolutionary processes. Applications from senior candidates will also be considered. The successful candidate will demonstrate innovation in addressing fundamental questions at the core of ecology and/or evolution. Interested applicants with a PhD must submit a CV, at least three selected reprints and preprints, and statements of research and teaching interests to http://tinyurl.com/eetheory2012. Applicants must also arrange for three letters of reference to be submitted to this site. Review of applications will begin after March 19, 2012 and continue until the position is filled.

Trevor Price <pricet@uchicago.edu>

UCincinnati LabTech PlantEvol

RESEARCH TECHNICIAN POSITION: PLANT EVOLUTIONARY/ECOLOGICAL GENETICS, UNIVERSITY OF CINCINNATI

A one-year, full-time technician position is available beginning June, 2012 in the Baucom lab in the Dept of Biological Sciences at the University of Cincinnati. General research in the laboratory addresses plant adaptation to environmental stresses. Duties will include working at the University's main campus in Cincinnati, OH and a nearby field research site. The technician's immediate responsibilities will be to carry out large field and greenhouse experiments, thus, the willingness and ability to work outside in the summer heat is a necessity. The technician will also be required to perform molecular genetics studies as well as general lab maintenance–previous experience with basic molecular techniques such as DNA isolation, PCR and cloning is desired.

The candidate should have a BA or BS in biology, genetics, horticulture or plant sciences, previous experience performing independent research, the ability to work well in a group environment, and the willingness to supervise undergraduates. The position is ideal for a highly motivated person interested in gaining field and laboratory skills prior to starting graduate school.

While I cannot accept official applications until this position is created at the University level, if this would be a position in which you might be interested, please email a CV, a cover letter of qualifications and interests, and the names and contact information of three references to regina.baucom@uc.edu. Please feel free to contact me with any questions at the above email. Review of applications will begin March 20, 2012 and continue until a suitable candidate is found. Salary is commensurate with experience and includes benefits.

Regina S. Baucom Assistant Professor Dept of Biological Sciences 721 Rieveschl Hall University of Cincinnati Cincinnati OH 45221 (513) 556-9721 Baucom Lab < http://homepages.uc.edu/ ~ baucomra/Baucom_Lab/-Home.html > gina.baucom@gmail.com

gina.baucom@gmail.com

UGoettingen PopulationGenomics

Dear colleagues,

the Faculty of Agricultural Sciences at Georg-August-Universitaet Goettingen, Germany, still invites further applications for a Junior Professorship (W1) described below. Please note that this position is especially suitable for (very) early career scientists. According to legal restrictions, to be eligible for the position the time of past employment (including the time as a PhD student) must not have exceeded six (!) years. So this job offer is actually directed to people who have finished their PhD and after that have worked a short time as a postdoc. If you fulfill this requirement, you have a background in population genetics, and you are willing to work with host-pathogen-systems in livestock (which should be clearly stated in the research statement), please give an application a serious consideration. The succesful applicant will lead an independent junior research group with an own budget and funding for scientific and technical staff. In case you need more information feel free to contact me (Henner Simianer, hsimian@gwdg.de) at any time.

And here comes again the posting:

The Faculty of Agricultural Sciences at Georg-August-Universitaet Goettingen, Germany, invites applications for a Junior Professorship (W1) for

Population Genomics of Host-Pathogen-Systems in Livestock

The position is to be filled at the earliest possible date.

The position is a fixed-term professorship for the duration of three years. Pending a positive evaluation, the position may be extended by another period of three years.

The successful candidate shall represent the subject in research and teaching. The approaches in research will aim at a better understanding of adaptation mechanisms and interactions between host and pathogens on the genomic level. Research activities will be concentrated on selected host-pathogen-systems in livestock (including aquaculture) and may have either an experimental or a more theoretical focus.

The candidate will hold an excellent PhD in a relevant discipline (e.g., agricultural science, biology, statistics). Experience in population genomics research and interest in interdisciplinary collaboration as well as in the participation in existing collaborative projects are supposed.

Please visit www.nutztierwissenschaften.uni-goettingen.de for additional information on this position (in German)

Further requirements for employment are stated in the Niedersächsische Hochschulgesetz (NHO) from February 26th, 2007. If the applicant was employed as a research assistant either before or after obtaining the doctoral degree, the entire duration of the period of employment and of the doctoral degree should not exceed six years.

The Georg-August-University Göttingen Public Law Foundation owns the right of appointment. Further details can be given upon request.

Applications of candidates from abroad are explicitly welcome. The University of Goettingen places particular emphasis on fostering career opportunities for female scientists and scholars and therefore strongly encourage qualified women to apply. Disabled persons with equivalent qualification will be given preference.

Applications should include a full CV, a list of publications, a statement of academic achievements including teaching, as well as an own representative research paper. Please submit your electronic application until March 31, 2012, to

Prof. Dr. Achim Spiller, Dean of the Faculty of Agricultural Sciences, Buesgenweg 5, D-37077 Goettingen, Germany, E-Mail: dekagrar@uni-goettingen.de

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>

UGuelph ResAssist PlantEvolution

Job Advertisement, Department of Integrative Biology, University of Guelph

Research Assistant, posted March 20 2012

The Caruso Lab is seeking a full time Research Assistant in Plant Evolutionary Ecology.

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

He/she must have (1) the ability to work independently and (2) some background in ecology and/or evolutionary biology. Experience working with plants is desirable, but not essential.

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

I am currently accepting applications, and will do so until the position is filled. The position will start in early August 2012. The initial appointment is for one year, but may be extended if funding is available. Salary will be commensurate with experience, and will include benefits.

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

– Christina M. (Chris) Caruso Associate Professor

Permanent address: Department of Integrative Biology, University of Guelph, Guelph, Ontario N1G 2W1 Canada 519-824-4120 x52030 carusoc@uoguelph.ca christinamariecaruso@gmail.com

Address until May 31 2012: National Evolutionary Synthesis Center (NESCent), 2024 W. Main Street, Suite A200, Durham, NC 27705-4667 USA 919-684-1615 carusoc@nescent.org

Chris Caruso <carusoc@uoguelph.ca>

UOregon Eugene NematodeEvolution

Research Assistant or Research Associate Institute of Ecology and Evolution Posting: 12096 Location: Eugene Closes: Open Until Filled

RESEARCH ASSOCIATE OR ASSISTANT. Full-time research position available at the University of Oregon, Eugene. Candidates having a B.A/B.S., M.S. or Ph.D. are invited to apply. We seek a highly motivated and responsible individual who enjoys participating in an interactive intellectual environment to join us in our studies of evolutionary genetics and genomics using the nematode Caenorhabditis elegans and its relatives as model systems. The candidate will be responsible for coordinating long-term selection projects, perform genetic crosses, prepare samples for whole genome sequencing, and perform general laboratory management/maintenance. Previous experience with basic molecular techniques is required, with experience with DNA sequencing and/or the genetics of model organisms preferred. Research assistant position would be under the direction of the investigator, research associate (PhD required) would participate in student training and conduct research under general guidance. Further details regarding ongoing research available at uoregon.edu/~pphil. Initial appointment for one year with salary commensurate with education and experience. Renewal possible based on performance, funding and need. Please send CV and names of three references to: Patrick Phillips, Ph.D., via ie2jobs@uoregon.edu reference search 12096 or c/o Search# 12096, Institute of Ecology and Evolution, 5289 University of Oregon, Eugene, OR 97403-5289.

The successful candidate will support and enhance a diverse learning and working environment. To assure full consideration, applications must be received by April 20, 2012, but position will remain open until filled.

The University of Oregon is an equal-opportunity, affirmative-action institution committed to cultural diversity and compliance with the Americans with Disabilities Act.

http://jobs.uoregon.edu/unclassified.php?id=3807 INSTITUTE OF ECOLOGY AND EVOLUTION 5289 University of Oregon, Eugene OR 97403-5289 F (541) 346-2364 http://IE2.uoregon.edu Equal-opportunity, affirmative-action institution committed to cultural diversity and compliance with the Americans with Disabilities Act

IE2jobs <ie2jobs@uoregon.edu>

UParis TermiteEvolution

job : position of assistant professor (CNU : 69 section, neurosciences ; Composante : LSHS, Université Paris 13) in Ecology and ethology of social insects (termites) Laboratory: BIOEMCO/LEEC Description : This position is a special MaÃtre de Conférences position called ≪ chaire mixte d'excellence ≫ based on cooperative research program , with several advantages for the successful candidate: 1) the teaching load is reduced to 1/3 of the normal teaching; 2) a scientific prize of about 10Kâper year in addition to the normal salary; 3) funding for research between 10K and 20 K per year.

Teaching: Psychophysiology in the Psycology curriculum for students in Licence and Ecology and Behaviour for students in Master 1 and 2 of Ethology. Lectures and practicals. Contact :Stéphane Chameron : chameron@leec.univ-paris13.fr

Research: Eco-ethological study of termite species of economical and ecological importance Qualifications: Applicants should have a solid and significant expertise in relevant aspects of insect biology and high profile publishing in their field. A good knowledge of insect ecology and ethology (communication, reproductive strategies, intra- and inter-specific interactions), and experience with working in the tropics will be appreciated.

Research project: The successful candidate will develop a collaborative research project involving the LEEC (University of Paris 13) and the IBIOS (Team BIOEMCO IRD France Nord). The project concerns investigation of the social organisation (division of labour, caste partitioning, nestmate recognition, reproductive strategies, etc.) and the biological and molecular features of several species of termites with different food regimes. The aim of this comparative and integrated approach should be to determine the evolutionary, ecological and ethological conditions responsible of the spreading of species that are potentially pest of tropical cultivars, in order to develop novel strategies for insect control.

deadline to Galaxie application: 27/03/2012, 16h The two laboratories to contact: 1) IRD France-Nord : UMR BIOEMCO Ãquipe IBIOS Corinne ROULAND-LEFEVRE, Director of IRD station France-Nord corinne.rouland-lefevre@ird.fr ; tel : 01 48 02 56 34

2) Université Paris 13 : LEEC EA 4443 Dominique Fresneau, lab's director mail : Dominique.Fresneau@leec.univ-paris13.fr ; Tél: 01 49 40 32 18 Patrizia d'Ettorre mail : dettorre@leec.univ-paris13.fr ; Tél : 01 49 40 31 96

Agricultural sciences, Tropical agriculture, Soil science, Forest science Environmental science, Ecology

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Chaire mixte IRD/Université Paris 13 Type : MaÃtre de Conférences(MC) CNU : 69 section, neurosciences Composante : LSHS, Université Paris 13 Laboratoire d'accueil : BIOEMCO/LEEC Profil court : Ecologie et éthologie des insectes sociaux

Description : Cette chaire mixte d'excellence IRD-Université Paris 13 est proposée en vue de développer un projet de recherche en collaboration entre le laboratoire IBIOS (Equipe BIOEMCO, IRD France Nord) et le LEEC (Université Paris 13) en éco-éthologie des termites. Ce poste présente plusieurs avantages : le lauréat devra assurer un service d'enseignement réduit à l'Université (1/3 d'un service normal) et bénéficiera d'une prime scientifique moyenne de 10Kâ¬*paranetsesrecherchesréaliséesÃl′IRDrecevrontunedotationannuelleentre10Kâet20Kâ*.

Enseignement : Filières de formation concernées : parcours de psychophysiologie en licence de psychologie (L1 ÃL3) et Master d'éthologie (M1et M2). - objectifs pédagogiques et besoin d'encadrement: Cours magistraux et Travaux Dirigés de Neurobiologie, Ethologie (L1 L3), Sciences du Comportement (Master 1 et 2). - Département : Département de Psychophysiologie Lieu(x) d'exercice : UFR Lettres et Sciences de l'Homme et des Sociétés Contact :Stéphane Chameron : chameron@leec.univ-paris13.fr

Recherche : Etude éco-éthologique d'espèces de termites ayant un impact économique et écologique Pré requis : Le candidat devra présenter une expérience avérée dans le domaine de la biologie des insectes et un très bon profil de publications. Une bonne connaissance de l'éthologie et l'écologie des insectes (communication, reproduction, relations intra- et inter- spécifiques) ainsi qu'une expérience de recherche en zones tropicales seront appréciées.

Recherche : Le candidat aura pour tÃche de développer un projet de recherche en collaboration entre le LEEC (Université Paris 13) et IBIOS (Equipe BIOEMCO, IRD France Nord) visant Ãcomparer l'organisation sociale (division du travail, régulation des castes, reconnaissance coloniale, reproduction), les caractéristiques biologiques et moléculaires chez

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UppsalaU MolEvolBiol

Permanent faculty-funded position Group leader in Molecular Evolutionary Biology

Evolutionary Biology Centre, Department of Ecology and Genetics, Sub-Department of Evolutionary Biology.

Application no later than 2012-05-04.

This is a faculty-funded permanent position for an independent researcher at the level equivalent to Assistant or Associate Professor. For an overview of on-going research at the Sub-Department, please see http://www.ebc.uu.se/Research/IEG/evbiol/research/ Work description: Independent research in evolutionary genomics, molecular evolution, or molecular ecology. Teaching including supervision of own PhD students may be included.

Required qualifications: PhD in a relevant subject area and several years of post-doctoral research experience. The research profile of the successful candidate is expected to complement and reveal synergism with ongoing research at the Sub-Department.

More information about the position can be obtained from Professor Hans Ellegren, tel. +46 18 471 6460, hans.ellegren@ebc.uu.se.

You are welcome to submit your application no later than May 4th, 2012.UFV-PA 2011/1345. Use the link below to access the application form.

http://www2.personalavd.uu.se/jobb/appform.php?lang=3Den&case=3DUFV-PA%202011/1345 How to apply: The application should include a short description of the applicant and his/her research interests. It should also include a CV, list of publications and other relevant documents including e.g. letters of recommendation or names of reference persons.

The Evolutionary Biology Centre (EBC) of Uppsala University is a leading international arena for research in evolutionary biology, see http://www.ebc.uu.se/Research/IEG/ and http://www.ebc.uu.se/Research/IOB_eng/. It offers a most stimulating atmosphere characterized by a high proportion of international students (at Master as well as PhD level) and post-docs, frequent seminars, an active grad school program geared towards the integration of genomic approaches in evolutionary biology (http://www.ebc.uu.se/education/postgrad/gradschool/) and unusual possibilities for cross-disciplinary work. EBC scientists have recently attracted five highly competitive European Research Council (ERC) Grants. EBC is connected to the Science for Life Laboratory initiative (http://www.scilifelab.se/) which is a competitive centre for high-throughput biosciences.

hans.ellegren@ebc.uu.se

USheffield EvolBiol

10 posts in Biology at Chair/Senior Lectureship/Lectureship levels

The University of Sheffield is an internationally leading centre of excellence in biology, with world-class research facilities. Biology at Sheffield was ranked 3rd in the UK in the 2008 Research Assessment exercise and 37th in the world (THE World University rankings 2011-12). We also have an outstanding reputation for the quality and breadth of expertise in biological teaching and are ranked 4th in the UK (Complete University Guide, 2012). We are looking to further our world-leading research portfolio and excellent undergraduate programmes by appointing outstanding scholars at Chair, Senior Lectureship and Lectureship levels.

Recruitment will be based on scientific excellence in research and teaching, and the successful candidates will be expected to enhance and develop our existing research/teaching strengths. The three biology departments (Animal and Plant Sciences, Biomedical Science, Molecular Biology and Biotechnology) contain around 100 academic staff and research fellows and teach 1500 students. The departments are renowned for cutting edge research and have internationally recognised strengths in evolutionary biology and genetics, cell and developmental biology, stem cell biology, behaviour and neuroscience, human health and disease, plant science and microbiology, ecology and environmental biology, and structural and quantitative biology.

Applications are invited from outstanding scholars who can demonstrate an excellent record of research publications for their career stage, proven performance in winning external research funding and who wish to play an active role in the delivery of high-quality and innovative research-led teaching. The closing date for applications is 24 April 2012 and further details, including how to apply, are available via www.sheffield.ac.uk/jobs For informal enquiries about opportunities in Evolutionary Biology, contact Roger Butlin - r.k.butlin@shef.ac.uk

r.k.butlin@sheffield.ac.uk

UTexasAustin LabTech FishParasiteInteractions

Job summary:

The Bolnick lab in the Section of Integrative Biology at the University of Texas at Austin, is seeking a highly motivated research technician to assist with a study of the evolution and quantitative genetic basis of interactions between helminth parasites and fish hosts. For more information on the Bolnick lab, visit: https://webspace.utexas.edu/dib73/Bolnicklab/-Bolnicklab.html Responsibilities will include: The primary responsibility of the lab technician will be animal care, including husbandry of a large laboratory population of fish (threespine stickleback), and maintaining a culture of a cestode parasite. Additional responsibilities, as time allows, will include surveying parasite abundance and identity in samples of wild-caught stickleback, DNA extraction, PCR, and sample preparation for next-gen sequencing. The technician will have the opportunity to assist with periodic field work on Vancouver Island, Canada, to obtain specimens. The technician may also assist with daily management of the laboratory, including purchasing, equipment maintenance, and database management.

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

Preferred qualifications: Experience with one or more of the following is desirable: fish care, molecular genetics, parasitology, or immunology.

Position Title: Research Technician 1

Employer: Howard Hughes Medical Institute

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

Classification: Full-time

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

Start date: No later than June 30 2012

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

To apply:

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

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

2) a curriculum vitae

3) the names of three references

The application may be sent via email as a pdf file (preferred) or word file to: danbolnick@mail.utexas.edu

HHMI is an Equal Opportunity Employer.

Dr. Daniel I. Bolnick

Early Career Scientist Howard Hughes Medical Institute

Associate Professor Section of Integrative Biology One University Station C0930 University of Texas at Austin Austin, TX 78712

512-471-2824 fax 512-471-3878 https://webspace.utexas.edu/dib73/TheBolnickLab/Home.html danbolnick@mail.utexas.edu

UToulouse EvolutionMicrobes

Ecole nationale de Formation agronomique de Toulouse Université de Toulouse Lecturer (MaÃtre de Conférences) in Integrative Biology and ecology of microorganisms MC 23-805 - Section CNECA nÂ2

A lecturer position will be opened at the Ecole nationale de Formation agronomique at the end of June 2012 or beginning of September 2012. The lecturer will join the team EVEC (évolution des traits d'historie de vie et écologie Comportementale) of the Laboratory ≪~Evolution et Diversité biologique~≫ (EDB~; UMR 5174 CNRS - Université Toulouse III - ENFA). The EDB laboratory aims at understanding the ecological and evolutionary processes that generate and maintain biological diversity at the gene, individual, population and community levels. By focusing on the interactions between organisms, the laboratory's objectives are to evaluate and characterize biodiversity, study the mechanism of change in biodiversity, and evaluate the role of selection in populations and speciation.

The successful applicant is expected to develop a research project in integrative biology and ecology of microorganisms. A member of EDB, he/she will be part of the Laboratory of Excellence (LABEX) TULIP. Through his/her strong contribution to microbiology, he/she will participate to research programmes on host-parasite interactions or on the impact of parasite transmission through sex, which are currently developed in EDB and other laboratories of TULIP. He/she will also reinforce research on interactions between microorganisms and their metacellular hosts. In this context, his/her project may pay more attention to microorganisms involved in interactions between prey and predators hence affecting speciation.

Qualifications and competencies: PhD in biological sciences; Abilities in experimental studies of molecular determinism of phenotypic traits in microorganisms Credentials in evolutionary biology; Teaching experience or any professional experience after the Ph D is expected

Contacts~: Director of ENFA~: M. Bascle - tél.~: 05 61 75 32 16 (michel.bascle@educagri.fr) EDB Chairman: E. Danchin - tél~: 05 61 55 73 84 (etienne.danchin@univ-tlse3.fr) EVEC~: J.-L. Hemptinne - tél~: 05 61 75 32 95 (jean-louis.hemptinne@educagri.fr)

Jean-Louis Hemptinne PR Ecologie et Didactique de l'Ecologie Université de Toulouse - Ecole nationale de Formation agronomique UMR CNRS 5174 Evolution et Diversité biologique BP 22687 F-31326 Castanet-Tolosan Cedex

Tel : (+33)0561753295 Fax : (+33)0561750309

JEAN-LOUIS HEMPTINNE <jean-louis.hemptinne@educagri.fr>

UWollongong MarineBiodiversity

Please post on Evoldir

Faculty of Science, School of Biological Sciences Applications are sought for a tenure-track Lecturer position (Lecturer level B) in the School of Biological Sciences at the University of Wollongong. The appointee will be expected to teach at all levels in subjects dealing with marine biodiversity, fisheries and aquaculture, and marine ecology.

Evolutionary biology is a strong theme within the school and the core research activity several staff. Marine Biologists with expertise in evolutionary biology are strongly encouraged to apply.

We are seeking candidates with experience in the area of marine biology. Candidates with research interests that would lead to productive collaborations with current academic staff are particularly encouraged to apply. Demonstrated excellence in research and the potential to attract external research funding is essential. The successful candidate will be expected to develop a research program within the School and to supervise honours and postgraduate research students.

The University of Wollongong has recently built a state-of-the-art research facility for contained animal and plant experiments, comprising 576 m2 of laboratory space. The successful candidate will be expected to become a member of and contribute to the Institute for Conservation Biology and Environmental Management (ICBEM http://www.uow.edu.au/science/biol/icb/index.html) , a key area of research strength within the University. Applicants must address the selection criteria specified in the Position Description, which is available from the University Website (http://employment.uow.edu.au). Further information can be obtained from Associate Professor Mark Dowton, by telephone (+61 2) 4221 3429 or by email (mdowton@uow.edu.au). Information about the School can be obtained from our website (http://www.uow.edu.au/science/biol/).

Applications Close 8 April 2012 Quote Ref No: 24211

David Ayre

David Ayre <dja@uow.edu.au>

UWyoming DirectorBiodiversity

Director University of Wyoming Biodiversity Institute

The newly founded University of Wyoming Biodiversity Institute is dedicated to world-class biodiversity research, education and training of graduate and undergraduate students, and dissemination of scholarship to support biodiversity conservation and management. We seek an energetic Director, hired at the rank of Full Professor, to develop this new program to its full potential as one of the world's leading biodiversity enterprises. This Institute provides an outstanding opportunity for a visionary leader to coordinate the University's resources in its internationally recognized programs in ecology, environmental sciences, and natural resource economics, and build an innovative interdisciplinary and collaborative program addressing multiple dimensions of the globally critical field of biodiversity research. While biodiversity sciences will anchor the Institute, human interactions with the natural environment are considered acritical focus of the Institute's work. For more i nformation about the University of Wyoming Biodiversity Institute please visit: www.uwyo.edu/acadaffairs/ad/biod.pdf . The Director will establish the Institute's curricula with opportunities for student research, field experiences and internships. The Director also will oversee outreach activities designed to serve the needs of the public and Wyoming state agencies and non-governmental organizations. The Biodiversity Institute will be housed in the University of Wyoming's Berry Biodiversity Conservation Center: www.uwyo.edu/berrycenter/ . The successful candidate will possess an internationally recognized reputation in biology, a passion for biodiversity, a commitment to the broadly inclusive mission of the Institute, proven leadership abilities, clear evidence of successful working relationships with faculty across disciplinary boundaries, and skills to represent the Institute effectively to state and national stakeholders and to the public. Preferred qualifications include: 1) leadership experience demonstrating vision, managerial ability, and communication skills; 2) the ability to create synergy with other University programs and with stakeholders; 3) a commitment to integrating academics, research excellence, and the outreach mission of the Institute; and 4) an internationally recognized record of teaching and research in biology, including a proven record of external grant support. Minimum qualifications include: 1) an earned doctorate; and 2) demonstrated excellence in research, teaching, and professi onal service commensurate with a tenured appointment at the rank ofFull Professor.

We seek to fill this full-time, 9-month position starting 21 August 2012. Applications should include: 1) a letter describing the applicant's qualifications and experience related to the position; 2) a curriculum vitae; and 3) names and addresses of three references. Review ofapplications will begin on April 30, 2012, but applications will be accepted until the position is filled. Please email all application materials as pdf attachments to Ms. Wilma Varga (wilmav@uwyo.edu) and reference the position number (#4916). Inquiries about the position can be made to Dr. David G. Williams (dgw@uwyo.edu).

The University of Wyoming is committed to diversity and endorses principles of affirmative action. We acknowledge that diversity enriches and sustains our scholarship and promotes equal access to our educational mission. We seek and welcome applications from individuals of all backgrounds, experiences, and perspectives.

Matt Carling Asst. Professor Department of Zoology & Physiology Berry Biodiversity Conservation Center University of Wyoming

www.uwyo.edu/carlinglab (p) 307.766.6169

mcarling@uwyo.edu

UZaragoza PlantEvolution

This is the announcement of an Araid-EU 2012 international call for the recruitment of permanent researches in Aragon (Spain). The call has been launched by the regional Aragon Government Araid Foundation and is co-funded by the EU. We are looking for a potential experienced postdoctoral candidate that would comply with the scientific requirements of the call and would have a good Curriculum in plant evolution, plant genetics, plant biology, or related lines, and would like to come to work with us to Huesca as a permanent researcher. Interested candidates please contact Prof. Pilar Catalan (pcatalan@unizar.es). The deadline for applications is 3.April.2012. sincerely,

Prof. Pilar Catalan Escuela Politecnica Superior de Huesca Universidad de Zaragoza Ctra. Cuarte km 1 22071 Huesca (Spain) phone +34 974233465 fax +34 974239302

Call for permanent research position ARAID-EU 2012: Bioflora research group

Scientific profile:

Biodiversity, evolution and conservation genetics of plants

We seek for potential candidates that would like to apply for a permanent research position within the ARAID-EU 2012 international call for applications (see attached information below) to work at the High Polytechnic School of Huesca ? University of Zaragoza (Huesca, Spain). We look for a specialist in evolutionary and population genetic analysis of plants. The researcher should have experience in molecular biology techniques and statistical and evolutionary analyses on genomics, phylogenies, population genetics, phylogeny and ecological and population dynamic modelling analyses applied to the investigation of evolutionary biology, comparative genomics, bio/phylogeography and the development predictive models for the study and conservation of the wild flora. The expert should have a good knowledge in statistic programming and biocomputing. Candidates with a postdoctoral training and expertise in Botany, Plant Genetics, Plant Ecology or similar background and with expertise in studies of plant biodiversity and conservation genetics are invited to apply to the job. We are looking for a motivated scientist with experience as leader of research projects and training of scientific staff. The expert will conduct the research and will supervise scientific and technical staff in evolutionary biology, inheritance patterns, functional and adaptive ecology, and genomic and transcriptomic analyses of wild plants. The selected candidate will be incorporated to the Bioflora research group at the High Polytechnic School of Huesca (University of Zaragoza). His/her research activities will include the collaboration in current research projects, the leading of new research projects submitted to national and European calls, the participation in master courses, and the transfer of the scientific results to administrations and agencies. Research centre: University of Zaragoza. High Polytechnic School of Huesca (Huesca, Spain). Plant Evolutionary Laboratory. Bioflora Research group (http:/-/bifi.es/bioflora/FrontPageBioFlora/History.htm). Interested candidates please contact Professor Pilar Catalán (pcatalan@unizar.es). Deadline for applications: 3.April.2012. ARAID area of priority: Environment and sustainability

International Call for the Recruitment of Researchers ARAID-EU PROGRAMME 2012

ARAID has launched an international call for applications to fill up to 18 research positions in different areas. The call for applications is open to any candidate that fits the requirements of mobility, academic background and postdoctoral experience. Only outstanding candidates with excellent research record and leadership capabilities will be considered. It is expected that the successful candidates will boost teams at Research Centres and Companies. ARAID researchers are expected to make a substantial contributions to their areas of research and be active members of the regional science-technology system. Applications must be submitted electronically through this website before 14.00h (GMT) April 3rd 2012. The final number of researchers to be hired depends on the quality of the proposals and budget availability.

Requisites for the candidates:

Research Experience: Candidates must be in possession of a doctoral degree and have at least six years of full-time equivalent research experience: Depending on their research experience they will be considered as: - Experienced fellows : PhDs with 6 to 10 years of research experience - Very experienced fellows: PhDs with more than 10 years of experience and an research stage of at least two years in a research institution/company located in a different country to the one were obtained its PhD. Mobility: Comply with one of these two types of trans-national mobility taken into account by the ARAID-EU Programme: Incoming mobility for non-residents in Spain or residents that have not

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YaleU ResAssist DNAanalysis

Research Assistant I

DNA Analysis Facility on Science Hill

Department of Ecology and Evolutionary Biology

Yale University

Location: New Haven, Connecticut

Official Start Date: Flexible but before July 29, 2012

The DNA Analysis Facility on Science Hill (http://dna- analysis.research.yale.edu//) is in the initial stages of recruiting for a Full-Time Research Assistant position, which will become open for hire in July 2012 with a flexible start date. Our Facility is located within the Laboratory of the Yale Institute for Biospheric Studies Molecular Systematics and Conservation Genetics Center (http://www.yale.edu/caccone/ecosave/index.html) bothunder the Direction of Dr. Adalgisa Caccone.

We are looking for an enthusiastic and self-motivated person, who enjoys acquiring new skills and working with a team of evolutionary geneticists and students. Although the primary responsibilities for the position are to assist with the daily operations of the Core Facility there is the possibility of participating in independent research projects connected with the YIBS-MSCG Center.

General Purpose: Work as part of a team within a high-volume DNA Analysis Core facility that provides services to researchers at Yale and the broader scientific community. Assist in preparing and processing DNA Sequencing and Fragment Analysis samples. Review data and provide troubleshooting support.

1. Assist with all day-to-day operations of the Facility including sample prep, processing and data review using a web- based Laboratory Information Management System to process and manage orders.

2. Follow established Standard Operating Procedures and ensure compliance with OEHS regulations.

3. Operate and perform routine maintenance of laboratory equipment including Applied Biosystems 3730xl Genetic Analyzer, Thermal Cyclers, manual and electronic single and multi-channel pipets and centrifuges.

4. Order and maintain stock solutions and lab supplies.

5. Effectively communicate and interact with facility users, in person, over the phone and through email to answer routine questions regarding setting up new user accounts, sample submission and preparation and general information regarding billing procedures.

6. Use a variety of software applications to analyze and review data for quality control and troubleshooting purposes.

7. Troubleshoot an array of issues with data pipelines and custom scripts written in Perl and Bash to ensure efficient delivery of data to users.

Education and Experience: a Bachelor degree in a biological field

Skills and Abilities:

1. Experience with Sanger Sequencing Data or Microsatellite Analysis, and/or involvement in a Population Genetics Project.

2. Experience in standard molecular biology and general laboratory techniques.

3. Ability to effectively communicate with scientists of various levels of training; from Principal Investigators to Undergraduates.

4. Work independently as well as part of a team.

5. Familiarity with MAC, PC, and common software packages such as MS Office, Adobe, Dreamweaver and SFTPs.

Additional Education and Experience: Educational emphasis in biology, genetics, or biochemistry preferred. Candidates with prior experience in Sanger Sequencing, Microsatelite Analysis, Population Genetics, Linux Administration, programming in Perl and Databasing with SQL, will be given immediate consideration.

Work Hours: minimum of 37.5 hours. Modified workweek with a combination of weekday and weekend hours, typical workday 10-6pm M-F, with overtime as needed.

Conditions of Appointment: Yale staff are offered a salary according to qualifications and work experience. The range of salaries for a level C Research Assistant technician is $19.47-$21.38/hour. This is a full time appointment (37.5 hours per week) initially for a two-year term, and subject to evaluation after the first year. For benefits description please refer to the following web site: www.yale.edu/hronline/benefits/ct.html For preliminary inquiries please contact Dr. Adalgisa Caccone at adalgisa.caccone@yale.edu and include a CV with your message.

Carol Mariani <carol.mariani@yale.edu>

Other

Best methods for Phylogenetics

Dear EvolDir Members,

When you were asked the question “What can phylogenetics and molecular dating do nowadays”, which top 3 papers would you cite? Which studies impressed you most regarding number of taxa included, number and quality of calibration points/available fossil data base, quality of methods used for phylogenetic inference, number/length of genes (genomes) included, methods for molecular dating used and so on....What is your personal gold standard today? Or in other words, which studies would you present in a class as today’s state of the art?

I would very much appreciate your suggestions. Best Lars

Dr. Lars Opgenoorth Department of Ecology University of Marburg Karl-von-Frisch Strasse 8 35043 Marburg

Phone: *49 (0) 6421 28-22080 Fax: *49 (0) 6421 28 23387

Lars.Opgenoorth@uni-marburg.de

Lars Opgenoorth <Lars.Opgenoorth@staff.uni-marburg.de>

BUCKy

Has anyone had this issue trying to run BUCKy (Bayesian Untangling of Concordance Knots), a species/gene tree reconciliation program (Ané et al.

(2007)? The program loads the *.in files (the individual locus input files generated from Mr.Bayes output using the component mbsum), but crashes for me whenever it starts to generate the main event, the concordance file wherein species trees are written. The concordance file will only have a single line with the word "translate" in it after the crash. I have written to both authors, and neither has responded. I have tried running the program in Windows 7 and Windows XP, but not (yet) Linux. That may be the problem - the Windows executable is I believe fairly new and may be buggy. Any ideas will be appreciated.

Thanks, Alan

Alan W. Meerow, Ph.D., Research Geneticist and Systematist USDA-ARS-SHRS, National Germplasm Repository 13601 Old Cutler Road, Miami, FL 33158 USA voice: 786-573-7075; cell: 786-412-1821; FAX: 786-573-7102 email: alan.meerow@ars.usda.gov

Alan.Meerow@ARS.USDA.GOV

Coalescent simulations

Hi,

I'm doing my Masters and am trying to figure a few things out about coalescent simulations in DNA SP.

If I am looking for recombination via the ZZ statistic of Linkage disequilibrium, then it is my understanding that ZZ increases as recombination increases. Am I right in thinking that because I need the value to be significantly HIGH, that I am looking for a p-value (in the DNA SP coalescent simulation tool) that is 0.975 or higher? My thinking is that this would mean that there is a $p<0.025$ chance of ZZ being higher than observed and therefore being classed as significant under a 95% confidence? If I got this value, would this be an indication of recombination within that population?

I have similar issues with Fu's Fs statistic, where I am looking for a significantly high value that would point towards a population bottle neck.

Thanks

Adrian Blake Adrian.Blake@Postgrad.Manchester.ac.uk

Estimates relatedness

Dear all,

As part of my masters thesis I will be applying genetic markers (microsatellites) to the management of captive breeding programs for Crocodylus species in Colombia. I am interested to know of any programs that incorporate information from multilocus genotype data to calculate estimates of relatedness and inbreeding coefficients as well as being able to incorporate pedigree data.

Thanks in advance,

Carolina

Carolina Ibáñez Rincón Zootecnista Grupo de Biodiversidad y Recursos Genéticos Instituto de Genética, Universidad Nacional de Colombia Tel 57-1-3165000 Ext 11614

lepidopteros@gmail.com

Evolution2012 UndergraduateDiversity Deadline

Undergraduate Diversity at Evolution 2012 - Application Deadline Approaching

We are pleased to announce an undergraduate travel award to bring talented and diverse undergraduates to the Evolution meetings this July 6-10 in Ottawa, Canada. For the 10th year in a row we will fly a cohort of undergraduates from throughout the US and Puerto Rico to present a poster at the meetings, receive mentoring from graduate students, postdocs and faculty, and participate in a career-oriented 'Undergraduate Futures in Evolutionary Biology' panel and discussion. The program covers the costs of travel, registration, food and accommodation at the meetings.

The application deadline is Friday, March 30th, and decisions will be announced by Friday, April 6th. Applications are welcomed from all undergraduates, and the admissions goal is to create a diverse pool of students.

An overview of the program and student eligibility can be found at:

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

www.nescent.org/Evo2012undergradapp Applications consist of a short statement of interest, a letter of recommendation and the title and abstract of the poster to be presented.

In addition, we will be soliciting names of graduate students, postdocs and faculty members who would like to serve as mentors during the meetings. Mentors meet with pairs of students and attend talks with them, introduce them to colleagues, network and generally make the meetings a welcoming place for them. Although costs are not covered for mentors it is an unusually rewarding experience. Contact Richard Kliman <rmkliman@cedarcrest.edu> if you are interested in serving as a mentor.

For inquires contact one of the organizers:

Scott Edwards - sedwards@oeb.harvard.edu Richard Kliman - rmkliman@cedarcrest.edu Jory Weintraub - jory@nescent.org

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

“Weintraub, Jory P” <lviscrst@live.unc.edu>

Intergenic hybrids

Hi everyone,

A colleague and I are looking for studies that have documented natural intergeneric (or other levels 'above' that of species) hybridization in animals and fungi.... having a harder time than expected in finding such studies. Citations or PDFs or further off-list discussion welcomed.

Thanks much.

Erin Tripp Rancho Santa Ana Botanic Garden Claremont, CA

etripp@rsabg.org

IntlJEvolBiol DiseaseEvolution CallPapers

We are currently looking for submissions for a special issue of International Journal of Evolutionary Biology on the evolution and epidemiology of bacterial pathogens. Topics to be addressed by the issue include, but are not limited to:

- Comparative genomics of pathogenic and non-pathogenic bacterial genomes - Molecular epidemiology of bacterial pathogens - Typing approaches for molecular epidemiology - Evolutionary forces affecting bacterial pathogens and populations - Metagenomic approaches in health and disease - Bioinformatics tools for bacterial genomics

More details can be found here: http://-www.hindawi.com/journals/ijeb/si/823204/cfp/ Lead Guest Editor: Iñaki Comas, Genomics and Health Unit, Centre for Public Health Research (CSISP), Avenida Cataluña 21, 46020 Valencia, Spain inaki.comas@uv.es

Guest Editors:

Kathryn E. Holt, Department of Microbiology and Immunology, The University of Melbourne, Parkville, VIC 3010, Australia kholt@unimelb.edu.au Laura Gómez-Valero, Biologie des Bactéries Intracellulaires, Institut Pasteur, 25 rue du Dr. Roux, 75724 Paris Cedex 15, France lgomez@pasteur.fr Darío García de Viedma, Clinical Microbiology and Infectious Diseases Service, Institute for Health Research, Gregorio Marañón, Calle Dr. Esquerdo 46, 28007 Madrid, Spain dgviedma2@gmail.com

Both review articles and data papers are encouraged. If you are thinking to submit a manuscript please write to inaki.comas@uv.es

Best regards,

Iñaki

IÑAKI COMAS , PhD

Genomics and Health Unit Centre for Public Health Research (CSISP) Avenida de Cataluña, 21 46020 Valencia Spain

email: inaki.comas@uv.es or icomas@nimr.mrc.ac.uk or comas_ina@gva.es Phone: (0034) 961925959

inaki.comas@uv.es inaki.comas@uv.es

IonTorrentReviews answers

Recently I posted a message asking for feedback from users of the Ion Torrent and how it compares to the Illumina MiSeq.I received many responses from others interested in the answer to this question, but unfortunately I did not receive any replies from anyone actually using this equipment. I did however receive some links to other sites with pertinent information and a very informative comparison of these two platforms.These are listed below.I would still appreciate any additional information on this topic.

Thank you,

Carla Hurt, Ph.D. hurtc@bio.miami.edu

Dept. of Biology Cox science center, rm 36 1301 Memorial Dr., University of Miami Coral Gables, Fl 33146

1.) Here are some blog posts that you might find helpful:

http://www.massgenomics.org/2011/02/small-ball-sequencing-on-the-benchtop.html http://www.massgenomics.org/2011/04/iontorrent-benchtop-sequencing-streamlined.html http://www.massgenomics.org/2011/06/first-look-data-from-iontorrents-316-chip.html

And then here is a recent anouncement from Life Technologies about a

new small sequencer:

http://goo.gl/9X8lc 2.) Here is a very helpful blog with information about many NGS platforms:

http://omicsomics.blogspot.com/ I also contacted Dr. Keith Robison - the author of this blog - and asked him specifically to compare the Ion Torrent and the Illumina MiSeq.His response is pasted below.

Just as a reminder – I haven't had hands on either machine (I have yet to see a MiSeq up close) but I have had data generated for me on both systems & have tried to seriously envision what each system would be like to have in a lab at my employer in terms of cost & labor.

Some key points to consider:

Both machines have a sequence output well suited for amplicon sequencing and for small genome sequencing (probably up through a few tens of megabases). Neither is well suited for really large genomes, metagenomes, for transcriptomes or for counting applications (e.g. ChIP-Seq) – the numbers of reads and amount of data are really too small and the cost per basepair is much higher than a system like HiSeq.

From a user's perspective, the main two reasons to go with these systems rather than HiSeq/GAIIx is the low cost per experiment and rapid turnaround time.

MiSeq has a greater range of software on the academic/freeware side; Ion doesn't really seem to have caught the bioinformatic developer community's imaginaition. Some software developed for 454 should work with Ion Torrent data, due to each having similar error profiles (homopolymer runs); this error profile also frustrates some software designed for Illumina. On the other hand, a lot of tool are platform-agnostic. On the commercial side, there does seem to be healthy support for all platforms.

Contrasting the two systems further are the read profiles. MiSeq offers a number of read lengths up to 150x2 paired end (which is longer than HiSeq and perhaps one reason why MiSeq may have an edge over HiSeq for genome assembly). Ion now has ˜250bp reads (you get a distribution) and a paired end protocol, though not a lot of groups are using it & I haven't seen 250x2 paired end data yet (which would be very cool to have!).

Both are probably going to have further read length improvements. I'm guessing the next Ion mark will be in the 300-350 range and probably be released sometime this spring. Several groups have demonstrated greater than 150 bp runs on the MiSeq, and Illumina will be releasing longer kits this summer (I think 250x2 is the first one).

Overall, I think the true end-to-end run times are getting very similar, but Ion may still be a bit better – if you are willing to put in the extra labor. Also, in planning throughput the timings can be troublesome. For example, right now the 150x2 mode takes 27 hours, which means if you were running just that & didn't have shifts 24x7, it is hard to keep the machine cranking all week (Illumina is finding clever ways to shorten cycle time; I think their reps told me the 250x2 will take /less/ time than that, though I could be remembering that wrong.).

it does appear that the 318 chip is the end of the PGM line, though LIFE has not made that explicit – Proton will be the instrument for doing big sequencing. MiSeq will get an upgrade this summer to allow reading both surfaces of the flowcell; this will roughly double the amount of data. Both will probably top out at a size suitable for targeted sequencing in model systems or with very focused exome arrays (but not whole exome).

— / —

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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OrthoMaM database update

Dear Evoldir members,

We are pleased to announce the release of OrthoMaM version 7: a major update of our database of orthologous single-copy nuclear markers (exons and CDS) for mammalian phylogenetics.

It can be browsed and queried at:

http://www.orthomam.univ-montp2.fr/ The new version 7 is based on EnsEMBL release v65 and now includes 6,111 exons and 13,111 CDS alignments for 39 mammalian species.

Major changes from the previous version 6 include:

* Requests on 39 species instead of 36 (based on EnsEMBL v65 December 2011). * Alignments have been improved and now rely on MACSE to detect potential frameshifts (indicated by "!"). * Unreliable alignment sites/sequences are removed using trimAl before phylogenetic analyses using RAxML (raw and filtered alignments are provided). * Exon orthology prediction has been improved and is now based on the corresponding CDS alignments. * Marker detail rendering is now compatible with most web browsers: Firefox, Internet Explorer, Safari, Chrome. * A visual rendering of GO annotation is now available based on the OntoFocus tool.

The article describing the original database is freely available from BMC Evolutionary Biology:

http://www.biomedcentral.com/1471-2148/7/241 OrthoMaM: A database of orthologous genomic markers for placental mammal phylogenetics Vincent Ranwez, Frederic Delsuc, Sylvie Ranwez, Khalid Belkhir, Marie-Ka Tilak and Emmanuel JP Douzery BMC Evolutionary Biology 2007, 7:241 (doi:10.1186/1471-2148-7-241)

We hope this will be of use to members of the evolutionary community.

Frederic Delsuc and co-authors

Frédéric DELSUC (Chargé de Recherche CNRS) Laboratoire de Paléontologie, Phylogénie et Paléobiologie CC064 Institut des Sciences de l'Evolution UMR5554-CNRS Université Montpellier II Place Eugène Bataillon 34095 Montpellier Cedex 05 France Tel: (+33) 4 67 14 39 64 FAX: (+33) 4 67 14 36 10 Email: Frederic.Delsuc@univ-montp2.fr Webpage: http://fdelsuc.perso.neuf.fr Frederic.Delsuc@univ-montp2.fr Frederic.Delsuc@univ-montp2.fr

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Panama VolFieldAssist SocialWasps

Volunteer Field Assistant Required Social Behaviour in Tropical Paper Wasps Mid April - Late June 2012

A volunteer field assistant is required to help with a field-based project on social behaviour in social wasps. The position is a fantastic opportunity to gain tropical field experience working in a vibrant research group, from the Institute of Zoology, Zoological Society of London (www.zsl.org/seiriansumner). The project is concerned with the evolution of castes (queens and workers) in Polistes paper wasps. These are a well-studied genus of social insects representing the early stages of social evolution where castes lack morphological differences, but have clear behavioural roles. Our study species is the tropical Polistes canadensis, found in Central and South America. It builds small nests (c20-60 females) that lack an envelope, so individually marked wasps can be easily observed and castes can be manipulated. The 2012 field site is based near the Smithsonian Tropical Research Station at Galatea, Colon, Republic of Panama and the field season will run from mid April until end of June.

The work involves marking wasps, conducting censuses and behavioural observations and simple manipulation experiments. Assistants are generally expected to be graduates with a good degree in the biological sciences, background in and keen interest in behavioural ecology and/or social evolution.Â Experience gained on the project will be especially useful for those soon to commence a field-based MSc or PhD project.Â Applicants should be fit, enthusiastic, hard working, and happy with living shared accommodation and working in uncomfortable conditions. Previous experience of working on social insects and/or in the tropics would be an advantage. A clean driving license and some basic knowledge of Spanish is also desirable. The applicant should be comfortable and must be able to commit to the full field season. NB these wasps do sting if provoked!

All work-related costs in Panama will be paid, including accommodation. In addition the assistant will receive a minimum of Â£500 towards travel costs (e.g.

air ticket). More details are available from Dr Seirian Sumner (Seirian.Sumner@ioz.ac.uk) and/or Dr Solenn Patalano (solenn.patalano@babraham.ac.uk). Applications should include CV (with email addresses for two referees) and a covering letter explaining why you would like to work on the Project. Applications should be submitted by e-mail to both Drs Sumner & Patalano by Thursday 24th February 2012. Shortlisted applicants will be notified by email by March 1st, and will be invited for interview either in person or over skype/phone soon afterwards.

Dr Seirian Sumner Research Fellow Institute of Zoology Zoological Society of London Regent's Park London, NW1 4RY

Tel: +44 (0) 207 449 6617 Fax: +44 (0) 207 586 2870 Home: +44 (0) 1491 652 882

Web: www.zsl.org/seiriansumner ZOOLOGICAL SOCIETY OF LONDON LIVING CONSERVATION Registered Charity no. 208728

Seirian Sumner <seirian.sumner@googlemail.com>

Phyloinformatics Summer of Code

Are you a student interested in evolutionary biology and open-source software development?

PHYLOINFORMATICS SUMMER OF CODE 2012

http://informatics.nescent.org/wiki/-Phyloinformatics_Summer_of_Code_2012 The Phyloinformatics Summer of Code program provides a unique opportunity for undergraduate, masters, and PhD students to obtain hands-on experience writing and extending open-source software for evolutionary informatics under the mentorship of experienced developers from around the world. The program is the participation of the US National Evolutionary Synthesis Center (NESCent) as a mentoring organization in the Google Summer of Code(tm) (http://code.google.com/soc/).

Students in the program receive a stipend from Google (and the coveted T-shirt upon completion!), and work from their home, or home institution, for the duration of the 3 month program. You will have to opportunity to collaborate with our enthusiastic mentor community, and will have at least one dedicated mentor to help you complete your project.

We are particularly targeting students interested in both evolutionary biology and software development. Our website, above, lists potential projects. Projects include many programming languages (e.g. C/C++, Java, Perl, R) and cover subjects ranging from visualization to algorithm implementation to data interoperability. You don't need to be an expert in either evolutionary biology or software development - find a project idea that interests you, and we can work with you to develop a proposal that fits your skills. We also welcome novel project ideas apart from those already on the list.

INTERESTED? Contact us phylosoc {at} nescent {dot} org. We strongly encourage all interested students to get in touch with us with their ideas as early on as possible. Admission is competitive, and we want plenty of time to work with you to develop a great project proposal.

TO APPLY: Apply online at the Google Summer of Code website:

http://www.google-melange.com/gsoc/homepage/-google/gsoc2012 where you will also find GSoC program rules and eligibility requirements. The 14-day application period for students opens on Monday March 26th and runs through Friday, April 6th, 2012.

Google Summer of Code FAQ: http://www.google-melange.com/gsoc/document/show/gsoc_program/-google/gsoc2012/faqs Karen Cranston and Jim Proctor National Evolutionary Synthesis Center http://nescent.org karen.cranston@gmail.com

Karen Cranston <karen.cranston@gmail.com>

Phyloseminar DavidLiberles

"Protein Structural, Biophysical, and Genomic Underpinnings of Protein Sequence Evolution" David Liberles (U Wyoming)

Common models for amino acid substitution assume that each site evolves independently according to average properties in the absence of a genomic, protein structural or functional context. Two characterizations of amino acid substitution will be presented. One approach extends a population genetic model to interspecific genomic data and a second approach evaluates the effects of selection for protein folding and protein-protein interaction on sequence evolution. Several take home lessons include the importance of considering linkage independent of protein structure, the importance of negative pleiotropy (or not statements in folding and binding), and the nature of the co-evolution of sites and how it links standard substitution models with covarion models when binding function is conserved and when it changes.

West Coast USA: 13:00 (01:00 PM) on Wednesday, March 28 East Coast USA: 16:00 (04:00 PM) on Wednesday, March 28 England: 21:00 (09:00 PM) on Wednesday, March 28 France: 22:00 (10:00 PM) on Wednesday, March 28 Japan: 05:00 (05:00 AM) on Thursday, March 29 New Zealand: 09:00 (09:00 AM) on Thursday, March 29

Frederick "Erick" Matsen, Assistant Member Fred Hutchinson Cancer Research Center http://matsen.fhcrc.org/ ematsen@gmail.com

Pyrenees VolFieldAssist EvolBiol

Field assistants: Volunteer positions in evolutionary biology

The Barton group (Evolutionary genetics) at IST Austria requires volunteers to assist with field work on plant speciation in the Pyrenees (Spain) this coming summer (May-July).

The project: We are studying the evolutionary dynamics underlying species diversification in the genus Antirrhinum (snapdragons). Several major loci have been identified that underlie interspecific variation in flower colour, which is the thought to be a primary driver of species diversification in snapdragons. We are using a range of ecological, molecular and population genetic studies to further investigate the dynamics underlying the speciation process in a hybrid zone between species with different flower colours. This is a great opportunity for anybody looking to obtain experience in field work relating to evolutionary biology, plant ecology and plant-animal interactions. You will also be part of a large multidisciplinary team including researchers from IST Austria (Vienna), John Innes Centre (Norwich, UK) and the University of Toulouse.

For these positions we are looking for hard working and enthusiastic biology students with a strong interest in working in the field with plants. We require people willing to work ˜6 days a week with potentially long days in the field. Some evening work may be required. You must also be comfortable working as part of a team. Familiarly with Spanish and a driver's license is preferred but not essential.

We require assistance between mid May and early July. Length of stay is flexible but a minimum stay of 3 weeks is required.

The field site is located close to the town of Planoles in the Eastern Pyrenees of Northern Spain. It is easy to get to by train from Barcelona (˜2 hours). The hybrid zone are located at ˜1200m altitude in open forest and all daily transport will be covered.

Food, accommodation and travel (within Europe) are covered. However, we cannot offer any further pay.

How to apply? Please send a statement of your background, CV, why you are interested and the length of time you would be available to:

david.field@ist.ac.at

Dr. David Field Postdoctoral Fellow Barton Group IST Austria AM Campus 1 Klosterneuburg 3400 Phone: +432243 9000 3008 Web: https://sites.google.com/site/davidfieldresearch/ Web: http://ist.ac.at/research-groups-pages/barton-group/ David Field <david.field@ist.ac.at>

Software Geneland

Dear all,

I am pleased to announce the release of version 4.0.0 of the Geneland program that includes a new model to deal with morphometric data.

Program homepage: http://www2.imm.dtu.dk/˜gigu/Geneland/ Reference on the model: G. Guillot, S. Renaud, R. Ledevin, J. Michaux, J. Claude. A Unifying Model for the Analysis of Phenotypic, Genetic and Geographic Data. To appear in Systematic Biology http://sysbio.oxfordjournals.org/content/early/2012/03/06/sysbio.sys038.abstract Gilles

– Gilles Guillot Department of Informatics and Mathematical Modelling Technical University of Denmark, Copenhagen, Denmark Richard Petersens Plads, Bygning 305, 2800 Lyngby Office phone +45 45 25 33 21 Mobile +45 26 95 39 44 / +46 737 319 754 http://www2.imm.dtu.dk/˜gigu gigu@imm.dtu.dk

Software GenGIS 2 0

Dear EvolDir members,

We have released version 2.0 of our GenGIS software. GenGIS is a geospatial information system for genomic data that allows interactive visualization of the relationship between geography, the environment, and biodiversity.

The GenGIS home page can be found at http://kiwi.cs.dal.ca/GenGIS/Main_Page and includes downloads, a complete manual and several tutorials that highlight different features of the program. We are currently supporting Windows XP, Windows 7 and Mac OSX 10.5, 10.6 and 10.7.

Here is a brief overview of what's new in version 2.0: - Plugins for data analysis, including regression, the Mantel test and visualizing distance matrices on a map - Support for saving and opening sessions - Expanded testing of linear gradients: now a user can test all possible gradients, instead of specifying a single one to test - Updated interface including new sequence and location legends and new ways to subselect data - Improved Mac version, with fixes to various GUI inconsistencies between the Windows and Mac version.

We encourage you to try it out and send in your feedback, and contribute examples to be featured in our gallery. GenGIS remains under active development, and user feedback will be incorporated into the next release.

Best wishes Rob Beiko

beiko@cs.dal.ca

Software OmegaPlus SelectiveSweeps

Dear Evoldir members,

We have developed OmegaPlus, a scalable implementation of the omega-statistic (Kim and Nielsen 2004) to detect selective sweeps in whole-genome data based on linkage disequilibrium patterns. OmegaPlus has been tested with fully phased data, but also with unphased data, where we can determine to which diploid individual a SNP belongs to, but we can not determine which of the two chromosomes carries the SNP. Outgroup information is not required. The program recognizes FASTA, Hudson's ms-like (http://home.uchicago.edu/rhudson1/source/mksamples.html) and MaCS-like (http://www-hsc.usc.edu/~garykche/) formats. OmegaPlus can scan the DPGP dataset (www.dpgp.org, reference release 1.0 September 2009, 37 sequences and ~340,000 SNPs) for positive selection within 55 seconds.

The software is open source and freely distributed under GNU GPL.

In addition to the efficient sequential implementation, we provide three parallelized versions that use fine-, coarse-, and multi-grained parallelism.

Availability: http://www.exelixis-lab.org/software.html User support: http://groups.google.com/group/omegaplus Contact: Pavlos Pavlidis pavlidisp@gmail.com and Nikos Alachiotis n.alachiotis@gmail.com

kind regards, pavlos

–

Pavlos Pavlidis

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

Schloss-Wolfsbrunnenweg 35 D-69118 Heidelberg Germany

Tel: +49 6221 533264 (Office)

Skype: idaios Email: pavlos.pavlidis@h-its.org WWW: http://bio.lmu.de/ ~ pavlidis/ Amtsgericht Mannheim/HRB 337446 Managing Directors: Dr. h. c. Dr.-Ing. E. h. Klaus Tschira/Prof. Dr.-Ing. Andreas Reuter

Pavlos Pavlidis <pavlidisp@gmail.com>

Software ViralSeqAnalysis

Dear Colleagues,

We have recently released several software tools optimized for ultra-deep sequence data sets for de novo genome assembly of viral genomes (AV454) and biological variant detection in genetically heterogeneous populations (RC454 & V-Phaser). The tools are available at:

http://www.broadinstitute.org/scientific-community/science/projects/viral-genomics/viral-genomics-analysis-software We hope that you will find these freely available tools useful for your research needs.

Best, M. Henn

Matthew Henn <mhenn@broadinstitute.org>

SSB ErnstMayr Award

Society of Systematic Biologists Ernst Mayr Award (Graduate Student Award)

The Ernst Mayr Award is given to the presenter of the outstanding student talk in the field of systematics at the annual meetings of the Society of Systematic Biologists (SSB). This is SSB's premier award, and is judged by the quality and creativity of the research completed over the course of the student's PhD program. The award consists of $1000, a certificate of distinction, and a two-year subscription to the journal Systematic Biology.

Eligibility: Members of the Society who are advanced PhD students or have completed their Ph.D. within the last 15 months are eligible. Applicants may be from any country, but must be members of SSB, and are advised to join the Society as soon as possible to be considered (to join go to: http://systbio.org/?q=node/6). Previous Mayr award winners are not eligible.

Application Procedure: 1. To be considered for this award, you will need to submit a 400-word abstract of your talk to the Evolution Ottawa meeting website (http://www.confersense.ca/Evolution2012/index.htm) at the time of registration. Instructions for registering as a potential Mayr award contender will be given on the meeting website. 2. Abstracts should clearly indicate methods used, conclusions, and the relevance to systematics. Presentations focusing on other areas of biology (ecology, behavior, genetics, populations or molecular biology, etc.) that lack a strong systematics emphasis are not eligible. 3. Applications for this award will be accepted only until the end of early registration (April 30, 2012). 4. At the closing of early registration, a subset of applicants will be selected by the SSB Awards Committee to present their talks in the Mayr Symposium during the meeting. All applicants will be notified about selection decisions by May 15.

Judging: Based on submitted abstracts, the Mayr Awards Committee (appointed by the Awards Chair, Sydney Cameron) will select a maximum of 16 applicants for inclusion in the Mayr Award symposium.

The Mayr symposium will be held at a single venue as a continuous session. Talks will be judged on creativity, depth and excellence of research, and on quality of presentation. Competitive students are expected to be in the final stages of their doctoral program, presenting results of a major body of work.

Co-Authors: The talk may be co-authored. It is understood that the ideas, data and conclusions presented are primarily and substantially the work of the student presenter, and the intention is that the student presenter will be senior author on the published version of the paper.

Notification of Winner: The winner of the award will be announced at the SSB business meeting in Ottawa and again during the banquet awards ceremony (complimentary ticket provided) at the conclusion of the Evolution Meetings, whereupon the winner will be given an award certificate. An announcement of the winner will be published in Systematic Biology and placed on the SSB website (see last year's winner at http://systbiol.org/).

Please see the SSB website (http://systbio.org/?q=node/10) for additional information or updates on this award. Questions via email may be addressed to Rhiannon Peery (ssb-apps@life.illinois.edu)

REMINDER: ABSTRACT SUBMISSION DEADLINE IS APRIL, 30 2012

Rhiannon Peery PhD Candidate in the lab of Stephen Downie University of Illinois at Urbana-Champaign Department of Plant Biology 265 Morrill Hall 505 S Goodwin Ave Urbana, IL 61801-3707

Rhiannon Peery <peery1@illinois.edu>

SSB Graduate Std Res Award

Society of Systematic Biology Graduate Student Research Award

The Society of Systematic Biologists (SSB) announces the 2012 annual Graduate Student Research Award competition. The purpose of these awards is to assist students in the initiation (FIRST TWO YEARS) of their systematics projects and in the collection of preliminary data to pursue additional sources of support (e.g., Doctoral Dissertation Improvement Grants from the National Science Foundation) or to enhance dissertation research (e.g., by visiting additional field collection sites or museums). Applicants may be from any country, but must be members of SSB, and are advised to join the Society as soon as possible to facilitate their applications (to join go to: http://systbio.org/?q=node/6). Previous awardees may not re-apply, but previous applicants who were not selected for funding are encouraged to re-apply. Awards range between $1,200 - $2000 and approximately 10 - 15 awards will be made.

How to Apply: applicants must submit 1. a curriculum vitae (one page) 2. brief research proposal including objectives, methods, significance, and schedule (max. three single-spaced pages including literature cited and any figures and tables) 3. budget and budget justification (1 page) 4. and arrange for two reference letters; one letter must be from the student's current graduate advisor.

All application materials must be in electronic format. Applicants and those writing reference letters are required to use pdf format to minimize difficulties in file transfer. Applicants should send all materials (except reference letters) in a SINGLE pdf file. Letters of reference should be sent separately by the referees in pdf format or in the text of an e-mail; please include the FULL NAME OF APPLICANT in reference letters.

Please email all application materials and queries to SSB Awards Committee (Chair, Sydney Cameron) at ssb-apps@life.illinois.edu. IN THE SUBJECT LINE OF THE E-MAIL, PLEASE INDICATE "Student Research" FOLLOWED BY FIRST INITIAL AND LAST NAME.

To be considered for this year's award, application materials, INCLUDING letters of recommendation, must be received electronically no later than March 31, 2012.

Please see the SSB website (http://systbio.org/?q=node/22) for additional details of this award. Questions via email may be addressed to Rhiannon Peery (ssb-apps@life.illinois.edu).

REMINDER: PROPOSAL SUBMISSION DEADLINE IS MARCH 31, 2012

Rhiannon Peery PhD Candidate in the lab of Stephen Downie University of Illinois at Urbana-Champaign Department of Plant Biology 265 Morrill Hall 505 S Goodwin Ave Urbana, IL 61801-3707

Rhiannon Peery <peery1@illinois.edu>

SSB Mini-Arts grant

SSB: Mini-ARTS Grant

The Society of Systematic Biologists is pleased to announce the availability of awards for revisionary taxonomy and systematics, modeled after the NSF Dear Colleague Letter: Advancing Revisionary Taxonomy and Systematics (ARTS) recently developed within the Systematics and Biodiversity Science Cluster. We are calling these 'mini-ARTS' grants. These awards are designed to allow SSB members (students, post-docs, and faculty) to spend a summer or semester apprenticed to an expert in a particular taxonomic group or to enhance revisionary taxonomic and systematics research in novel ways. Goals of this award program are to address constraints on our knowledge of undescribed biodiversity, assist in passing on taxonomic expertise before it is lost, increase the number of students with broad training in organismal biology and systematics, and support projects in biodiversity and taxonomy informatics as well as monographic and revisionary taxonomy. Activities can include a trip to the taxonomist's laboratory, pay for the taxonomist to visit the applicant's laboratory for a period of time, or pay for costs of computer time or development of interactive keys for electronic dissemination of systematics results. Requests for support may be in any amount up to $3,000. We will fund two or three of these awards this year.

Please visit NSF's website http://www.nsf.gov/pubs/2011/nsf11037/nsf11037.jsp for more information about their ARTS program.

How to apply (deadline March 31, 2012) A complete application includes 1) a brief description of the project, including a separate section justifying the importance of the taxon and the revisionary work, 2) an itemized budget, 3) the applicant's CV, and 4) a letter of support from the taxonomic expert or collaborator. If the applicant is a student or post-doc, please also include a reference letter from the advisor. Applicants may be from any country, but must be members of SSB, and are advised to join the Society as soon as possible to facilitate their applications (to join go to: http://systbio.org/?q=node/6). The narrative part of the application should be no more than two pages, including the budget, but not including the curriculum vitae and letter(s).

Grant applications should be sent to the SSB Awards Committee (ssb-apps@life.illinois.edu), Committee Chair Sydney Cameron. E-mail submissions are required, and applicants should use pdf format for all documents. In the subject line of the email, please indicate the SSB award category as 'mini-ARTS'.

Please see the SSB website (http://systbio.org/?q=node/26) for any updates or additional information about this award. Questions via email may be addressed to Rhiannon Peery (ssb-apps@life.illinois.edu).

APPLICATION DEADLINE IS MARCH 31, 2012

Rhiannon Peery PhD Candidate in the lab of Stephen Downie University of Illinois at Urbana-Champaign Department of Plant Biology 265 Morrill Hall 505 S Goodwin Ave Urbana, IL 61801-3707

Rhiannon Peery <peery1@illinois.edu>

TravelGrants SpeciationResearch

Dear colleagues,

The European Research Networking Programme "Frontiers of Speciation Research", supported by 18 National Funding Organizations in member countries of the European Science Foundation, is inviting applications for travel grants intended to foster collaborations between European researchers working on topics related to the Programme.

Support is available for short visits (up to 2 weeks) and exchange grants (up to 3 months), with preference given to junior researchers at a graduate or postdoctoral level. A typical grant covers between EUR 1500 and EUR 2000. Applicants will want to keep in mind that, reflecting the availability of funds, applications for smaller grants are more likely to succeed than applications for larger grants, and that granted amounts are typically adjusted relative to solicited amounts so as to promote equity among selected candidates.

Applications are reviewed quarterly after a submission deadline of 24:00 CET on 15 March, 15 June, 15 September, and 15 December. About 4-6 weeks after each deadline, the ESF will inform applicants about the outcome of evaluations.

Further information and instructions on how to apply are available at www.iiasa.ac.at/Research/EEP/FroSpects/Travel_Grants.html .

For general information about the FroSpects Research Networking Programme, please see www.iiasa.ac.at/Research/EEP/FroSpects .

With best wishes,

Ãke Brännström & Ulf Dieckmann, on behalf of the FroSpects Steering Committee

Ulf Dieckmann Program Leader Evolution and Ecology Program International Institute for Applied Systems Analysis A-2361 Laxenburg Austria

Email dieckmann@iiasa.ac.at Phone +43 2236 807 386 Phone secretary +43 2236 807 231 Fax +43 2236 807 466 or +43 2236 71313 Web http://www.iiasa.ac.at/Research/EEP Online reprints http://www.iiasa.ac.at/˜dieckman FishACE Network http://www.iiasa.ac.at/Research/EEP/FishACE FinE Network http://www.iiasa.ac.at/Research/EEP/FinE FroSpects Network http://www.iiasa.ac.at/Research/EEP/FroSpects

dieckmann@iiasa.ac.at

Trypsination caco-2 cells

Dear everyone,

I'm looking for a protocol for trypsine caco-2 cells. Does someone have an very efficient procedure?

Best regards,

Stéphane.

Stéphane MAZIERES, Ph.D.

Anthropologie, Droit, Ethique et Santé UMR 7268, Aix-Marseille Université, EFS-AM Faculté de Médecine - Secteur Nord Bâtiment A - CS80011 Bd Pierre Dramard 13344 MARSEILLE Cedex 15 - FRANCE

phone: +33 (0)4 9169 8876 http://www.anthropologie-biologique.cnrs.fr/ mazieres_stephane@yahoo.fr

UBath VoluntaryFieldAssist BirdBehaviour

Field Assistant position in behavioural ecology in Cape Verde, North Africa ? Sept to Dec 2012

We are seeking 1 Voluntary Field Assistant for a bird evolutionary ecological project in the Republic of Cape Verde. The assistant is required from 1 September until 15 December 2012. Basic food, accommodation and research expenses are provided, although the assistant has to cover his/her journey to (and from) Maio, Cape Verde.

The project We are investigating breeding ecology and behaviour of Kentish plover Charadrius alexandrinus in Cape Verde by monitoring colour-ringed individuals. This is an all-year resident population and many individuals are already ringed from previous years.

The place The study sites are in Maio Island, Cape Verde, at the Salina Porto Ingles and nearby lagoons (see the Bradt Guide to Cape Verde Islands). Accommodation on the islands is in an apartment, with occasional water and electricity. The island has spectacular wildlife, including endemic birds, corals and marine mammals; it is a beautiful and inspiring place to work. However, the island is a small and isolated place with basic commodities, the weather can be harsh, and a great deal of walking and cycling are required.

The job The fieldwork will run from 1 September to mid December 2012. It will be unsupervised, and will involve ? among other tasks ? searching for plover nests and marked plovers and their families, taking behavioural observations and monitoring nest survival. It will also involve capturing, ringing and bleeding adults and young.

The candidates This is a voluntary post ? applicants must be willing to pay for their own transport to Maio. Once in Maio, however, accommodation, basic food and expenses associated with research will be covered. Phone calls and internet costs will not be covered.

You will be a keen birder with sharp eyes and plenty of experience in trapping, handling and ringing birds. Clean driving licence is essential. You must be personable and happy to engage with locals to explain the project; some Spanish or Portuguese is helpful. You must be physically fit, hard-working and meticulous, and have a proven ability to work independently.

As you will appreciate from its description, the project will involve many different challenges. A proven ability to collect high-quality data is essential (i.e. a good degree in a biological subject or equivalent experience), and you should be prepared to type up your data in the evenings. You must have a positive attitude and an ability to look after yourself ? this means cooking your own meals, dealing with logistics, and most importantly being capable of organising your own work for a long period of time.

If you like chatting on the phone, or feel the need to text and email people all the time, this position is not for you. The cost of living is high, and fancy food is expensive.

Costs It is possible to fly through Lisbon from the UK that costs about £700. Internal flights from Praia to Maio should be under £100 one way, and the Praia-Maio ferry costs about £15.

Interested? Please send a current CV with an email stating why you feel you are a strong candidate to me (Professor Tamás Székely) at T.Szekely@bath.ac.uk. Application deadline: 15 April 2012. Telephone Interviews will be carried out in late April 2012.

I will also need the contact details (email and telephone) of two referees. If you have any questions, please direct them to me at the same email address, or call me at +44 1225 383676.

Professor Tamas Szekely Professor of Biodiversity Dept of Biology and Biochemistry, University of Bath, Bath BA2 7AY, UK 01225 383676 (phone), 01225 386779 (fax), T.Szekely@bath.ac.uk (email) http://www.bath.ac.uk/bio-sci/biodiversity-lab/index.htm http://www.maioconservation.org Social Behaviour: Genes, Ecology and Evolution, 2010, Edited by Tamas Szekely, Allen J Moore & Jan Komdeur. Cambridge University Press, 2010 http://www.cambridge.org/gb/knowledge/isbn/item5708507/?site_locale=en_GB bssts@bath.ac.uk

Undergraduate travel grants

PLANTS Grants Preparing Leaders and Nurturing Tomorrows Scientists Undergraduate Travel Awards: Enhancing Diversity at the Botanical Society of America Conferences

We are pleased to announce the PLANTS program funded by the National Science Foundation and Botanical Society of America to bring talented and diverse undergraduates to the BOTANY 2012 meeting on July 7-11, 2012 in Columbus, Ohio.

BOTANY 2012 is the annual scientific conference for the Botanical Society of America, Canadian Botanical Association/L'Association Botanique du Canada, American Bryological and Lichenological Society, American Fern Society, American Society of Plant Taxonomists and the International Association for Plant Taxonomy.

The theme of the meetings this year is "Botany - The Next Generation". Topics range across all levels of botany and include talks on carnivorous plants, plant genomics, rhizosphere interactions, plant systematics, and botanical education. There are also a number of social functions, specifically targeted at students for networking and fun. The meetings are a great way to understand the breadth of botanical research and education, to meet undergraduate and graduate students with similar interests, and to network with professionals in your area of interest. This is really a friendly community, so please consider joining us!

The PLANTS program (Preparing Leaders and Nurturing Tomorrow's Scientists: Increasing the diversity of plant scientists) will fund up to 12 undergraduates from throughout the US to attend the meeting, receive mentoring from graduate students, postdocs and faculty, and participate in networking events including the Diversity Luncheon and career-oriented activities. The program covers the normal costs of travel, registration, and food and accommodation at the meetings. An overview of the meetings is available at http://www.2012.botanyconference.org/ APPLICATIONS: Applications are due by MARCH 15, 2012 and include completion of the online form providing your statement of interest, a letter of recommendation, and unofficical transcripts. Applications will be reviewed as they are received, so the earlier you apply, the better. Applications are welcome from all undergraduates who have interest in plant science; the admissions goal is to create a diverse pool of students. The application form is located online at http://www.botany.org/awards/F_PLANTS.php. We encourage you to review the online form thoroughly before filling it out. Please have letters of recommendation and unofficial transcripts sent directly to Heather Cacanindin at HCacanindin@Botany.org.

MENTORS: In addition, we are soliciting names of graduate students, postdocs and faculty members who would like to serve as mentors during the meetings. Mentors work with PLANTS students and attend talks with them, introduce them to colleagues, network and generally make the meetings a welcoming place for them. Although costs are not covered for mentors, it is a very rewarding experience to mentor this group of students. Contact Ann Hirsch (ahirsch@ucla.edu) if you are interested in serving as a mentor.

CONTACTS: For further inquiries, please contact one of the organizers: Ann Sakai – aksakai@uci.edu Ann Hirsch – ahirsch@ucla.edu Heather Cacanindin – hcacanindin@botany.org

DEADLINE: March 15, 2012

aksakai@uci.edu

Workshops Courses in Genomics

Colleagues,

An increasing number of labs I work with are moving towards 454, Illumina, or similar next generation genome or transcriptome sequencing projects. I am frequently asked about North American or UK workshops or courses for molecular biologists that wish to learn about generation and analysis of these data, particularly genome assembly. Most of these are Ph.D. level investigators but often without sophisticated computational skills. Could you please suggest appropriate courses for these investigators (Sanger, Woods Hole, Cold Spring Harbor?). Please reply to me directly and I will post a summary to EvolDir.

Much thanks, Andrew McArthur

Andrew G. McArthur, Ph.D. Bioinformatics Consulting Services Email: amcarthur@mac.com, Web: http://mcarthurbioinformatics.ca/ Phone: 905.296.3252, Mobile: 905.745.2794, Fax: 647.439.0829 Skype: agmcarthur

Based in Gothenburg, Sweden July 2012 through August 2013. Gothenburg is 6 hours ahead of the Eastern Time Zone (e.g. Toronto/Boston) and 9 hours ahead of the Pacific Time Zone (e.g. Los Angeles).

amcarthur@mac.com

PostDocs

AlbertEinstein PopGen

A postdoctoral position is available in the laboratory of Dr. Adam Auton, in the Department of Genetics at Albert Einstein College of Medicine in New York,USA(http://autonlab.einstein.yu.edu/). Research goals of the lab are to use statistical methods in conjunction with high-throughputDNAsequencing to examine patterns of recombination in the human genome, and to quantify how these patterns vary across individuals. The focus of the position will be to develop methods for the study of recombination.

We welcome candidates with a background in Biology, Population and Statistical Genetics, Bioinformatics or related disciplines. Experience with high-throughput sequencing data and/or experimental techniques would be an advantage. Salary will be based on theNIH scale. Please email a CV including list of publications and names of two references toadam.auton@einstein.yu.edu by March 29th 2012.

The Albert Einstein College of Medicine is a leading medical research institution located in a residential area of the Bronx, NY, and is a short commute from Manhattan. The Auton Lab is part of the Computational Genetics Division, situated in the Michael F. Price Center for Genetic and Translational Medicine.

adam.auton@gmail.com

Barcelona MarieCurie Chordate EvoDevo Genomics

Marie Curie POST-DOC fellowship application University of Barcelona, Department of Genetics

Our new group on the field of Functional Evo-Devo and Genomics on Chordates is looking for candidates to apply for the forthcoming FP7 POST-DOC FELLOWSHIP from the Marie Curie program (Opening call March 13)

Candidates have to be enthusiastic, and need to have a competitive CV to successfully apply for the fellowship. Experience in Molecular Genetics, Transgenesis and Developmental Biology, and (or) Background in Bioinformatics, and Comparative Genomics will be positively considered.

Our main research interest is to understand the impact of gene losses on the evolutionary diversification of mechanisms of development in chordates. Our work focuses on comparative approaches between vertebrates (zebrafish), urochordates and cephalochordates. Our main subject of study is Oikopleura dioica, a new emergent urochordate model within our own phylum, with the smallest genome size known so far in all metazoans, and with an outstanding amount of gene losses (Denoeud et al., Science, 2010).

Interested candidates, please send a brief letter of interest and a CV in ONE single pdf file to Cristian Cañestro (canestro@ub.edu)

Interested candidates for future POST- or PRE-DOCTORAL applications, please feel free to contact too.

For an outline of our group's research: http://www.ub.edu/genetica/evo-devoen/canestro.htm http://www.uoneuro.uoregon.edu/ ˜ cristian/Canestro.html FP7 fellowship link: http://ec.europa.eu/research/participants/portal/page/people&state=3Dforthcoming oikocris@gmail.com

Barcelona OpenCalls MarieCurie Chordate EvoDevo

Reminder: Marie Curie POST-DOC fellowship application (IIF and IEF Calls now opened) University of Barcelona, Department of Genetics

Our new group on the field of Functional Evo-Devo and Genomics on Chordates is looking for candidates to apply for the forthcoming FP7 POST-DOC FELLOWSHIP from the Marie Curie program

Candidates have to be enthusiastic, and need to have a competitive CV to successfully apply for the fellowship. Experience in Molecular Genetics, Transgenesis and Developmental Biology, and (or) Background in Bioinformatics, and Comparative Genomics will be positively considered.

Our main research interest is to understand the impact of gene losses on the evolutionary diversification of mechanisms of development in chordates. Our work focuses on comparative approaches between vertebrates (zebrafish), urochordates and cephalochordates. Our main subject of study is Oikopleura dioica, a new emergent urochordate model within our own phylum, with the smallest genome size known so far in all metazoans, and with an outstanding amount of gene losses (Denoeud et al., Science, 2010).

Interested candidates, please send a brief letter of interest and a CV in ONE single pdf file to Cristian Cañestro (canestro@ub.edu)

Interested candidates for future POST- or PRE-DOCTORAL applications, please feel free to contact too.

For an outline of our group's research: http://www.ub.edu/genetica/evo-devoen/canestro.htm http://www.uoneuro.uoregon.edu/ ˜ cristian/Canestro.html FP7 fellowship link: http://ec.europa.eu/research/participants/portal/page/people&state=3Dforthcoming oikocris@gmail.com

California Microarrays

Post-doctoral Microarray Researcher/Lab Manager/Instructor sought for Profile Genomics, Peralta Foundation, Alameda California, USA

DESCRIPTION OF WORK: Primarily Microarray development as a managing level position for this area, and part-time Genomics education. Profile Genomics is a new non-profit Genomics training and service facility. We are looking for original thinking applicants able to apply for postdoctoral funding through NSF and NIH or other international funding sources. This new lab in Alameda, California embraces research as well as training of a diverse Community College student population of all ages, all races, and all financial backgrounds; students have diverse academic preparation ranging from Bachelors, Masters and even Ph.D.s, and are coming for real life skill-sets training in Genomic science and technologies.

APPLICANT QUALIFICATIONS: Applicants are expected to have a PhD and strong expertise and interest in Comparative Genomic Expression work, especially with proficiency in Microarrays.

RESOURCES:

The following Genomic resources are available for development on site:

Over twelve thousand frozen tissue samples (primarily snap-frozen) from over 34 countries; we have one of the largest Amphibian and Reptile frozen tissue collections in the world, and it is by far the most valuable. For example, we have the largest collection of frozen tissues from Western China and Tibet, Turkmenistan, Iran, Afghanistan, The Arabian Peninsula (U.A.E., Oman, and Yemen), and Somalia, and other regions. We also have microbiota of mother and daughter human gut cloned into Fosmid libraries. We have six complete nuclear genomes of non-mammalian amniotes cloned into BAC libraries.

APPLICATION:

Please send a cover letter, a CV and any other pertinent information. In your cover letter please address the following issues: (1) tell us about your expertise in Comparative Genomic Expression work, (2) your Microarray background, and (3) your thoughts on how this relates to the better understanding of Evolutionary Biology. Funding is not available for this position on its own, however postdoctoral grant support with a joint application is highly encouraged. Additional salary base could come from teaching as well as outside Genomic/Microarray contractual services that are supporting the program.

CONTACT INFO:

J. Robert Macey, Ph.D., Profile Genomics, 860 Atlantic Avenue Alameda, California 94501-2200 Contact info: J. Robert Macey <jrobertmacey@gmail.com>

barowning@gmail.com

ClarkU FungalPhylogenetics

Post-doctoral Position in Fungal Phylogenetics

A Post-Doctoral position in fungal phylogenetics is available in the Hibbett laboratory at Clark University (http://www.clarku.edu/faculty/dhibbett/). The Post-doc will participate in a large collaborative endeavor supported by the NSF AVATOL Program that is aimed at synthesizing a comprehensive tree of life from published analyses, and developing novel tools for community-driven annotation of the tree. Specific responsibilities will include (1) assembly and integration of phylogenetic datasets and trees representing all groups of Fungi; (2) coordination with a multi-laboratory team including software developers and systematists to develop and test new methods for tree integration and annotation; (3) outreach to the fungal systematics community; (4) contribution to a distributed web-based undergraduate course on assembling the tree of life, and co-instruction of a linked undergraduate course at Clark University.

The ideal candidate will be a productive researcher with interests in fungal systematics and the construction and interpretation of large-scale phylogenetic trees, will have excellent communication and interpersonal skills, and will seek a career involving both research and education. Candidates lacking background in fungal systematics, but with strong qualifications in phylogenetics, and excellent potential as educators, may be considered.

It is anticipated that the position will be available beginning May 1, 2012. Up to three years of support is possible, depending on progress. Funding is contingent on final NSF approval.

To apply, e-mail a curriculum vitae, statement of research interests and career goals, PDFs of major publications, and names and e-mail addresses for three references. Applications from women and members of underrepresented groups in science are encouraged.

Clark University is an EEO/AA Employer.

David S. Hibbett Biology Department Clark University Worcester, MA 01610 (508) 793-7332 Dhibbett@clarku.edu

David Hibbett <DHibbett@clarku.edu>

Dublin ForestGeneticDiversity

Position: Research Fellow

Duration: 12 months

Location: National Botanic Gardens, Dublin, Ireland

A research position is available immediately for a fixed term of one year on a project investigating provenance and gene diversity in forest trees. The position will be based in the National Botanic Gardens of Ireland and is part of a project in collaboration with a research team in University College Dublin, Coillte and Teagasc. The research will focus on identifying genetic provenance of Irish forestry trees and also aims to characterise and screen gene regions for selection of suitable material for future planting and breeding programmes. The project will focus on broadleaves such as birch and alder, and conifers such as pine and spruce. The post will primarily be lab based with an element of fieldwork to sample material. The candidate will ideally have considerable laboratory experience in genotyping and DNA sequencing. They will have proven experience of self-motivated research and will work well alone and be able to network with other researchers. They will be expected to publish from the results and to report regularly. They will be expected to help in the running of the lab and the supervision of students. Experience of genomic technologies or bioinformatic techniques would be a distinct advantage. A driving licence and access to a vehicle are also necessary. The salary scale will be at postdoctoral level from EUR37,750 to EUR44,930 per annum, depending on experience.

The DBN Plant Molecular Laboratory in the National Botanic Gardens is equipped for DNA sequencing and genotyping. The gardens are located to the north of the city of Dublin. The lab research focuses on biogeography and genetic variation in natural populations, conservation genetics and taxonomy. The Research Fellow would be encouraged and supported to develop further funding potential. Informal queries to Dr Colin Kelleher, National Botanic Gardens, colin.kelleher@opw.ie.

Applications by way of cover letter and CV with a list of three referees to be sent to: botanicgardens@opw.ie, noting “Forgen Research Fellow” in subject heading. Closing date for receipt of applications is the 2^nd of April.

Colin Kelleher MSc PhD Herbarium and Molecular Lab National Botanic Gardens Glasnevin Dublin 9 Ireland T:+353-1-8040326 E:colin.kelleher@opw.ie

Colin Kelleher <colin.kelleher@opw.ie>

DukeU EvolutionaryGenetics

DukeU.EvolutionaryGenetics

Duke University, Biology Department, Postdoctoral Researcher

A Postdoctoral Researcher is wanted to participate in an NSF funded project on the genetic basis and adaptive significance of pleiotropy in /FLC/-regulated germination and flowering.The project involves determining the extent of pleiotropy expressed by genes involved in /FLC/-mediated germination and flowering, manipulating /FLC/ expression to assess its pleiotropic effects, and measuring natural selection on /FLC /genotypes. The ideal applicant would have a PhD in evolutionary biology or comparable field, and have skills in RNA quantification, promoter construction, RNAi implementation, quantitative genetics, and selection analysis.A motivating interest in evolutionary processes is necessary, as is independence in methodological development and troubleshooting, and evidence of success in publication.

Available May 15, 2012. One year, renewable for up to three years.Competitive salary and full Duke benefits.Duke University is an Equal Opportunity/Affirmative Action employer.Please send CV and names and contact information for three references to Kathleen Donohue: k.donohue@duke.edu

DEADLINE FOR CONSIDERATION: APRIL 15, 2011

– Kathleen Donohue Biology Department Duke University Box 90338 Durham, NC 27708 USA Tel: (919) 613-7467 Fax: (919) 660-7293

Kathleen Donohue <k.donohue@duke.edu>

Guelph PathogenGenomics

POST DOCTORAL POSITION IN PATHOGEN GENOMICS AT THE PUBLIC HEALTH AGENCY OF CANADA (PHAC)

Applications are invited for a post doctoral fellowship position available April 2012 in a Genomics Research and Development Initiative (GRDI) project at the PHACs Laboratory for Foodborne Zoonoses, Guelph, Ontario, Canada. Fellowships are awarded initially for one year with the possibility of renewal for a second year.

The project is focused on development of high resolution molecular subtyping of the highly clonal enteric pathogen, Salmonella Enteritidis. The approach is to use whole genome sequencing to identify variably present or absent loci or SNPs that will provide highly discriminatory identification of related and unrelated strains.

With open whole genome sequences of numerous selected strains now available, the candidate will undertake genome assembly, annotation and analysis to identify panels of loci and/or SNPs that potentially will provide the required discriminatory power. These panels will then be evaluated on a broad range of strains.

The successful candidate should have PhD/post doctoral experience in molecular biology, bioinformatics and computational genomics of microbes. Previous experience with genomics of pathogens will be an advantage.

The lead scientists on the project are Roger Johnson and Kim Ziebell, supported by PHAC collaborators including Vic Gannon, Matthew Gilmour, Andrew Kropinski, Chad Laing and John Nash.

For more information: Roger.Johnson@phac-aspc.gc.ca

Starting date: Spring/Summer 2012, Year 1: to March 31 2013. Year 2: April 1 2013- March 31 2014.

Application deadline: April 15 2012

Stipend: approx: CDN$47,200 per year, under the Visiting Fellowships in Canadian Government Laboratories program of the National and Scientific and Engineering Research Council of Canada. http://www.nserc-crsng.gc.ca/Students-Etudiants/PD-NP/Laboratories-Laboratoires/index_eng.asp How to apply: Email your application to Roger.Johnson@phac-aspc.gc.ca as a single pdf file containing your CV with publications, contact details of two referees, and a letter (maximum 1 page) with a description of your research interests and why you would be a suitable candidate for the position.

Roger Johnson MVSc, PhD, Research Scientist & Director of Reference Laboratories, Public Health Agency of Canada, Laboratory for Foodborne Zoonoses 110 Stone Road West, Guelph, ON, N1G 3W4 Tel: 519 826 2644; Fax: 519 822 2280; email: Roger.Johnson@phac-aspc.gc.ca

Roger Johnson <Roger.Johnson@phac-aspc.gc.ca>

LinnaeusU EvolutionAvianImmunity

Postdoc:

LinnaeusU.avian.innate.immunity

Postdoctoral researcher in Ecology, specifically entailing the ecology and evolution of avian innate immunity, ref PA 2012/144

Linnaeus University is a modern, international university in southern Sweden. The university is situated in Kalmar and Växjö, and has 34,000 students and 2,000 employees. For more information see: Lnu.se. The school of Natural Sciences is part of the Faculty of science and engineering. The research activities within this multidisciplinary school include the areas of Biochemistry, Biotechnology, Biomedical Sciences, Organic Chemistry, Marine Ecology and Microbiology.

The Linnaeus Centre for Ecology and Evolution in Microbial Model Systems (EEMiS) now seeks a postdoctoral researcher with a strong background in molecular biology and ecology.

The research project is centered on ecological and evolutionary interactions between pathogens and host innate immunity in wild bird populations. Pathogenic microorganisms are a reality for all living animals and infectious diseases shape the ecology and evolution of the host species they infect. The co-evolution between pathogens and hosts can be viewed as an arms race, with selection on both host and pathogen genomes. The current project aims to understand how genetic variations at innate immune gene loci in Mallards give rise to differences in susceptibility to naturally occurring bacterial and viral pathogens. As a starting point, the postdoctoral researcher will investigate the genetic basis for innate immune genes and the degree of allelic variation within and between duck species. This information will then be used to link allelic variation with data on pathogen susceptibility using both culture- and genetic-based approaches.

The EEMiS environment is a centre of excellence within Linnaeus University involving larger teams of multidisciplinary researchers. Therefore, the successful applicant will interact with other existing research projects within EEMiS.

Applicants should have a Ph.D. degree in a subject area of relevance for the present project, such as molecular biology, genetics or ecology. Excellent written and oral communication skills in English are essential. Documented experience with characterizations of immune genes, gene function or disease susceptibility is desirable.

The position is available for two years. We offer excellent working conditions, a competitive income, access to state-of-the-art laboratory facilities and an opportunity to develop your career in a dynamic environment. The position is located in Kalmar.

For further information please contact Dr. Jonas Waldenström at +46-480-446195, (jonas.waldenstrom@lnu.se), Dr. Olof Hellgren +46-

70-6473522 (olof.hellgren@lnu.se), Head of School Prof. Ian Nicholls, +46-480-446258 (ian.nicholls@lnu.se) or Personnel Officer Leif Eriksson at +46-480- 446028, (leif.eriksson@lnu.se). Union representatives may be contacted via the university switchboard at +46-772-28 80 00.

Please apply through: lnu.se, and go to "jobs and vacancies". The application should arrive no later than April 15, 2012. Mark your application with reference number PA 2012/144. The application (in English) should contain a CV, copy of doctoral certificate, a list of at least two referees (with telephone, fax, and/or e-mail), at least two letters of recommendation, and a description of motivation and experience relevant to the research project.

Olof Hellgren <Olof.Hellgren@biol.lu.se>

Liverpool Malaria

$* is no longer supported at /home/brian/src/delete_blank_lines.pl line 3. Post Doctoral Research Assistant (Ref 619) Vector Group

Salary: £31,020 - £33,884

Full-Time, Fixed-Term 12 month appointment

The Liverpool School of Tropical Medicine (LSTM) is an international centre of excellence and our researchers have access to the most up to date, cutting edge technology, making us world leaders in our field.

This post will work with Dr Martin Donnelly's team within LSTM's Vector Group and will be responsible for providing support to a number of different country projects including Benin, Cameroon, India, Kenya and Sudan by investigating the impacts of insecticide resistance on malaria control programmes. You will be expected to travel to each of the countries to collect specimens for gene expression studies which are to be conducted at LSTM in collaboration with project partners.

Possessing a PhD in Biology, you will be an ambitious and self motivated researcher with experience of gene expression studies and the design and implementation of DNA based diagnostic assays. Previous experience working with insect vectors and/ or in malaria endemic countries is highly desirable but is not essential.

You will have very strong analytical skills and have the ability to identify problems and suggest viable solutions when necessary. Computer literacy, time management and organisational skills are also essential to the role, as is the ability to work both collaboratively and independently across a multi-disciplinary research team. Further details of the post can be found by visiting our website at http://lstmliverpool.ac.uk If you are interested in applying, please return your completed Application Form, Personal Details Form and Equal Opportunities Monitoring Form together with a copy of your CV, stating vacancy reference number (619), via email to Lstmjobs@liverpool.ac.uk, or by post to HR, Liverpool School of Tropical Medicine, Pembroke Place, Liverpool L3 5QA.

Informal enquiries may be directed to Dr Martin Donnelly (m.j.donnelly@liv.ac.uk).

Closing Date: Tuesday 3rd April 2012 (5pm)

Interview Date: To take place in Liverpool week commencing 23rd April 2012.

LSTM actively promotes an Equal Opportunities Policy

M.J.Donnelly@liverpool.ac.uk

Lyon Bioinformatics

Dear colleagues,

We are seeking a bioinformatics post-doc for 24 months in Lyon, France. Please see the details below.

Thank you Best regards Julien Varaldi

Insects are hosts to numerous bacterial symbionts shaping their phenotypes. Recently, we have found that in addition to bacterial symbionts, heritable viruses may also deeply impact the phenotype of insect, as observed in the parasitoid wasp Leptopilina boulardi. In this system, the maternally inherited virus LbFV pushes infected females to lay their eggs in previously parasitised hosts. This behaviour, called superparasitism, is adaptive for the virus since it allows it to colonize new parasitoid lineages through horizontal transmission (Varaldi et al. 2003, Gandon et al. 2006). Although this example shows that heritable viruses may have a dramatic impact on the phenotype of insects, the diversity and distribution of such viruses is mostly unknown in any ecological system. The ANR-funded project âViromics' aims at delineating the diversity and circulation of these viruses in a well characterised Drosophila-parasitoid community. This issue will be addressed using a virus-targeted metagenomic approach involving NGS sequencing. The identification of heritable viruses present in this community, their respective host ranges and prevalence in different environments should allow us to identity viruses involved in the adaptation of insects to their local environment. In addition to this exploratory work, the project will aim at identifying the genes involved in the above-described behaviour manipulation induced by LbFV using RNAseq (project 2). Part of the data are already available. We are seeking a two-years post-doc that could lead these projects. The candidate should have expertise in NGS data analysis in the field of genomics and metagenomics assembly and annotation (project 1), and/or in the field of transcriptome assembly, annotation and differential expression analysis (project 2). Experience in the field of host-symbiont interactions is also welcome. The project can start as soon as June 2012. If you are interested by this position, please send a CV and brief statement on your motivations to Julien Varaldi <julien.varaldi@univ-lyon1.fr>.

Gandon, S., Rivero, A., & Varaldi, J. 2006. Superparasitism evolution: Adaptation or manipulation? The American naturalist 167: E1-E22.

Varaldi, J., Fouillet, P., Ravallec, M., Lopez-Ferber, M., Boulétreau, M., & Fleury, F. 2003. Infectious behavior in a parasitoid. Science 302: 1930.

Julien Varaldi Biometry and Evolutionary Biology University Lyon1 43 boulevard du 11 novembre 1918 69622 Villeurbanne FRANCE

julien.varaldi@univ-lyon1.fr tel: 00334 72448101 fax: 00334 72431388

VARALDI JULIEN <Julien.Varaldi@univ-lyon1.fr>

Madrid PlantVirusEvol

*_POSTDOCTORAL POSITION AVAILABLE_*

In *Plant-Virus Interaction and Co-Evolution*

_Research topics_*: The long-term goal of the group is to understand the evolution of plant-virus interactions*. Recent work in the group has been directed at developing /Arabidopsis thaliana/ as a system for the study of plant-virus co-evolution. Within the broad field of the evolution of plant-virus interactions *the post-doctoral scientist to be recruited will participate in defining a specific programme of research that should be related to one of the following subjects: 1) Ecology of virus emergence, 2) Population genetics of plant-virus interactions, 3) Genetics and dynamics of plant colonisation by viruses. *

*_Period_*: Starting any time from now.

*_Conditions_*: Contract conditions will be equivalent to those of the Spanish "Juan de la Cierva" Programme.

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*_Requisites_*: Experience in virus evolution or/and population genetics of plants or/and evolutionary biology of host-parasite interactions.

INTERESTED CANDIDATES PLEASE CONTACT

Prof. *FERNANDO GARCÍA-ARENAL *_fernando.garciaarenal@upm.es

BEFORE *MARCH 20^th * 2012

For further information about the group: http://www.cbgp.upm.es/plant_virus.php *_ _*

*_Recent publications of the group related to the above-specified topics:_** *

* ** *

Pagán I. /et al/. (2008). Host responses in life-history traits and tolerance to virus infection in /Arabidopsis thaliana. *PLoS Pathogens */4:e1000134

González-Jara P. /et al./ (2009). Multiplicity of infection of a plant virus varies during colonization of its eukaryotic host. */Journal of Virology /*83:7487-7494.

Pagán I. /et al./ (2009). Differential tolerance to direct and indirect density-dependent costs of viral infection in /Arabidopsis thaliana/. */PLoS Pathogens/ *5:e1000531.

Pagán I. /et al/. (2010). /Arabidopsis thaliana/ as a model for the study of plant-virus co-evolution. */Philosophical Transactions of the Royal Society B/ *365:1983-1995.

Fraile A /et al/. (2011). Rapid genetic diversification and high fitness penalties associated with pathogenicity evolution in a plant virus*. /Molecular Biology and Evolution/*/./ 28: 1425-1437.

For additional information on CBGP, please visit http://www.cbgp.upm Fernando García-Arenal Rodríguez Catedrático de la Universidad Politécnica de Madrid Director del Centro de Biotecnología y Genómica de Plantas UPM - INIA Campus de Montegancedo Autopista M40, Km38 28223 Pozuelo de Alarcón Madrid T: + 34 91 336 4550/4539 F: + 34 91 715 77 21 E –mail: fernando.garciaarenal@upm.es fernando garcia arenal <fernando.garciaarenal@upm.es>

MasseyU ComputationalFungalGenomics

Postdoctoral Position in Computational Fungal Genomics (A091-12ZZ)

I am looking for a motivated and productive postdoctoral fellow to study the evolution of fungal genomes, including the role of lateral gene transfer, using comparative genomics and next generation sequencing technologies. The successful candidate will have scope to drive his/her own research program within the bounds of the group's larger research direction, but will also be invited to engage with ongoing collaborative research projects.

This computational position requires solid quantitative skills, preferably with a background in bioinformatics, statistics, next generation sequencing and basic scripting/programming. Training in fungal biology and genetics can be provided as needed, and candidates with compatible, but non-standard, research backgrounds are strongly encouraged to apply.

Funding is available for three years subject to satisfactory performance, with an initial probationary period of one year. The salary is extremely competitive, starting at NZ $65,000 (˜US $55,000) per year.

The postdoc will be based in the Computational Biology Research Group at Massey University, New Zealand. My interdisciplinary research team is intellectually diverse, has a strong high-impact publication culture, and is firmly embedded in the international scientific community with extensive collaborative links to the United States, France, Australia and Indonesia. This position offers a rare opportunity to experience New Zealand's unique natural and cultural environment. Palmerston North, a university town with a large international community, offers the full range of social and cultural amenities. The city is located close to both mountains and the sea, and presents regular opportunities for hiking, skiing, surfing and adventure sports. A strong cafe culture will appeal to more urbane types.

If you have any questions, please contact Dr Murray Cox (email m.p.cox@massey.ac.nz). Information about the Computational Biology Research Group (http://massey.genomicus.com/), the Institute of Molecular BioSciences (http://imbs.massey.ac.nz/-) and the Bio-Protection Research Centre (http://-bioprotection.org.nz/) is available online.

To apply for this position, upload the following documents (PDF format) at the official Massey University job website: http://jobs.massey.ac.nz/ 1. A brief statement of research interests, qualifications and experience. 2. A curriculum vitae, including a list of scientific publications. 3. The names and contact details of three referees willing to provide a confidential letter of recommendation upon request.

Dr Murray P. Cox Institute of Molecular BioSciences Massey University Private Bag 11 222 Palmerston North 4442 NEW ZEALAND

http://massey.genomicus.com/ m.p.cox@massey.ac.nz

Informal enquiries are welcome. Formal applications are due by 22 April 2012.

M.P.Cox@massey.ac.nz

Montpellier RNAseq Speciation

Postdoctoral position in transcriptomics and speciation at CNRS ' Institute for Evolutionary Biology, Montpellier, France.

A 18-month post-doctoral position is available at CNRS Montpellier, France (Institut des Sciences de l^{1}Evolution) to work with Carole Smadja and Pierre Boursot on the genomics of speciation in the house mouse (Mus musculus).

This ANR and EU-funded project is devoted to characterise the genomics of speciation in the house mouse. The successful candidate will be in charge of the transcriptomics side of the project, which will seek for expression divergence between two subspecies of mice. RNAseq will be used to tackle gene expression in different organs and individuals and test for divergence at candidate genes. The role of the job-holder will be to analyse and interpret next-generation sequencing data from RNAseq experiments and to handle manuscript preparation.

Applicants should have a PhD in any relevant area (evolutionary biology, genomics, molecular biology). We are seeking for someone with a strong experience in RNAseq data analysis and a vivid interest in the role of gene expression in evolution. Skills in bioinformatics and biostatistics are essential as well as experience in handling Next-Generation-Sequencing data. A strong track record and good communication skills are expected, and some interest in speciation and population genomics research would be a plus. Proficiency in English is required.

The post will be based in Montpellier (South of France), European centre of excellence in biodiversity research and known for its quality of life in the Mediterranean region. The Institute for Evolutionary Biology has a long lasting history of research excellence in genetics and evolution and the successful applicant will directly benefit from this outstanding scientific environment while building a strong and valuable experience in biodiversity informatics and genomics. Candidates will not need to speak French and the working language will be English.

Net monthly salary will be 2100-2500 Euros depending on experience.

Applications should be sent by email to carole.smadja-at-univ-montp2.fr AND Pierre.boursot-at-univ-montp2.fr by ***10 April 2012*** and should include 1-page research statement with date of availability, a detailed CV, and the names and contact details of 3 referees.

Dr. Carole Smadja CNRS research scientist Chargée de recherches CNRS http://www.carole-smadja.staff.shef.ac.uk/ Institut des Sciences de l^{1}Evolution cc065, Université Montpellier 2 34095 Montpellier France Phone: +33 (0)4 67 14 92 70

carole.smadja@univ-montp2.fr

MountainLake BiologicalStation EarlyCareerFellowships

REMINDER: Review of proposals has begun. Please send in your application.

Mountain Lake Biological Station announces Early-Career Fellowships.

The University of Virginia's, MLBS is excited to offer a limited number of fellowships to support station and residency costs for researchers to explore new projects or collect preliminary data. This is a rare opportunity to make an extended stay of up to 2 months at one of North America's premier field stations at no cost to the researcher. Preference will be given to individuals and projects with the potential to develop into long-term research activities at the Station. We especially encourage applications from individuals in the postdoctoral or early faculty phases of their careers, but will not exclude other individuals from consideration.

Interested individuals should submit a single pdf file including CV and a 2-3 pp proposal outlining the proposed research to MLBS@virginia.edu. Review of proposals will begin February 20, 2012. For more information about the fellowship program, research opportunities or Mountain Lake Biological Station (mlbs.org), please contact the Director - Butch Brodie (bbrodie@virginia.edu).

Yours, Melissa Ivy Wender Office Manager Mountain Lake Biological Station University of Virginia 223 Gilmer Hall 1-434-982-5486 www.mlbs.org "Wender, Melissa (miw2m)" <miw2m@eservices.virginia.edu>

NewYorkU AbuDhabi EvolutionaryGenomics

POSTDOC: EVOLUTIONARY GENOMICS AT NEW YORK UNIVERSITY/ABU DHABI

Several postdoctoral and technician positions are available immediately in the Purugganan Laboratory to study plant evolutionary genomics in the new NYU Abu Dhabi Center for Genomics and Systems Biology. Candidates must have a Ph.D. and experience in molecular evolutionary research. The position is available immediately and the postdoctoral scientist will be based in a satellite laboratory of the Purugganan group in Abu Dhabi at the United Arab Emirates.

The researchers at the new NYU Abu Dhabi Center will work primarily and initially on re-sequencing of date palm genomes for a comprehensive study of their evolution. Other secondary projects involve the evolution of Chlamydomonas and other marine algae, and possibly microbiome work in extreme environments and coral reefs in the region. We are looking for researchers who have a pioneering spirit and will be able to work well in an interdisciplinary setting. The researchers will also have to be involved in establishing the Center and setting up an intellectual community at NYU AD with physicists, chemists, neuroscientists and engineers.

The position will have a generous pay and housing/travel allowance package and is for an initial one-year period renewable annually for 5 years. Applicants should send a CV and names of 3 referees to Michael Purugganan (mp132@nyu.edu). Applications will be considered immediately until the position is filled.

NYU Abu Dhabi is a research university with a fully integrated liberal arts and science college (http://nyuad.nyu.edu/). It draws students from around the world, and prepares them for the challenges and opportunities of our interconnected world. NYU Abu Dhabi and NYU New York form the backbone of a fully connected Global Network University. The new NYU Abu Dhabi Center for Genomics and Systems Biology will house researchers in evolutionary genomics, algal systems biology, chemical genomics and neuronal systems biology.

– Michael Purugganan Dorothy Schiff Professor of Genomics

Department of Biology Center for Genomics and Systems Biology 12 Waverly Place New York University New York, NY 10003

Tel. (212) 992 9628 Web: http://biology.as.nyu.edu/object/MichaelPurugganan.html mp132@nyu.edu

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NorthCarolinaStateU ModelingPopDynamics

Postdoc: Mathematical Modeling of Evolutionary Strategies to combat vector-borne disease

PROJECT DESCRIPTION: The incumbent will work on an NIH-funded project that will build, test and refine stochastic, spatially explicit, simulation models that link insect population genetics/dynamics with human disease epidemiology. We aim to develop a city-scale model for the transmission of dengue virus, utilizing rich entomological, epidemiological and human movement data sets from a research collaboration focused in Iquitos, Peru. A major goal of the work is to predict the impacts of various interventions (such as conventional mosquito control, vaccines, and novel transgenic mosquito management methods) on dengue. The culmination of the project will be the execution of a large-scale mosquito control study and a comparison between observed and model-predicted population genetics/dynamics.

Our major new modeling efforts will be to develop the epidemiological component of our model and to use parallel computing to increase the spatial scale of our mosquito population dynamics/genetics models. We are also interested in building simple spatial and non-spatial, deterministic models as heuristic tools for better understanding basic principles, but we are not looking for applicants who are only interested in working with simple, generic models.

An important part of our project involves field experiments to acquire data that will inform the structure and parameterization of the models, and a large-scale mosquito control study to provide data against which model predictions will be tested. We anticipate that this position will involve analysis of these and other data, so statistical experience, particularly involving parameter estimation and/or uncertainty quantification, would be beneficial. The person in this position will have the opportunity to travel to Peru and assist in design of field experiments. Some hands on field- work is also possible.

The funding for this postdoctoral position is through an NIH research grant. However, our group also has an NSF-IGERT graduate training grant titled “Genetic Engineering and Society: The case of transgenic pests”. Six students in the first IGERT cohort will focus on mosquitoes and dengue. The person in this postdoctoral position will have the opportunity to work with the students and faculty involved in the IGERT program. http://geneticengsoc.ncsu.edu/ Qualifications: Training in ecological or epidemiological modeling and experience with development of computer simulation models. Experience in C++ would be highly desirable, as would strong statistical skills.

To apply: email a cover letter and CV to Fred_Gould@ncsu.edu and Alun_Lloyd@ncsu.edu

For more details on the project see the following publications:

Magori, K., M. Legros, M. Puente, D. A. Focks, T. W. Scott, A. Lloyd, F, Gould. 2009. Skeeter Buster: a stochastic, spatially-explicit modeling tool for studying Aedes aegypti population replacement and population suppression strategies. PLoS Negl Trop Dis 3(9): e508. doi:10.1371/journal.pntd. 0000508

Xu, C., Legros, M., Gould, F, Lloyd, A. L. 2010.Understanding Uncertainties in Model-Based Predictions of Aedes aegypti Population Dynamics. PLoS Negl. Trop. Dis. 4(9): e830. doi:10.1371/journal.pntd.0000830 Legros, M., Magori, K., Morrison, A.C., Xu, C., Scott, T.W., Lloyd, A.L.,

Gould, F. 2011. Evaluation of location-specific predictions by a detailed simulation model of Aedes aegypti populations. PLoS ONE 6(7), e22701. doi:10.1371/journal.pone.0022701 Gould, F.,

K. Magori, Y. X. Huang 2006 Genetic strategies for controlling mosquito-borne diseases. American Scientist. 94 (3): 238-246.

fred_Gould@NCSU.EDU

Okinawa QuantitativeBiodiversity

Postdoc: Quantitative Biodiversity Scientist

The Biodiversity and Biocomplexity Unit (http://www.oist.jp/biodiversity-and-biocomplexity-unit, PI: Evan Economo) at the Okinawa Institute of Science and Technology, Japan, is seeking a postdoctoral researcher.

We are looking for a postdoc with interests in computational, theoretical, or statistical approaches to biodiversity science from evolutionary and/or ecological perspectives. The lab has a focus on the ecology, evolution, and biogeography of ant biodiversity in the Pacific region but prior experience with ant biology is not necessary for this position. Applicants having experience with model-based inference of population and evolutionary processes and working with next-generation sequence data are especially encouraged to apply. However, the position is flexible and all interested parties are encouraged to contact the PI. There will be numerous opportunities to work closely with other research groups at OIST (e.g. Ecology & Evolution Unit, PI: A. Mikheyev), the nearby University of the Ryukyus, the U. of Michigan, and elsewhere.

To apply, please send your CV, including a list of references, and a letter describing your scientific background and interests by email to <recruiting-economo@oist.jp> by March 12. Informal enquiries or questions are also welcome, and I will be at ESJ in Otsu in March for those who would like to meet then. The position would begin in summer 2012.

About OIST: The Okinawa Institute of Science and Technology (www.oist.jp) is a new interdisciplinary research institute and graduate university located in the seaside village of Onna-son. The institute is international by design; the working language is English and researchers are split between Japanese and foreign nationalities. The institute is located in a beautiful ecological setting adjacent to coral reefs and subtropical forest, and offers a highly competitive package for postdoctoral scientists. For more information on OIST, see recent articles in Nature (http://www.nature.com/news/2011/110629/full/474553a.html) (http://www.nature.com/nature/journal/v474/n7353/full/474541b.html) and the Economist (http://www.economist.com/node/21540228).

Evan P. Economo Michigan Society of Fellows Department of Ecology & Evolutionary Biology University of Michigan

evaneconomo@gmail.com

Oxford EvolutionaryComputational

Postdoctoral Research Assistant Behavioural and Evolutionary Ecologist/Computational Biologist

Fixed-term for up to three years Department of Zoology, South Parks Road, Oxford Grade 7: £29,249-£35,938 p.a.

A postdoctoral position is available, for up to three years, from 1April 2012 or as soon as possible thereafter, to study social structure in wild bird populations from an ecological and evolutionary perspective. The post is funded as part of an ERC Advanced Investigator grant of 2.5M over five years to Prof Ben Sheldon. The post will be based in the Edward Grey Institute, Department of Zoology, University of Oxford. The postholder will join a research team examining the causes and consequences of variation in social structure in wild populations.

Candidates should have a PhD in behavioural or evolutionary ecology, or a related subject or in computational biology,particularly as applied to the study of social networks, group and population structure or collective behaviour. The successful candidate will have proven skills in computationally intensive analyses of biological systems and in writing and publishing papers in leading journals in the field.

The post is based in a dynamic research-active institute, of c. 55 people, fully integrated within the Department of Zoology. Further details about the institute available at: http://www.zoo.ox.ac.uk/egi/ Informal inquiries (with CV) to Prof Ben Sheldon (ben.sheldon@zoo.ox.ac.uk). Only applications received before midday on 29 March 2012 can be considered. If you would like to apply please go to http://www.ox.ac.uk/about_the_university/jobs/research/ and search using reference 102358.

Cheers, Colin

Further particulars: DEPARTMENT OF ZOOLOGY TINBERGEN BUILDING SOUTH PARKS ROAD OXFORD OX1 3PS Tel: 01865271278

Job description and selection criteria

Job title Postdoctoral Research Assistant Division MPLS Department Zoology Location South Parks Road Grade and salary Grade 7: £29,249-£35,938 per annum Hours Full time Contract type Fixed-term for up to three years Reporting to Professor Ben Sheldon Vacancy reference 102358

Introduction

The University

The University of Oxford is a complex and stimulating organisation, which enjoys an international reputation as a world-class centre of excellence in research and teaching. It employs over 10,000 staff and has a student population of over 21,000.

Most staff are directly appointed and managed by one of the University¿s 130 departments or other units within a highly devolved operational structure - this includes 5,900 academicrelated staff (postgraduate research, computing, senior library, and administrative staff) and 2,820 support staff (including clerical, library, technical, and manual staff). There are also over 1,600 academic staff (professors, readers, lecturers), whose appointments are in the main overseen by a combination of broader divisional and local faculty board/departmental structures. Academics are generally all also employed by one of the 38 constituent colleges of the University as well as by the central University itself.

Our annual income in 2010/11 was £919.6m. Oxford is one of Europe's most innovative universities: income from external research contracts exceeds £376m p.a., and more than 70 spin-off companies have been created.

For more information please visit www.ox.ac.uk About the Mathematical, Physical, and Life Sciences Division

The Mathematical, Physical, and Life Sciences Division (MPLS) is one of the four academic divisions within the University, (that is, Humanities Division, Social Sciences Division, Mathematical, Physical, and Life Sciences Division, Medical Sciences Division). It comprises ten academic departments: Chemistry, Computing Laboratory, Earth Sciences, Engineering Sciences, Materials, the Mathematical Institute, Physics, Plant Sciences, Statistics, Zoology. The MPLS Division also encompasses the Begbroke Science Park, the Life Sciences Interface Doctoral Training Centre, and the Oxford e-Research Centre. The constituent units of the Division enjoy an international reputation for excellence in the mathematical, physical, and life sciences, as well as in interdisciplinary areas, particularly at the interface with the medical and environmental sciences.

Each division has its own academic Head of Division and a divisional secretariat, led by the Divisional Secretary. Each division is responsible for academic oversight of the teaching and research of its various departments and faculties, for strategic and operational planning, and for personnel and resource management. Much of this is undertaken by the divisional board and its principal committees.

The Head of the Mathematical, Physical, and Life Sciences Division

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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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PennStateU Metagenomicist

Penn State University and U.S. Geological Survey's Leetown Science Center have an immediate opening for a metagenomicist (two-year position, with full benefits) that will conduct species inventories using next generation sequencing of genomic shotgun libraries generated from environmental (e)DNA samples. Most of the sampling has (and will) involve the collection of eDNA and the detection of invasive, injurious, and rare species. We believe this research will provide the benefits of a more robust comparison of the invasive or rare species genomes, researchers involved in biodiversity monitoring will have more robust answers to fundamental questions such as ?What is the species composition of a particular ecosystem??? and ??How does biodiversity change over time, space, and in relation to future environmental change in threatened habitats???.

The successful applicant will be employed by Penn State University (Dr. Jay Stauffer) and stationed in Dr. Tim King's Laboratory at the U.S. Geological Survey?s Leetown Science Center (LSC) in Kearneysville, West Virginia. The incumbent will lead a project designed to collect eDNA samples, construct genomic DNA shotgun libraries, and perform sequencing on in-house Illumina (GA IIx), Roche 454 (GS Jr.), and Ion Torrent (PGM) platforms. There are several data management challenges that must be overcome including accurate post-sequencing community composition estimates, binning, chimeric contig identification and removal; and downstream comparative analyses of pre- and post-impact community composition surveys. Sequencing results will be used to create a species-specific database containing annotated contigs and singleton sequences for many aquatic invasive, nuisance, and rare species. This BLASTable database will allow researchers to compare the results of eDNA sequences to efficiently detect the presence of invasive and/or rare species. The assembled and annotated genome sequences (including organelles), single nucleotide polymorphisms (SNPs), and microsatellite markers for each rare and invasive species incorporated into the study will be made available via the Aquatic Invasives and Rare Species database (AIRSBase) at USGS?LSC.

Knowledge Required by the Position

Advanced professional knowledge of genetics and genomics, metagenomics, comparative genomics, community ecology, and issues related to detecting aquatic invasive species.

Comprehensive knowledge of molecular biology techniques to analyze samples of fish and wildlife, including DNA, RNA (mRNA and miRNA), and eDNA extraction and quantification, genomic shotgun DNA and cDNA library creation, qPCR library quantitation, high throughput (e.g., massively parallel) and Sanger (capillary electrophoresis) DNA sequencing, polymerase chain reaction (PCR) methodology, restrictase digests, and electrophoretic analysis; and skill in modifying or adapting techniques to meet project goals.

Comprehensive knowledge of next generation sequencing technology, including genomic shotgun, cDNA, and paired-end library preparation for sequence analysis and operation of the Agilent Technologies 2100 Bioanalyzer, the Roche 454 GS Jr., the Ion Torrent, and Illumina GA IIx sequencers. Candidates with an advanced background in bioinformatics will be given special considerations.

If you are interested in this position, please contact Dr. Tim King (tlking@usgs.gov ; 304-724-4450) or Dr. Jay Stauffer (vc5@psu.edu ; 814 863-0645).

Fair Winds and Following Seas,

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

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

tlking@usgs.gov

PennStateU MolPopulationGenomics

An NIH funded position for a Postdoctoral Scholar in Molecular Population Genomics is available immediately in the lab of Dr. Stephen W. Schaeffer, Professor, Department of Biology, The Pennsylvania State University, University Park, PA, USA. The aim of this project is to determine the molecular population genetic mechanisms for the origin and maintenance of chromosomal inversions in natural populations of Drosophila pseudoobscura. This project will involve the analysis of 50 genomes of Drosophila pseudoobscura using next generation sequencing. This position will include teaching one academic course (Advanced Genetics) during the fall semester under the guidance of Dr. Schaeffer, where students in the course will aid in the analysis of next generation sequence data. A PhD with expertise in one or more of the following areas is required: molecular population genetics, bioinformatics, or genomics. Applicants should send a cover letter briefly describing their experience and how it relates to the advertised position, their CV, and names and contact information for three references by email to Dr. Schaeffer at (sws4@psu.edu) For further information please call Dr. Schaeffer at 814-865-3269. Review of applications will begin immediately and continue until the position is filled.

Penn State is committed to affirmative action, equal opportunity, and the diversity of its workforce.

Stephen W. Schaeffer, Ph.D. Department of Biology The Pennsylvania State University 208 Erwin W. Mueller Laboratories University Park, PA 16802-5301 Office Telephone: (814) 865-3269 Laboratory Telephone: (814) 863-1650 FAX: (814) 865-9131 Email: swschaeffer@psu.edu WWW: http://www.bio.psu.edu/directory/sws4

swschaeffer@psu.edu

Smithsonian BiodiversityGenomics

Smithsonian Biodiversity Genomics and Bioinformatics Postdoctoral Fellowship Program

The Smithsonian Institution (SI) Postdoctoral Fellowships in Biodiversity Genomics and Bioinformatics promote collaborative research in these fields (60%), plus a well-defined outreach component (40%) oriented toward building genomics expertise in the greater SI research community. Research should involve comparative genomic approaches such as phylogenomics, population genomics, metagenomics or transcriptomics, and have a component that involves significant bioinformatics analysis. Your proposal should also detail in at least one page your bioinformatics outreach plan, which can include collaborative work with other SI projects and teams, training workshops or development of software,pipelines or tutorials. We plan to fill three or more Fellowships in the area of Biodiversity Genomics and are especially interested in recruiting a team of Fellows who will work together to advance bioinformatics at the Institution. Coordinated applications dealing with multiple genomic approaches are strongly encouraged. The Smithsonian's molecular research facilities are located at National Museum of Natural History (NMNH), National Zoological Park (NZP), and the Smithsonian Tropical Research Institute (STRI) in the Republic of Panama. Collaboration with other SI facilities (Smithsonian Environmental Research Center, Museum Conservation Institute, etc.) is encouraged. Applicants must propose to conduct research in-residence for a period of 12 to 24 months. Applicants must have completed or be near completion of the Ph.D. Recipients who have not completed the Ph.D. at the time of application must provide proof of completion of the degree before the fellowship begins. Applicants interested in conducting research at these facilities are strongly encouraged to contact potential advisors/hosts at any of the Smithsonian's various Museums and Research Institutes prior to proposal preparation and submission, as well as the Biodiversity Genomics Steering Committee (via Michael Braun, braunm@si.edu). Please consult the research staff listed for the Museum, Research Institutes, and Offices http://www.si.edu/ofg/mrirolist.htm. Proposals are due 1 April 2012 and application materials are available via https://solaa.si.edu . "Fleischer, Robert" <FleischerR@si.edu>

Smithsonian BiodiversityGenomics 2

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Please consult the research staff listed for the Museum, Research Institutes, and Offices http://www.si.edu/ofg/mrirolist.htm . Proposals are due 1 April 2012. Application instructions are online at http://www.si.edu/ofg/Applications/BGB/BGBappOnline.htm. Submit applications via https://solaa.si.edu . "Fleischer, Robert" <FleischerR@si.edu>

Stockholm Computational Phylogenetics

Two post-docs in computational phylogenetics

Two 24-month post-doctoral positions are available in the Department of Biodiversity Informatics at the Swedish Museum of Natural History in Stockholm to work with Dr Fredrik Ronquist on Bayesian phylogenetic inference. In this project, funded by the Swedish Research Council, we are developing an R-like computational environment making it possible to build complex evolutionary models for simulation and Bayesian inference. You will be expected to contribute to the computational environment while developing an independent, methodological or empirical research project where Bayesian phylogenetic computation plays a central role. The choice of research topic is quite flexible within these general constraints.

The successful candidates will be part of the Stockholm Phylogenomics Group, involving mathematicians, computer scientists and biologists at the Karolinska Institute, the Royal Institute of Technology (KTH), the Swedish Museum of Natural History, and Stockholm University. The group offers an excellent interactive environment for cross-disciplinary research in bioinformatics. Through the Swedish National Infrastructure for Computing (SNIC) and the Bioinformatics Infrastructure for Life Sciences (BILS), the group has access to high-performance computing resources and support services.

You should have a doctoral degree in a relevant area, such as bioinformatics, mathematics, statistics, computer science or evolutionary biology. You should be comfortable with mathematical and statistical reasoning, be a skilled programmer, and have experience with empirical research problems of scientific significance. A strong track record and good communication skills are expected, including proficiency in English.

Monthly salary will be 3,100-3,600 Euros depending on experience. Starting date is flexible but should be no later than December 31, 2012. Please indicate desired starting date in the application.

For more information about the positions, contact Professor Fredrik Ronquist, Head of the Department of Biodiversity Informatics at the Swedish Museum of Natural History (fredrik.ronquist@nrm.se; +46-8 5195 4094).

The application should consist of a personal letter, a description of the planned research project (3-5 pages), and a CV. Mark the application with "dnr 33-119/2012", and send it by e-mail to rekrytering@nrm.se by *** March 30, 2012 ***.

Fredrik Ronquist <Fredrik.Ronquist@nrm.se>

Switzerland ModellingPopulations

Modelling large-scale population processes in Swiss breeding birds

The Swiss Ornithological Institute in Sempach (Switzerland) is seeking a highly motivated postdoctoral researcher to model large-scale population processes in Swiss breeding birds. The project aims 1) to develop methods that allow the estimation of survival and recruitment from monitoring data and 2) to model spatial and temporal variation of survival and recruitment in selected species to better understand population trends.

The main data source in the project will be the Swiss breeding bird survey (MHB), which has been producing 2-3 replicated counts per breeding season in 267 1 km2 quadrats in every breeding season since 1999. These data allow estimation of population trends in abundance while accommodating imperfect detection. However, the demographic mechanisms underlying these trends remain unknown. The model of Dail and Madsen (Biometrics 2011) enables the estimation of survival and recruitment from such data. Exploring the potential of the Dail-Madsen-model at the scale of Switzerland will be a first part of the project. A possible topic is also to develop extensions of the model, such as the inclusion of correlated spatial effects or the integration of MHB data with other data sets that are directly informative about demographic rates, such as ring-recoveries. A second part of the project is the application of the modelling framework to address relevant ecological and management questions. Candidates include the patterns of survival and recruitment along the altitudinal gradient in Switzerland or whether particular habitat types or regions are associated with higher survival or recruitment. It will be one of the duties of the selected candidate to identify relevant research topics in this field and then to expand on the identified issues using our data and the modelling framework to be developed.

The ideal candidate has solid experience in population modelling, in Bayesian statistical modelling and is a proficient programmer in the R and BUGS languages. Further, a demonstrated ability and willingness to produce high-quality publications will be an important selection criterion.

The work will be conducted in collaboration with Michael Schaub (michael.schaub@vogelwarte.ch) and Marc Kéry (marc.kery@vogelwarte.ch), which both are available for further information.

The position is initially for two years, but may be extended to a third year. The ideal starting date would be June 2012. Information on the Institute can be found at www.vogelwarte.ch/startseite-english.html Applications (preferably by e-mail) should be submitted to Michael Schaub (michael.schaub@vogelwarte.ch), Swiss Ornithological Institute, 6204 Sempach, Switzerland, before 30 April 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 May 2012.

Schaub Michael <michael.schaub@vogelwarte.ch>

SyracuseU InsectMolPhylo

Postdoctoral Position in Insect Molecular Phylogenetics.

A postdoctoral position on the molecular phylogenetics of tri-trophic interactions is available in the laboratory of Dr. David Althoff at Syracuse University. Specifically, traditional molecular techniques and NextGen sequencing will be used to conduct simultaneous analyses of phylogeographic and phylogenetic patterns in yuccas, yucca moths and their insect natural enemies. The overall goal is to examine the importance of host specialization in diversification at multiple trophic and hierarchical levels.

The position will require field collections, voucher preparation, and the development and application of molecular markers (SNPs, microsatellites, and single copy loci) to analyze genetic structure of plants and insects. The position will be awarded for one year with the possibility of renewal for additional years. The ideal candidate will have strong interests in plant-insect interactions and the use of molecular phylogenetics to test evolutionary hypotheses, be proficient in phylogenetic analyses, and have extensive experience with NextGen Sequencing data collection and analysis.

Applicants should send an e-mail to Dr. David Althoff (dmalthof@syr.edu) explaining their interest in the position, a CV, and the names and contact information for at least two references. The position will begin after July 1, 2012. Review of applicants will begin March 25, 2012 and will continue until the position is filled.

David Althoff Assistant Professor Dept. of Biology Syracuse University 107 College Place Syracuse, NY 13244 Office: 315.443.1096 Lab: 315.443.9368 FAX: 315.443.2012 plantecology.syr.edu/althoff/

David M Althoff <dmalthof@syr.edu>

SyracuseU PlantEvolGenetics

Post-Doctoral Position in Plant Evolutionary/Ecological Genetics

A post-doctoral position is available in the laboratory of Jannice Friedman, in the Department of Biology at Syracuse University. Work in my lab is focused on both the ecological causes and the genetic underpinnings of the evolution of reproductive strategies in plants. Current work is focused on understanding life history transitions between annual and perennial strategies in Mimulus guttatus, yellow monkeyflower. Other projects include investigating the evolution of wind pollination from animal pollination in the angiosperms.

I am interested in recruiting an individual to work on the genetics of adaptation of reproductive strategies. The focus of this research position will be tailored to the skills and expertise of the successful applicant, but projects will likely involve greenhouse and molecular work, field experiments, and analysis of next-gen sequence data. A strong background in evolutionary or population genetics, experience with molecular techniques, and data analysis and/or programming would be valuable. The ideal candidate will have a clear vision of promising directions and unresolved questions in ecological and evolutionary genetics, and use this appointment as an opportunity to develop and pursue novel and exciting questions.

Interested candidates should contact me by email at friedman@syr.edu. Applications should include: a brief description of past research accomplishments and future goals, CV, PDFs of top two publications, and contact information for three references. Funding is guaranteed for 1 year, with a second year renewable depending on progress. Salary will be competitive with full benefits.

Jannice Friedman Assistant Professor Department of Biology Syracuse University 107 College Place Syracuse NY 13244

friedman@syr.edu http://friedmanlab.syr.edu friedman@syr.edu

TromsoU Museum AncientDNA

Postdoctoral fellow on ancient DNA studies, Tromsø University Museum, Norway

Application deadline: March 29th 2012 The following reference number must be quoted in your application: 2012/989

The University of Tromsø has vacant a Postdoctoral fellow on the project ancient DNA analyses of flora and fauna in NW Europe. The starting date is as soon as possible.

The position is a fixed term of three years.

The position is attached to Tromsø University Museum, Department of Natural Sciences.

For further information, please contact project leader Inger Greve Alsos, e-mail: inger.g.alsos@uit.no, tel + 47 77 62 07 96 or head of Department of natural sciences Arne C. Nilssen, e-mail arne.c.nilssen@uit.no, tel +47 77 64 50 12.

The Department of Natural Sciences presently employs 25 staff members, including 10 permanent scientific positions, one researcher, and 5 PhD students (http://-uit.no). The department has large scientific collections, documenting more than 130 years of research in North Norway and other northern regions. The department includes a research group in taxonomy and biodiversity. The group focuses on diversity, phylogeography, and taxonomy of northern organism using molecular as well as traditional methods.

The position is on the project “Ancient DNA of NW Europe reveals responses to climate Change” funded by the Research Council of Norway. The primary objective of the project is to explore the occurrence of boreal species at northern latitudes by ancient DNA analyses. Subgoals are to 1) Confirm the occurrence of trees and other boreal taxa during the LGM period (22,000 - 13,000 BP) at Andøya (Parducci et al. Science 2012), 2) Determine the occurrence of boreal species on Svalbard during the Holocene warm period, 3) Evaluate the representation of current surrounding vegetation in modern lake DNA, 4) Test if pollen may contribute to DNA recovered in ancient soils, and 5) Evaluate implications for inferred species migration rates as well as climate reconstruction.

See full annoucement at : http://www.jobbnorge.no/-job.aspx?jobid=81767 Assoc. Prof. Inger Greve Alsos Tromsø University Museum NO-9037 Tromsø Norway Telephone: +47 77 62 07 96 Telefax: +47 77 64 51 05 Email: inger.g.alsos@uit.no http://www.svalbardflora.net/ Alsos Inger Greve <inger.g.alsos@uit.no>

TulaneU AmphibianEvol

POSTDOCTORAL RESEARCH ASSOCIATE

Tulane University, New Orleans

AMPHIBIAN EVOLUTIONARY ECOLOGY

The Richards-Zawacki lab at Tulane University is seeking a Postdoctoral Research Associate to participate in an NSF funded project investigating the evolutionary ecology of Panamanian poison frogs. The successful applicant will collaborate on projects to investigate the roles of natural and sexual selection in driving diversification among poison frog populations in Panama. Potential projects could include (1) studies of mating behavior/sexual selection and/or natural selection on aposematic signal variants, (2) studies of the genetic/genomic architecture of variation in aposematic signals and their reception, or (3) studies of the impact of habitat quality on visual/chemical signals.

The successful applicant will have (1) a Ph.D. in evolution, molecular biology, ecology or related field, (2) the ability to organize and lead field studies in Panama and/or molecular studies in New Orleans, (3) strong writing skills, and (4) the ability to work independently. Candidates with experience working with genomic/transcriptomic data and a working knowledge of Spanish are preferred.

Funds are available for one year with the possibility of a second year pending satisfactory progress. Starting salary is dependent upon experience.

The position is available starting May 2012 (negotiable). Review of applications will begin April 1, 2012 and continue until a suitable candidate is found.

To apply, please send (1) a cover letter, (2) CV, (3) statement of research interests/experiences, and (4) names and contact information for three references to Dr. Corinne Richards-Zawacki (cori@tulane.edu).

For additional information about this and other research programs going on in our laboratory, please visit our website at http://tulane.edu/sse/eebio/people/cori/index.cfm Corinne L. Richards Zawacki, Ph.D. email:cori@tulane.edu Assistant Professor Department of Ecology and Evolutionary Biology Tulane University, New Orleans, Louisiana

Cori Richards-Zawacki <cori@tulane.edu>

TulaneU TeachingPlantEvol

KOCH POSTDOCTORAL TEACHING FELLOW

The Department of Ecology and Evolutionary Biology (EEB) at Tulane University seeks to fill the inaugural Koch Postdoctoral Teaching Fellowship in Plant Ecology And Evolution, pending budgetary approval (website:http://tulane.edu/sse/eebio/about/kochfellow.cfm). The position is a two-year appointment, with faculty status and a start date of July 1. The department aims to recruit outstanding researchers with a Ph.D. and prior postdoctoral research experience who will merge excellence in teaching (30%), research (60%), and service (10%). Applicants are encouraged to identify a potential faculty collaborator in EEB, although those interested in independent research will be given consideration. Applicants should describe botanical courses they would be able to teach, including courses that are not in the existing curriculum and could be taught as special topics. An application (curriculum vitae, statement of research interests, and statement of teaching philosophy and interests) and three letters of recommendation focusing on both research excellence and teaching potential should be submitted electronically to the Search Committee (e-mail: ecolevol@tulane.edu). Please write "Koch Fellow" in the subject line. Application review will begin immediately, and the position will remain open until filled.

Tulane University is an Equal Employment Opportunity/Affirmative Action/ADA employer committed to excellence through diversity. All eligible candidates are invited to apply.

Michael J. Blum Arnold Early Career Professor in Earth and Ecological Science Dept of Ecology & Evolutionary Biology Tulane University New Orleans, LA 70118

www.tulane.edu/~mjblum< http://www.tulane.edu/%7Emjblum >

"Blum, Michael J" <mjblum@tulane.edu>

UAdelaide AncientDNA

Microbiology (medical/dental) / Ancient DNA / Archaeology

ARC Post-doctoral position available at the Australian Centre for Ancient DNA

School of Earth and Environmental Sciences, University of Adelaide http://www.adelaide.edu.au/acad/ Due to an administrative delay posting the job description, the closing date for this position has been extended until March 7, 2012.

Salary: (Level A) Aus $68,751 - $73,800 // (Level B) $75,425 - $89,569 per year. (Appointment to either level will be commensurate with qualifications and experience).

We are searching for a post-doctoral researcher to lead a 3-year Australian Research Council funded project A powerful new genetic view of the recent evolutionary history of humans and their diseases' which will use DNA from calcified oral microbial plaques to trace the evolution of a variety of human diseases, and the relationship to culture, diet, migration patterns and geography.

The project will use Next Generation Sequencing approaches to explore microbial diversity over the past 10,000 years, in one of the first studies of how human commensals have evolved through time and the potential disease consequences. Primary study areas are Neolithic Europe and the Americas, and international travel is likely.

We are looking for an unusually capable and motivated individual with wide interests who enjoys challenging and unusual research, and has the ability to work closely with archaeologists and museum personnel as well as dental microbiologists and evolutionary biologists. Expertise in microbial evolution, genetics, archaeology, bioinformatics, and natural history are key requirements. Evidence of strong independent research and writing/publishing skills are also essential.

The successful applicant will have been awarded a PhD at the time of taking up the appointment, and will have a strong record of publishing papers throughout their career, preferably in high profile journals.

Enquiries of an academic nature can be directed to Professor Alan Cooper, Australian Centre for Ancient DNA, University of Adelaide, email: alan.cooper@adelaide.edu.au

Fixed-term for three years starting as soon as possible

Applicants can visit http://www.adelaide.edu.au/jobs/current/ Job No. 17258 for relevant information on the application process, and the selection criteria. Applications will be accepted until the 7 March, 2012.

alan.cooper@adelaide.edu.au

UArizona Evolution

Post-Doc Position Opening

I am seeking a full-time post-doctoral researcher to join my lab at the School of Information Resources and Library Science, University of Arizona. The researcher will work full time on a NSF funded project that will employ natural language processing techniques to extract organism character/trait information from the evolutionary literature for the purpose of constructing the tree of life. At the University of Arizona, our focus is on natural language processing techniques, but the researcher will also have the opportunity to work with a team of biologists, computer scientists, and paleontologists from ten universities. Cost of relocation from another state will be reimbursed.

Position start date: As soon as a candidate is selected.

Salary: $45,000 with 3% increase annually

Qualifications: 1. Must have an earned Ph.D (or close to completion) in Computer Science, Information Science, Biology, or related fields 2. Must have experience with Java programming language and application development environment such as Eclipse. 3. Knowledge and experience in natural language processing such as regular expression pattern match, syntactic parsing, and/or semantic analysis are highly desirable but not required 4. Knowledge and background in systematics and/or evolutionary biology are highly desirable but not required

Responsibilities: The post-doc researcher will be involved in 1) activities related to developing, implementing, and evaluating natural language processing algorithms, 2) communicating with other collaborators and participating in project meetings, including short visits to other sites, 3) activities related to project management, such as project reporting to NSF., 4) activities related to publish and present research findings, and 5) other miscellaneous activities related to the project in general.

Application: Applications are reviewed immediately until a candidate is selected. Please send cover page, CV, and three letters of recommendation via the UA Career application system (https://www.uacareertrack.com/, search for Job Number: 49679) .

Questions? Contact: Hong Cui, Ph.D Assistant Professor, Information Technologies School of Information Resources and Library Science University of Arizona hongcui@email.arizona.edu

Hong cui <hong1.cui@gmail.com>

UBuffalo EvolPlantGenomics

POSTDOCTORAL FELLOW IN EVOLUTIONARY PLANT GENOMICS

We invite applications for a Postdoctoral Fellowship in Evolutionary Plant Genomics. Candidates should have recently completed, or will soon complete, their PhD with an emphasis on bioinformatics or computational genomics. Experience with genomic data bases, genome assembly, annotation and comparison software desirable. Knowledge of combinatorial optimization and graph algorithms will be useful. The position is for two years, subject to review after one year, and can begin immediately. The successful applicant will be co-supervised, in the context of a joint project, by Victor Albert in the Biological Sciences department at the University at Buffalo (where the postdoc will be physically based), and David Sankoff in the Mathematics department of the University of Ottawa. Contact vaalbert@buffalo.edu for details.

Victor A. Albert Empire Innovation Professor of Biological Sciences University at Buffalo http://biology.buffalo.edu/Faculty/Albert/albert.html vaalbert@buffalo.edu

UCIrvine MosquitoChromosomeEvolution

UCIrvine.MosquitoChromosomeEvolution

Applications are invited for a postdoctoral scholar position in the laboratory of Dr. José M. Ranz at University of California Irvine. The major goal of the project is to study the functional genomics of chromosomal rearrangements in the malaria vector Anopheles arabiensis. The position is available starting in June 2012 for two years. The successful applicant will be based the first 9 months at the Institut de Recherche en Sciences de la Santé (IRSS), Bobo-Dioulasso, Burkina Faso. The project involves the molecular analysis of breakpoints of chromosomal inversions involved in the adaptation of Anopheles arabiensis and the characterization of genome-wide patterns of expression divergence between alternative chromosomal arrangements. A strong background in mosquito genetics is required and some experience in cytogenetics, molecular biology, and bioinformatics is desired. Particularly encouraged are applicants with prior experience in field malaria research. Salary commensurate with experience. Applications should include a covering letter describing previous experience and fit to the position, full CV with a list of publications, and the name and address of two references. The deadline for applications is May 4th 2012. Applications should be sent to the email addresses below:

Dr. José M. Ranz jranz@uci.edu

Dr. Diego Ayala diego.ayala@nd.edu

Dr. Roch Dabiré dabire_roch@hotmail.com

The University of California, Irvine is an equal opportunity employer committed to excellence through diversity, has an active career partner program and a National Science Foundation Advance Gender Equity Program.

Jose Ranz <jranz@uci.edu>

UExeter MicrobeEvolutionModels

Postdoctoral research associate: Mathematical and Empirical Models of Microbial Evolution

Fixed-term position for 24 months, starting April, 2012

Biosciences, University of Exeter, UK

Funded by EPSRC, we seek an enthusiastic evolutionary biologist or computational/mathematical modeller to work on microbial adaptation and evolution in the shared laboratory of Robert Beardmore and Ivana Gudelj. You should already hold, or be about to complete, a PhD and the project would start as soon as possible.

Strong statisticians, physicists, engineers, or computer scientists looking for a change of direction would be of interest to our group as we have a range of interdisciplinary projects that require skills from a multitude of disciplines.

The successful candidate will be able to choose one from a range of projects, but the main current focus of our group is the evolution of resistance of microbes in response to antimicrobial drugs and viruses. Likely projects involve active collaboration with laboratories at ETH, Michigan, Harvard, Bath and elsewhere and possible titles are as follows:

(1) Single-cell observations of bacteria in single and multi-antibiotic environments (2) Understanding the co-adaptation of synthetic phage and their pathogenic hosts. (3) The nonlinear dynamics of gene regulation: how do bacteria decide to move?

A successful candidate with an empirical background will be encouraged to interact with theoretical researchers already in the group, conversely an incoming theoretical researcher would have the opportunity to undertake empirical work in-house.

To apply, send a copy of your CV with a cover letter and two academic references to r.e.beardmore@exeter.ac.uk

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Robert Beardmore Professor of Mathematical Biosciences

EPSRC Leadership Fellow Biosciences, Geoffrey Pope Building Streatham Campus Exeter University

t: +44 (0)1392 725 839 w: http://people.exeter.ac.uk/-reb217/home.html "Beardmore, Robert" <R.E.Beardmore@exeter.ac.uk>

UGreifswald PopGenetics

Applied Zoology and Conservation, Zoological Institute and Museum, University of Greifswald, Germany

Postdoctoral Researcher - 'Conservation/Population Genetics'

Application deadline: 10.05.2012

We are seeking a highly motivated team-oriented researcher with a strong background in Conservation/Population/Socio-Genetics and good skills in statistics and modeling. The person appointed is expected to lead the DNA lab, teach the module Evolutionary Conservation Genetics (4 h urs/ week and semester in English) and supervise bachelor / master students. Post-doc experience and basic knowledge in German is of advantage.

Education: PhD with experience in Conservation and/or Population Genetics

Entrance: starting July 01, 2012

Duration of appointment: up to 6 years

Salary and benefits: according to a public service position in Germany (E 13)

Please send your application by email (all material in one attached pdf please) to Gerald Kerth (gerald.kerth@uni-greifswald.de). Include your CV, a short description of your research interests and research experience (including a list of methods you are familiar with), and names and email addresses of 2-3 references who could be contacted.

The research group 'Applied Zoology and Conservation' uses an integrative approach, combining behavioral, ecological, and molecular methods to investigate questions at the interface of evolutionary, behavioral, and conservation biology. We study bats and species interacting (e.g. parasites) with them as well as hornets, but our research is not restricted to a specific group of animals. Research interests include the causes and consequences of sociality (incl. cooperative behavior and host-parasite interactions), mate and habitat choice, dispersal, as well as applied and basic animal conservation. In the field, we apply automatic monitoring of animals marked with PIT- tags, radio-telemetry, thermography, and infrared-video. Genetic methods include analyses of nuclear and mitochondrial DNA microsatellites and sequences.

Greifswald, a lively town with 55.000 inhabitants and rich medieval architecture, is situated in Northern Germany at the Baltic Sea. It has good connections to the nearby islands of Usedom and Ruegen with their lovely beaches and is a train-ride of 2.5 hours away from Berlin. In its vicinity are several National Parks, harboring a diverse wildlife.

For further information contact gerald.kerth@uni-greifswald.de or see:

www.mnf.uni-greifswald.de/institute/fr-biologie/-zool-institut-museum/angewandte-zoologie-und-naturschutz.html Professor Dr. Gerald Kerth

Angewandte Zoologie und Naturschutz Zoologisches Institut Johann Sebastian Bach-Str. 11/12 D - 17489 Greifswald

Tel.: +49 (0)3834 864100 Fax: +49 (0)3834 864252

gerald.kerth@uni-greifswald.de

UGroningen EvolutionaryTheory

PhD (4 years) or Post-doc (3 years) position in Theoretical Evolutionary Ecology

"Causes and consequences of variation in dispersal behaviour"

Organization

This research project 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 University of Groningen (The Netherlands). The research is funded by a TopGrant (ALW-TOP/11.017) allocated to Prof. Jan Komdeur from the Netherlands Science Foundation (NWO).

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 post-doctoral 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.

Qualifications

- 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

For the PhD

The University of Groningen offers a salary of 2042 (scale 50, number 0) gross per month in the first year, up to a maximum of 2612 (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.

For the Post-Doc

The university offers a gross salary depending on qualifications and experience, ranging between 2744 gross (scale 10, number 3) per month and a maximum of 3755 (scale 10, number 12) gross per month for a full-time post-doctoral 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 June 1, 2012. The position will be filled as soon as suitable candidates have been found.

Additional information

Information about the University of Groningen can be found at the website www.rug.nl. Detailed information about the Theoretical Biology and the

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UHelsinki EvolutionaryGenomics

Department of Biosciences, University of Helsinki, invites applications for

POST-DOCTORAL POSITION

in Evolutionary Genomics.

The postdoctoral researcher will be a part of the

Ecological Genetics Research Unit (EGRU; http://www.helsinki.fi/biosci/egru/index.html) lead by Prof. Juha Merilä. The assignment can start in April 2012 (start date is flexible - early start preferred) and continue until April 2014, possibly longer.

The post-doctoral fellow to be employed is expected work with projects focused on application of next-generation sequencing technologies to address broad and generally interesting problems relating to population differentiation and genetics of adaptation. The model systems in these studies will be the nine-spined (Pungitius pungitius) and three-spined (Gasterosteus aculeatus) sticklebacks. Leeway and funds be will be provided to pursue side-projects as long as the general goals of these are aligned with the general goals of the main project.

An ideal candidate for this position would have a broad interest in evolutionary biology and a background in one or several of the following fields: bioinformatics, evolutionary genomics, statistical or population genetics/genomics, animal or plant breeding sciences.

We are looking for an individual who is highly motivated and can work both independently and in a team. Capacity to face intellectual challenges, willingness to learn new skills, and to explore new intellectual territories are qualities expected from a strong candidate. A demonstrated track-record in research, doctoral degree and experience in bioinformatics analysis of next-generation sequencing data are required. The working language will be English. An overview of our past and current research can be found at http://www.helsinki.fi/biosci/egru/index.html. The salary will be based on level 5 of the demands level chart for teaching and research personnel in the salary system of Finnish Universities. In addition, the appointee will be paid a salary component based on personal work performance (total salary will be approximately 3050-3400 EUR per month).

Help will be provided in relocation to Helsinki.

The application should include (i) CV, (ii) Publication list, (iii) statement of research interests and motivation for applying this position not exceeding two pages and (iv) contact information of two reference persons who have agreed to provide a written statement on behalf of the applicant.

Applications should be addressed to the Department of Biological Sciences, P. O. Box 65 (Viikinkaari 1), FIN-00014 University of Helsinki, and sent to egru-mail@helsinki.fi. The review of application starts immediately and the position will be filled when a suitable candidate has been found. More information on this position is available from Prof. Juha Merilä (e-mail: juha.merila@helsinki.fi).

More information about Helsinki, University of Helsinki, and Department Biosciences can be found from the following links: http://www.helsinki.fi/en/index.html (city) http://www.helsinki.fi/university/ (university) http://www.helsinki.fi/biosciences/ (department) http://www.helsinki.fi/intstaff/ (University of Helsinki International Staff Services)

Juha Merilä Ecological Genetics Research Unit Department of Biosciences PO Box 65 (Biocenter 3, Viikinkaari 1) FIN-00014 University of Helsinki Finland

E-mail: juha.merila@helsinki.fi Gsm: +358-40-8374165 Fax: +358-9-19157694 www: http://www.helsinki.fi/biosci/egru/ Blog: http://blogs.helsinki.fi/egru-blog/ Juha Merilä <juha.merila@helsinki.fi>

UHelsinki PathogenEvolution

POST DOC POSITION IN PATHOGEN EVOLUTION AT THE UNIVERSITY OF HELSINKI

Applications are invited for a 2-year (with a possibility of continuation) post doctoral position in the ERC funded PATHEVOL (Linking Pathogen Evolution and Epidemiology) project led by Dr Anna-Liisa Laine at the University of Helsinki.

The project is centered on the interaction between host plant Plantago lanceolata and its fungal pathogen Podosphaera plantaginis in the Aland Islands. With 11 years of epidemiological data from over 4000 host populations, sequenced pathogen transcriptome and solid experimental protocols, this system offers unique opportunities for testing classic hypotheses regarding pathogen evolution with direct links to epidemiological dynamics.

The successful candidate should have PhD / post doctoral experience in evolutionary biology, and a strong interest in studying disease in natural populations. Prior experience studying host-parasite interactions using genetic approaches will be considered an advantage. She/he will lead large scale SNP analyses to answer questions of how pathogen metapopulation genetic structure changes through space and time. The candidate is expected to bring a strong intellectual input to the research, and collaborate closely with other post docs and PhD students in the group.

The research group of Dr Anna-Liisa Laine is part of a consortium of 8 Principal Investigators that form the Metapopulation Research Group, a Centre-of-Excellence appointed by the Academy of Finland for years 2012-2017.

More information: www.helsinki.fi/ ~ allaine www.helsinki.fi/science/metapop Starting date: Summer / Autumn of 2012 Application deadline: 15 April 2012 Salary: 3235-3910 EUR (depending on experience) How to apply: Mail your application (CV with publications included, contact details of two references, and a letter (MAX 1 page) with a description of your research interests and why you would be a suitable candidate for the project) as a single pdf file to biotiede-mrg@helsinki.fi with title PATHEVOL / post doc.

Informal inquiries to anna-liisa.laine@helsinki.fi

Anna-Liisa Laine <anna-liisa.laine@helsinki.fi>

UIllinois GrassGenomics

Postdoctoral position in sorghum genomics

A postdoctoral position is available immediately in the Energy Biosciences Institute at the University of Illinois to study the genetic architecture of plant height and flowering time in sorghum. The successful candidate will map major genes in a large set of sorghum introgression lines using genotyping-by sequencing, characterize their phenotypic and transcriptional effects (alone and in combination) in near-isogenic lines, and integrate the results into current models of internode elongation and phase change in grasses. This is a mature project with good opportunities for rapid publication for the motivated candidate.

The Energy Biosciences Institute (http://www.energybiosciencesinstitute.org/) is a large, multidisciplinary, public-private partnership between the University of Illinois, the University of California-Berkeley, Lawrence Berkeley National Laboratory, and BP. This position will be located in the Institute for Genomic Biology (http://www.igb.uiuc.edu/), one of the newest buildings on campus. Champaign-Urbana is one of 13 "micro-urban" communities recognized in Wikipedia for their combination of big-city culture and small-town affordability.

Requirements: PhD in plant genetics or a related discipline and strong scientific writing skills.

Preferred Qualifications: Previous experience with next-generation sequence data analysis. Physiologists/developmental biologists with a strong motivation to learn genomics are also encouraged to apply.

The position is for 2 years with the possibility of extension. Review of applications will begin April 16th and continue until the position is filled. To apply please send a cover letter summarizing your previous research experience, future research goals, and interest in this position, as well as a CV and email addresses for 3 references, to:

Patrick J. Brown Assistant Professor Department of Crop Sciences University of Illinois 1408 Institute for Genomic Biology 1206 W Gregory Drive Urbana, IL 61801 pjb34@illinois.edu

pjb34@illinois.edu

UManchester MicrobialInteractions

Postdoctoral research assistant: Microbial Ecology/Insect-Microbe interactions

Fixed-term position for 7 months.

Faculty of Life Sciences, University of Manchester

We seek an enthusiastic and highly motivated evolutionary biologist/ microbial ecologist to study competitive and coevolutionary interactions between bacteria and burying beetles for access to carrion. You will use complementary methods to characterize decomposer microbial communities and their associated toxins, as well as behavioural, physiological and biochemical counterstrategies used by beetle adults and larvae to contend with microbial competitors. This project is a collaboration between Drs. Daniel Rozen and Andrew McBain at the University of Manchester and Dr. Per Smiseth at the University of Edinburgh.

You should hold a PhD in a relevant biological discipline and have a strong background in evolutionary biology. Experience in microbial ecology is desirable.

Funded by the Leverhulme Trust, this position is tenable from 1 April 2012 until 9 November 2012.

Please send informal inquires and applications (CV and cover letter) to Daniel Rozen (daniel.rozen@manchester.ac.uk).

The application deadline is April 4.

Daniel Rozen Faculty of Life Sciences Michael Smith

Building Oxford Road, Manchester M13 9PT UK

phone: +44 (0)161 275 5094 fax: +44 (0)161 275 5082

Daniel.Rozen@manchester.ac.uk

UMelbourne ColourAdaptation

POSTDOC - ADAPTIVE SIGNIFICANCE OF COLOUR CHANGE

A post-doctoral position is available based in the Department of Zoology at the University of Melbourne, Australia to join an ARC-funded interdisciplinary collaboration between Dr Devi Stuart-Fox (The University of Melbourne), Prof. John Endler (Deakin University - near Melbourne) and Prof. Warren Porter (University of Wisconsin, USA). We are seeking a highly motivated and enthusiastic person to work on the adaptive significance of visible and near-infrared (NIR) colour change in bearded dragon lizards. The aim of the project is to understand the evolutionary drivers of colour change. Specifically, the project will assess the relationship between animal-visible and NIR colour and colour changes, and how that relationship varies within and between individuals and in relation to environmental and visual parameters. The research fellow will conduct extensive fieldwork at a range of sites in semi-arid Australia, and apply a range of techniques including spectrodadiometry, thermal imaging and potentially radio-tracking. The research fellow will also learn and apply visual and biophysical modelling techniques to assess the consequences of animal-visible and NIR colour change for signalling or camouflage and thermoregulation. Applicants should have a background in sensory and/or biophysical ecology, excellent interpersonal and written and oral communication skills, and ability to work to deadlines on research publications and grant applications. Experience with spectroradiometry, thermal imaging and/or biophysical modelling is highly advantageous.

The successful candidate will be expected to start on the 1st August 2012. Application details, including specific selection criteria, can be found at www.jobs.unimelb.edu.au, Position number 0028711.

Applications will close Monday 2nd April 2012. For further information please contact: Dr. Devi Stuart-Fox Tel +61 3 83444846 devis@unimelb.edu.au

PhD POSITION - ADAPTIVE SIGNIFICANCE OF COLOUR CHANGE

A PhD project is available to investigate the causes and consequences of colour change in bearded dragon lizards. The project is part of an ARC-funded interdisciplinary collaboration between Dr Devi Stuart-Fox (The University of Melbourne), Prof. John Endler (Deakin University - near Melbourne) and Prof. Warren Porter (University of Wisconsin, USA). The student will be based in the Department of Zoology at the University of Melbourne but will also regularly visit and work closely with Prof. John Endler's research group at Deakin University.

The aim of the project is to understand the evolutionary drivers of colour change. Specifically, the project will assess the relationship between animal-visible and near-infrared (NIR) colour and colour changes, and how that relationship varies within and between individuals and in relation to the environment. The project addresses the consequences of colour change for thermoregulation, camouflage and signalling, and therefore straddles the fields of biophysical and sensory ecology. The project will involve field work in southern-central and eastern semi-arid Australia, where bearded dragon lizards are relatively common, and vary in coloration. The project will also involve captive maintenance of bearded dragons and laboratory-based behavioural experiments. The student will be an integral part of a team comprising the project leaders, a postdoctoral research fellow and potentially a Masters student and volunteers.

The student will need to obtain a scholarship at the University of Melbourne (Australian Postgraduate Award (APA) or equivalent). Thus a first class honours or masters degree and/or evidence of publishing in international peer-reviewed scientific journals will be essential. Experience working with reptiles and evidence of field skills will be a bonus. The preferred starting date for this project is early to August/September 2012, but a later start date is possible.

Closing date for expressions of interest is April 30th 2012. Please submit a brief cover letter and comprehensive CV with contact details for two referees to: Dr Devi Stuart-Fox, Department of Zoology, University of Melbourne, Victoria 3010 - devis@unimelb.edu.au. For further information, contact Dr Devi Stuart-Fox - devis@unimelb.edu.au.

Devi Meian Stuart-Fox <d.stuart-fox@unimelb.edu.au>

UMichigan Phylogenomics

Postdocs: Phylogenomics, Quantitative Macroevolution, & Evolutionary Morphology.

I am seeking 1-2 postdoctoral researchers to join my lab in the Department of Ecology and Evolutionary Biology at the University of Michigan in late summer or fall of 2012.

I welcome applications from researchers whose interests complement any conceptual aspects of our research program (see below!). However, applicants with interests and/or skills in any of the following areas are especially encouraged to apply:

1) Phylogenomics and macroevolution. The objective of this work is to generate and analyze genomic datasets at the species and population level for several major groups of Australian squamate reptiles to better understand the speciation process and large-scale patterns of diversification. The ideal candidate would have experience in generating, assembling, and analyzing next-generation sequence data. An interest in understanding Australia's amazing reptile diversity is also desirable, but no prior experience with reptiles is required.

2) Modeling phenotypic evolution across vertebrates, particularly towards the development of new methods for data acquisition and analysis. Candidates with strong backgrounds in vertebrate paleobiology and evolutionary morphology or involving the integration of morphology and computer science (e.g., applications of computer vision; 3D morphometrics) are especially encouraged to apply.

3) Computational macroevolution, particularly towards the development of new methods for integrating fossils and phylogenies or for analyzing the tempo and mode of speciation, extinction, and phenotypic evolution. Programming skills in R, C++, and/or Python are highly desirable, but limited prior experience will suffice provided the applicant has genuine enthusiasm to learn.

Research in the Rabosky lab focuses on three primary areas: (i) evolutionary biology and ecological biogeography of Australian squamate reptiles; (ii) the causes of variation in speciation, extinction, and phenotypic evolutionary rates across phylogenetically diverse taxa; and (iii) development of computational and mathematical approaches for studying large-scale patterns and processes in evolutionary biology, as applied to molecular phylogenetic, paleontological, and ecological data. Our primary conceptual objective is to understand why species richness and phenotypic/ecological diversity vary so dramatically across the tree of life.

The positions offer excellent opportunities for independent research, career development, and quantitative skills training. The U of Michigan has an outstanding community of researchers in quantitative/computational evolutionary biology as well as foundational biodiversity science (including many researchers affiliated with the UM Museum of Zoology and Museum of Paleontology).

Applications should be sent to drabosky@umich.edu. Please include a cover letter describing your experience and research interests, a C.V., and contact information for three references. Review of applications will begin in late March and will continue until the positions are filled.

Daniel L Rabosky Miller Research Fellow Department of Integrative Biology University of California, Berkeley Berkeley, CA 94720

[starting 2012] Assistant Professor Department of Ecology and Evolutionary Biology University of Michigan

Assistant Curator of Herpetology, University of Michigan Museum of Zoology

email: drabosky@umich.edu website: http://-cteg.berkeley.edu/ ˜ rabosky drabosky@berkeley.edu drabosky@berkeley.edu

UMinnesota PopulationFragments correctedURL

A postdoctoral position is available on a project examining evolutionary consequences of population fragmentation of Echinacea angustifolia (purple coneflower) in North American prairie. This study, now in its 17th year and funded by NSF's Evolutionary Genetics Program, joins demography of remnant populations and quantitative genetic experiments in the field with modeling efforts to shed light on the feedbacks between numerical dynamics and genetic dynamics of Echinacea, and on its interactions with insects. The postdoc will collaborate with Stuart Wagenius (Chicago Botanic Garden) and Ruth Shaw (University of Minnesota) on quantitative genetic and demographic studies of the fragmented population and associated field experiments and will have the opportunity to participate in developing evolutionary models that incorporate our accumulating understanding of genetic and demographic processes within the study system. There is considerable potential for the postdoc to develop further research projects pertinent to the overall goals of this study.

To learn more about this project, please consult: Shaw, R.G., C.J. Geyer, S. Wagenius, H.H. Hangelbroek, J.R. Etterson. 2008. Unifying life history analyses for inference of fitness and population growth. American Naturalist 172: E35-E47.

Lopez, S., F. Rousset, F. H. Shaw, R. G. Shaw, O. Ronce. 2009 Joint effects of inbreeding and local adaptation on the evolution of genetic load after fragmentation. Conservation Biology 23: 1618-1627.

Wagenius, S., H. H. Hangelbroek, C. E. Ridley, R. G. Shaw. 2010. Biparental inbreeding and interremnant mating in a perennial prairie plant: fitness consequences for progeny in their first eight years. Evolution 64:761-771.

Wagenius, S., A. Dykstra, C. E. Ridley, and R. G. Shaw. 2011. Seedling recruitment in the long-lived perennial, Echinacea angustifolia: a ten year experiment. Restoration Ecology. DOI: 10.1111/j.1526-100X.2011.00775.x

Ridley, C. E., H. H. Hangelbroek, S. Wagenius, J. Stanton-Geddes and R. G. Shaw. 2011. The effect of plant inbreeding and stoichiometry on interactions with herbivores in nature: Echinacea angustifolia and its specialist aphid. PLoS One 6(9): e24762. doi: 10.1371/journal.pone.0024762

More information on the project, including links to papers, available at http://echinaceaproject.org/ The position is offered for an initial year, with the opportunity to renew for a second year. During the summer, the postdoc will be based, along with the rest of the research team, at the field site near Alexandria MN. During the academic year, the postdoc will be based in the Department of Ecology, Evolution and Behavior at the University of Minnesota. Both are stimulating and interactive communities. To learn more about the project, interested individuals may email Ruth Shaw (rshaw@superb.ecology.umn.edu) or Stuart Wagenius (swagenius@chicagobotanic.org).

To apply, submit a letter of interest describing research interests and experience, CV, and names and contact information of three individuals willing to send letters of reference at https://employment.umn.edu/ The requisition number for this position is: 176618

Review of applications will begin March 19, 2012 and continue until the position has been filled.

The University of Minnesota provides equal access to and opportunity in its programs, facilities, and employment without regard to race, color, creed, religion, national origin, gender, age, marital status, disability, public assistance status, veteran status, sexual orientation, gender identity, or gender expression.

Ruth Shaw <shawx016@umn.edu>

UMinnesota SexualSelection

Postdoctoral Position Available: University of Minnesota, Department of Ecology, Evolution, and Behavior

A position for a postdoctoral research associate is available in the laboratory of Marlene Zuk. I am moving from UC Riverside to the EEB department at the University of Minnesota, and am seeking a postdoc to collaborate on research into sexual selection, signaling, and rapid evolution in field crickets.

Our lab focuses on the recent spread of a new silent morph in several populations of Teleogryllus oceanicus, an Australasian cricket that has been introduced to Hawaii. We are examining the role of behavior in the establishment of this novel trait, and are particularly interested in the importance of parasitoid-host interactions in the system. Research involves both laboratory and field components, and is described in more detail at http://www.faculty.ucr.edu/~mzuk/. In recent years we have added a significant molecular component to the work, and are collaborating with scientists from the University of St. Andrews on a project examining the genetic basis for the silent morph. In addition to the research, the postdoc will help establish a new laboratory and supervise undergraduate research assistants as well as work with graduate students.

Qualifications and start date: Applicants should have completed the PhD in evolutionary biology or a related discipline by spring 2012. Experience in some combination of behavioral ecology, molecular evolution, phylogeography, and/or entomology is desirable. Anticipated start date is flexible, but no earlier than June 1, 2012. Salary will be in the range of $39,000 per year, depending on qualifications and experience. Initial funding is available for one year, with the opportunity for extension to a second and third year.

To apply: Send a complete CV, the names and contact information for at least two references, and a short statement of research interests and accomplishments to: employment.umn.edu, requisition #177088. Review of applications begins immediately.

Environment: Founded in 1851, the University of Minnesota, with its five campuses and 67,932 students, is one of the largest, most comprehensive universities in the United States, and ranks among the most prestigious research universities in the world. It is both a major research institution, with scholars of national and international reputation, and a state land-grant university, with a strong tradition of education and public engagement.

EEB is part of the College of Biological Sciences at the University of Minnesota and is one of the Universitys most highly ranked units. The department is located in the Ecology Building on the St. Paul campus, but also has two major field stations where students and faculty conduct field research.

The University of Minnesota provides equal access to and opportunity in its programs, facilities, and employment without regard to race, color, creed, religion, national origin, gender, age, marital status, disability, public assistance status, veteran status, sexual orientation, gender identity, or gender expression.

Marlene Zuk Professor of Biology University of California Riverside, CA 92521

Ph: 951-827-3952

http://biology.ucr.edu/people/faculty/Zuk.html Sex on Six Legs: Lessons on Life, Love, and Language from the Insect World Available now! Buy it on Amazon, B&N, or from your independent bookseller

Marlene Zuk <marlene.zuk@ucr.edu>

UNebraska PopBiol 2

This ad contains updated application instructions, but is otherwise identical to the previously posted ad.

POPULATION BIOLOGY POSTDOCTORAL RESEARCH FELLOWSHIP

THE UNIVERSITY OF NEBRASKA-LINCOLN is seeking applications for two 2-year postdoctoral fellows in Population Biology.

A Ph.D. completed in an area of the biological sciences with expertise in any aspect of population biology is required. Qualified candidates are required to contact a potential faculty advisor to develop a 2-year research project. Advisors may be in the School of Biological Sciences (biosci.unl.edu), School of Natural Resources (snr.unl.edu), or Department of Mathematics (math.unl.edu) and must be qualified to advise projects in population biology. Fellows will pursue research with a faculty advisor and will teach a graduate seminar in each year of their fellowship.

To apply go to http://unl.employment.unl.edu, search for requisition #120198, and complete the Faculty/Administrative application. In addition, application materials should be assembled into a single pdf (Lastname_Firstname_PopBio) and emailed as an attachment to biologysearch@unl.edu. This pdf must include a CV, a 1-page research proposal, a 1-page description of prior research, and a 1-page description of potential graduate seminars. Finally, the applicant must arrange for three letters of reference (one of which must be from the proposed faculty sponsor) to be emailed to the same address. Questions about the program should be sent to Dr. Diana Pilson (dpilson1@unl.edu).

Applications should be received by 15 April 2012 in order to ensure full consideration, but the position will remain open until filled. The salary range is in line with international standards for postdoctoral positions. We strongly encourage applications from women, and members of minority groups. The University of Nebraska has an active National Science foundation ADVANCE gender equity program, and is committed to a pluralistic campus community through affirmative action, equal opportunity, work-life balance, and dual careers.

Diana Pilson School of Biological Sciences 348 Manter Hall University of Nebraska Lincoln NE 68588-0118

402-472-2347 402-472-2083 (fax)

Diana Pilson <dpilson1@unl.edu>

UNebraska PopulationBiology

POPULATION BIOLOGY POSTDOCTORAL RESEARCH FELLOWSHIP

THE UNIVERSITY OF NEBRASKA-LINCOLN is seeking applications for two 2-year postdoctoral fellows in Population Biology.

A Ph.D. in Biology, Ecology, Evolution, Genetics, or

Mathematics, and expertise in any aspect of population biology is required. Qualified candidates are *required** *to contact a potential faculty advisor to develop a 2-year research project. Advisors may be in the School of Biological Sciences (biosci.unl.edu), School of Natural Resources (snr.unl.edu), or Department of Mathematics (math.unl.edu) and must be qualified to advise projects in population biology. Fellows will pursue research with a faculty advisor and will teach a graduate seminar in each year of their fellowship. Applications must include a CV, a 1-page research proposal, a 1-page description of prior research, and a 1-page description of potential graduate seminars. Application materials should be assembled into a single pdf (Lastname_Firstname_PopBio) and emailed as an attachment to biologysearch@unl.edu. In addition, the applicant must arrange for three letters of reference (one of which must be from the proposed faculty sponsor) to be emailed to the same address. Questions about the program should be sent to Dr. Diana Pilson (dpilson1@unl.edu).

Applications should be received by 15 April 2012 in order to ensure full consideration, but the position will remain open until filled. The salary range is in line with international standards for postdoctoral positions. We strongly encourage applications from women, and members of minority groups. UNL is committed to a pluralistic campus community through Affirmative Action and Equal Opportunity, and is responsive to the needs of dual career couples. We assure responsible accommodation under the Americans with Disabilities Act. For further information contact Dr. Valery Forbes at 402-472-6676 for assistance.

Diana Pilson School of Biological Sciences 348 Manter Hall University of Nebraska Lincoln NE 68588-0118

402-472-2347 402-472-2083 (fax)

Diana Pilson <dpilson1@unl.edu>

UNotreDame MosquitoGenomics

POSTDOC: Functional Genomics of malaria mosquitoes

An NIH-funded postdoctoral position is available immediately in the lab of Nora Besansky, Department of Biological Sciences, University of Notre Dame. The goal of the project is to uncover the genetic basis of a physiological trait– saltwater tolerance– in an African malaria vector mosquito, Anopheles merus. This primarily coastal species is sister to An. gambiae, an obligate freshwater breeder that is the main vector of malaria across most of tropical Africa. The two morphologically indistinguishable species are very closely related, and can be crossed to produce viable and fertile F1 females. Laboratory colonies of both species and insectary rearing facilities are available at Notre Dame; other tools include completely sequenced genomes (for An. gambiae, since 2002; for An. merus, later this year). Genetic analysis of saltwater tolerance will involve two experimental approaches: QTL mapping based on next generation sequencing, and comparative transcriptomics based on RNASeq. As such, the project will involve the collection and analysis of large next-generation sequencing datasets. The successful candidate will work with Dr. Besansky in collaboration with Dr. Romero-Severson at Notre Dame, and Dr. Peter Andolfatto at Princeton. The Besansky lab has other ecological and evolutionary genomics projects ongoing in An. gambiae; for more information, please see:

http://nd.edu/˜nbesansk/ http://biology.nd.edu/people/faculty/besansky/ http://www.ncbi.nlm.nih.gov/pubmed?term=3Dbesansky%20n EDUCATION/EXPERIENCE/SKILLS: REQUIRED: Ph.D. in biology, computer science, or related field. Strong motivation, good laboratory and analytical skills, demonstrated track record of writing and publicaton. PREFERRED: Experience in population genetics, statistical genetics, bioinformatics. Laboratory experience with molecular methods (DNA/RNA). Programming skills, familiarity with R, and experience with NGS data.

HOW TO APPLY: Applicants should submit a single PDF file containing a brief cover letter, curriculum vitae, and the names and contact information for two references, to nbesansk@nd.edu. Screening of applications will begin immediately and continue until the position is filled.

TERM OF APPOINTMENT: The initial term is set for one year but is renewable for another year, with the possibility of renewal for additional years.

ADDITIONAL INFORMATION: The Department of Biological Sciences is the center for research and teaching in the life sciences at the University of Notre Dame. Housed mainly in the Galvin Life Sciences Building, the department is home to some 50 research and/or teaching faculty, 120 graduate students, 30 postdoctoral fellows, 300 undergraduate majors, and 75 technical and administrative staff. This vibrant research and teaching community continues to expand its faculty, both within the Department and with new associated faculty in the nearby Indiana University School of Medicine - South Bend, and in other departments in the College of Science and the College of Engineering. New centers in our building enhance our intellectual mission, and include the Eck Institute for Global Health, Center for Rare and Neglected Diseases, Environmental Change Initiative and Center for Aquatic Conservation, Center for Zebrafish Research, and the Notre Dame Integrated Imaging Facility. We also house a Genomics Core and the Freimann Animal Facility and support an outstanding field station, the University of Notre Dame Environmental Research Center - a NSF NEON site. Other available resources on campus include the Harper Cancer Research Institute, Keck Center for Transgene Research, Center for the Study of Biocomplexity, as well as Proteomics Cores and high-performance computing resources. Information on department and other college faculty and facilities can be found at http://-biology.nd.edu and http://science.nd.edu . The University of Notre Dame is located on the northern limits of South Bend, Indiana (90 miles east of Chicago). The University of Notre Dame is an Equal Opportunity / Affirmative Action Employer.

Nora J. Besansky, PhD Rev. John Cardinal O'Hara, C.S.C. Professor of Biological Sciences Eck Institute for Global Health Department of Biological Sciences 317 Galvin Life Sciences Bldg University of Notre Dame Notre Dame, IN 46556-0369 Tel: 574-631-9321 Fax: 574-631-3996 nbesansk@nd.edu

nbesansk@nd.edu

UOregon NematodeEvolution

Postdoctoral Research Associate Institute of Ecology and Evolution Posting: 12098 Location: Eugene Closes: Open Until Filled

POSTDOCTORAL POSITION: EVOLUTIONARY

GENETICS OF SEXUAL CONFLICT AND MATING SYSTEMS EVOLUTION

A postdoctoral scholar is sought to contribute to an NSF funded project in the laboratory of Patrick Phillips, Institute of Ecology and Evolution, University of Oregon using the nematode Caenorhabditis elegans and its relatives as model systems for studying the origins and consequences of sexual conflict. The project uses experimental evolution, molecular quantitative genetics, functional analysis, and high throughput genomics and proteomics to understand both natural and experimentally derived variation in sexual interations and sex-specific function. See http://-www.uoregon.edu/~pphil for lab projects.

The University of Oregon is located in Eugene, OR, one of the most outstanding small cities in the US. The campus is one hour from the beautiful Oregon coast and one hour from mountain hiking and skiing. Candidates should have completed their Ph.D. before beginning the position. The successful candidate will have the ability to work effectively with faculty, staff and students from a variety of diverse backgrounds. The initial appointment is for one year with extension for an additional year. Although the postion is available immediately, the start date can be flexible based on the needs of the candidate. To assure full consideration applications must be received by April 15, 2012, but position will remain open until filled. Please send a statement of research interests, publications, CV, and letters from three references to Patrick Phillips via ie2jobs@uoregon.edu, Subject Posting 12098 or c/o Search #12098, Institute of Ecology and Evolution, 5289 University of Oregon, Eugene, OR 97403-5289.

The University of Oregon is an equal-opportunity, affirmative-action institution committed to cultural diversity and compliance with the Americans with Disabilities Act.

http://jobs.uoregon.edu/unclassified.php?id=3792 INSTITUTE OF ECOLOGY AND EVOLUTION 5289 University of Oregon, Eugene OR 97403-5289 F (541) 346-2364 http://IE2.uoregon.edu Equal-opportunity, affirmative-action institution committed to cultural diversity and compliance with the Americans with Disabilities Act

IE2jobs <ie2jobs@uoregon.edu>

UOregon PrimatePopGenomics

Postdoctoral Research Associate Posting: 12068 Location: Eugene Closes: Open Until Filled

The Department of Anthropology and the Institute of Ecology and Evolution (IE2) at the University of Oregon invite applications for a post-doctoral researcher to study the relationships among genetics, environmental change, demography, and disease transmission in wild non-human primates. This research is part of a new NIH-funded project focused on the biological and human dimensions of primate retroviral transmission. Specifically, the successful candidate will be using molecular methods to infer patterns of relatedness and migration in a primate community occupying a fragmented landscape (Kibale National Park, Uganda), contributing to a larger effort aimed at understanding disease transmission. S/he will be part of an international and multidisciplinary collaborative research team, an integral member of the Molecular Anthropology Group at the University of Oregon (http://molecular-anthro.uoregon.edu/), and will work closely with other labs in the Institute of Ecology and Evolution (http://ie2.uoregon.edu/). The following criteria apply:

1) Candidates must have completed a PhD in Anthropology, Biology, or a relevant discipline within the biological sciences prior to start date.

2) Candidates must have strong interests in evolutionary biology and/or ecology with a demonstrated commitment to publishing and a career in research. Interests in molecular ecology, conservation biology, and disease ecology are a plus.

3) Strong preference will be given to candidates who have expertise in (or are dedicated to learning) computational approaches that can be used to assemble 2nd generation sequence data and conduct evolutionary population genetic/genomic analyses.

4) Preference will be given to candidates who have experience with molecular genetic wet lab methods, especially as applied to eukaryotic organisms.

5) Candidates must be team players who are able to thrive in a collaborative working environment and work effectively with faculty, staff and students from a variety of diverse backgrounds.

6) Candidates must be willing to relocate to Eugene, Oregon for 2 years.

The successful candidate will gain experience in using state of the art molecular methods to address pressing environmental, conservation, and health concerns. S/he will be intimately involved in the continuing development of latest-generation sequencing methods for acquiring population genomic data from non-model organisms and non-invasively collected samples. Duties will include assembly and analysis of genomic data, publication and presentation of results, and helping mentor graduate and undergraduate students in collaboration with colleagues from Africa, North America, and the UK. The successful applicant will also be encouraged to engage in fieldwork and explore new research directions of his/her choosing, assisted by a strong team of collaborators.

The University of Oregon is a highly ranked public research university (R1) and one of the 61 esteemed members of the Association of American Universities (AAU). Eugene is the second largest city in Oregon and an excellent place for the arts and outdoors. It is perfectly situated in the Willamette Valley with Portland, the Pacific Coast, and the Cascade Mountains all within a short drive.

A complete application consists of a current CV, statement of research interests and qualifications specifically addressing the referenced criteria, and a list of three people (names, affiliations, email addresses) who can serve as references. Please direct inquiries to Dr. Nelson Ting (nting@uoregon.edu).

Application materials should be sent to ie2jobs@uoregon.edu with subject Posting 12068 and must be received by March 28, 2012 to assure full consideration, although the position will remain open until filled. Start date is negotiable but no later than September 2012.

The University of Oregon is an equal-opportunity, affirmative-action institution committed to cultural diversity and compliance with the Americans with Disabilities Act

– Nelson Ting, Ph.D. Assistant Professor Department of Anthropology University of Oregon 308 Condon Hall Eugene, OR 97403 Office: (541) 346-5509 http://molecular-anthro.uoregon.edu/index.html nelson ting <nting@uoregon.edu>

UPoitiers EndosymbiontGenomics-Bioinfomatics

Postdoctoral Position in Bioinformatics

A European Research Council (ERC)-funded postdoctoral position is available to investigate the impact of Wolbachia endosymbionts on the mechanisms of sex determination in isopod crustaceans. The project is supervised by Dr. Richard Cordaux at the Laboratoire Ecologie & Biologie des Interactions (EBI, UMR CNRS 7267), University of Poitiers, France.

Wolbachia are intracellular, maternally-inherited bacteria of arthropods and nematodes, with whom they interact through a variety of symbiotic associations, ranging from parasitism to mutualism. These bacteria are gaining increasing interest as a biological model because of their potential roles in evolutionary processes, insect disease vector and agricultural pest control, and human filarial diseases. Notably, in several isopod crustaceans, Wolbachia endosymbionts can convert non-transmitting male hosts into transmitting females through feminization of genetic males (Cordaux et al. 2004 Heredity 93, 78-84; Cordaux et al. 2011 Trends Genet 27, 332-341).

The area of emphasis for this position will be bioinformatics and genomics. The successful applicant will analyze next-generation sequencing datasets obtained from various isopods and Wolbachia strains to investigate the molecular genetic basis and evolution of sex-determination mechanisms in the isopod-Wolbachia system.

Qualifications include: - Ph.D. in genomics, computational biology or related field, - Computer programming skills (C/C++, Python, PERL and/or R), - Familiarity with the UNIX/LINUX computer-operating environment and with databases, - Experience in and/or knowledge of bioinformatics and statistical analysis.

Other preferred qualifications include: - Experience working with next-generation sequencing datasets and analysis tools, - Knowledge of molecular evolution and/or population genetics.

Applicants are requested to send a curriculum vitae, a statement of research interests, reprints of recent papers, and the names and contact details of three referees. Please provide information regarding timing of availability for this position.

Applications and informal enquiries should be sent to Richard Cordaux (richard.cordaux@univ-poitiers.fr).

Richard Cordaux, Ph.D.

Université de Poitiers UMR CNRS 7267 Ecologie et Biologie des Interactions Equipe Ecologie Evolution Symbiose, Bat. B8 40 Avenue du Recteur Pineau 86022 Poitiers Cedex France Tel: +33 (0)5 49 45 36 51 Fax: +33 (0)5 49 45 40 15 E-mail: richard.cordaux@univ-poitiers.fr Lab website: http://ecoevol.labo.univ-poitiers.fr/ Personal website: http://rcordaux.voila.net/ NEW: 7th International Wolbachia Conference, June 7-14, France http://wolbachia2012.conference.univ-poitiers.fr/ richard.cordaux@univ-poitiers.fr richard.cordaux@univ-poitiers.fr

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UPorto NGS Domestication Adaptation

POST DOCTORAL RESEARCH ASSOCIATE IN BIOINFORMATICS AND POPULATION GENETICS

The Population Genomics and Traits Group of researchers at CIBIO-University of Porto (http://cibio.up.pt) are seeking two candidates for a Posdoctoral fellowship. The successful candidate will be expected to engage in a vigorous basic and applied research program focused on NGS (next generation sequencing) data from several domestic species and their wild relative species. The initial appointment to this position is for three years with a possible extension to six years. Requires a PhD in biological or computer sciences with a solid background on population genetics and evolution as well strong experience with bioinformatics programming languages in a unix environment (Perl, Python, Javascript, SQL) and compiled languages (e.g. C++), relational databases, and construction of computational pipelines. Ability to work independently and with theoretical and empirical population genetics researchers is important. Prior experience with NGS data and large datasets of SNPs is preferred. The goal of the research is to test hypotheses related to animal domestication and molecular adaptation of populations and species to extreme environments. The postdoctoral research will be mainly focused in population genomics, selection, and demography of wild/domestic (livestock) species their parasites from all over the world. This work will include a large amount of data analysis, simulation, and bioinformatics. Several interesting datasets are in hand, which will allow the postdoc to analyze data and publish quality manuscripts relatively quickly to advance the field.

Instructions to Applicants: Applicants should submit by email a cover letter describing interests, skills (including any specific experience with the job responsibilities listed above), prior scientific experience, and 2-3 publications (.pdfs) from peer-reviewed journals, their CV, and the names and contact information of 3 people who can provide letters of reference. Applications as well as demands for further information should be sent to Albano Beja-Pereira to the following email address: posdoc_call2012@cibio.up.pt

The successful candidate will apply to the Portuguese

National Science Agency (FCT) and it's expected to start working in the first months of 2013. Fellowship wage will be 1495 euros /month (tax-free), with social security and national health system assess included. The successful applicants are encouraged to spend part of their time in the United States, e.g. at University of Montana, working with collaborators.

Application review will start at March 12, 2012 and continue until the position is filled.

albanobp@fc.up.pt

USantander CSIC EvolutionaryGenomics

Postdoctoral Position in Evolutionary Genomics at IFCA (Universidad of Santander-CSIC).

A postdoctoral position is available immediately to work with Rafael Zardoya (Madrid), Julio Rozas (Barcelona), David Posada (Vigo), and Jesus Marco (Santander) on a common Project related with gastropod phylogenomics. The position has a term of 1 year and mobility among the referred labs.

Prerrequisites: A PhD in Biology, Chemistry, Computer Science or related fields, with proved skills in computational biology.

Priority will be given to candidates with previous experience in NGS data analysis (assembling, gene annotation, etc), and with expertise in in bioinformatics programing languages (Perl, Python, C, etc).

It will be desirable some experience with Phylogenetics and/or Comparative Genomics or evolutionary biology in general, and with Relational databases (MySQL).

If interested please contact Rafael Zardoya, Department of Biodiversity and Evolutionary Biology, Museo Nacional de Ciencias Naturales, rafaz@mncn.csic.es. Application review will begin on March 5, 2012 and continue until the position is filled. To apply, please send the following: 1. A curriculum vitae 2. Names of 2 referees willing to provide a letter of recommendation upon request 3. A brief statement of research interests and goals.

Rafael Zardoya Research Professor CSIC Museo Nacional de Ciencias Naturales CSIC Jose Gutierrez Abascal, 2 28006 Madrid email: rafaz@mncn.csic.es

rafaz@mncn.csic.es

WayneStateU EvolutionaryGenomics

A postdoctoral position is immediately available in the Hao Group at Wayne State University in the field of evolutionary genomics.

The Hao laboratory is interested in developing a better understanding of the highly dynamic processes and the corresponding functional consequences of genome evolution. To accomplish this research we conduct comparative genomic studies using next-generation sequencing, computational/bioinformatics approaches and mathematical modelling in the context of rigorous, statistical frameworks.

Current projects include: whole genome sequencing of emerging bacterial pathogens, understanding the evolution and epidemiology of bacterial pathogens, developing new models to detect/quantify fine-scale homologous recombination and horizontal gene transfer (in both prokaryotes and eukarytoes), and the birth and death of gene families.

A minimum qualification is a PhD in evolutionary biology, computational biology, genomics or related field. Applicants should be highly motivated, have strong writing skills, and have expertise with some or all of the following skills: phylogenetics, genome assembly, comparative genomics, and computational genomics.

To apply, applicants should send a curriculum vitae, a cover letter with a brief statement of research interests, PDFs of two publications, and contact information for three references. Application material should be sent by email in a single PDF file to HaoW@wayne.edu.

For more information, please email HaoW@wayne.edu or call 313-577-6450.

Wayne State University is an equal opportunity, affirmative action employer. Applications from women and minorities are encouraged.

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WorkshopsCourses

AWI Germany MarineEvolution Sep17-21

Sylt, Germany - Evolutionary potential in marine populations 17-21 Sept.

Workshop: 17-21 September 2012 Evolutionary potential in marine populations

Organisers: Lisa Shama & Mathias Wegner. Helmholtz-Zentrum für Ozeanforschung Kiel (GEOMAR) & Alfred Wegener Institut für Polar und Meeresforschung (AWI)

Venue: AWI Wadden Sea Station, List auf Sylt, Germany

http://www.awi.de/en/research/research_divisions/biosciences/coastal_ecology/events_courses/ http://en.sylt.de/ Workshop content: Our climate is changing at an unprecedented rate, and there is ample evidence that these changes have ecological consequences. The key question now being asked is whether species will be able to adapt fast enough to keep pace with changing environments. Some species will be evolutionary winners (e.g. invasive species), whereas others may not fare as well (e.g. ephemeral populations). This especially applies to marine ecosystems, where climate change has multi-facetted consequences (e.g. ocean warming and acidification, high rates of biological invasions and emerging diseases). Despite the growing awareness of this, very few studies to date have quantified the evolutionary potential of marine populations or the underlying mechanisms of adaptation. Moreover, with the increasing importance of epigenetic inheritance, the balance between genetic adaptation (selection on standing genetic variation) and epigenetic effects (e.g. transgenerational phenotypic plasticity) in response to fast-changing selective agents in the marine environment needs to be reset. In this workshop we will bring together researchers with a primary focus on the evolutionary potential of marine populations to adapt to rapidly changing environments. The workshop will be arranged into three broad topics that include:

1. Molecular and quantitative genetic approaches (e.g. neutral and adaptive genetic variation, standing genetic variation, candidate genes) to investigate adaptation in marine populations

2. Abiotic and biotic selective agents (e.g. climate variability, parasites) that lead to changes in genetic variation in marine populations

3. Epigenetic inheritance (e.g. transgenerational plasticity) as a mechanism to cope with rapid environmental change

Talks and posters will be presented in a relatively informal setting with the aim of promoting discussions, developing new ideas, and providing opportunities for collaborations and networking.

Confirmed plenary speakers:

Philip Munday, ARC Centre of Excellence for Coral Reef Studies andâSchool of Marine and Tropical Biology, âJames Cook University, Australia.

Jennifer Sunday, Earth to Oceans Research Group, Department of Biological Sciences, Simon Fraser University, Burnaby, Canada.

Juha Merilä, Ecological Genetics Research Unit, University of Helsinki, Finland.

Sinéad Collins, Royal Society University Research Fellow, University of Edinburgh, Scotland.

Hans-Otto Pörtner, Marine Biology/Ecological and Evolutionary Physiology, Alfred Wegener Institute, Bremerhaven, Germany

Abstract submission: please apply by 29 April 2012 by submitting an abstract (max. 300 words) to Lisa Shama (lisa.shama@awi.de). Please indicate in which of the three broad topics you prefer to present. Note: the workshop is limited to approx. 50 participants, and we will aim to have a wide variety of presentations within each of the three main topics.

Cost: Depending on the final budget and sources of funding, we expect the registration cost to be approx. 100âper person. Registration includes accommodation in the AWI Guesthouse and meals during the workshop. Participants must cover the costs of travel to Sylt themselves.

Programme: Travel should be planned with arrival during the afternoon/evening on Monday, 17 Sept. The workshop begins with a welcome BBQ on Monday evening. The main body of the workshop takes place over 3 days, with departure on Friday morning 21 Sept.

Download a flyer and find details for travel to Sylt (announcement) at:

http://www.awi.de/en/research/research_divisions/-biosciences/coastal_ecology/events_courses/ For more information contact Lisa Shama (lisa.shama@awi.de).

Lisa Shama <Lisa.Shama@awi.de>

Barcelona Morphometrics Apr10-13 LastCall

This is the last call for the course “Integration and Modularity with Geometric Morphometrics”. This course will be held in the Sabadell facilities of the Institut Català de Paleontologia (Barcelona, Spain) on April 10-13 2012. Instructor: Dr. Chris Klingenberg (University of Manchester, UK).

You can find more information at: http://-www.transmittingscience.org/imgm.htm or writing to courses@transmittingscience.org. There are few places left, and will be occupied by strict inscription order.

With best regards

Soledad De Esteban Trivigno Area de Paleobiología Institut Català de Paleontologia Edifici ICP, Campus de la UAB 08193 Cerdanyola del Vallès Barcelona. Spain 00-34-935868334 www.icp.cat Soledad Esteban <soledad.esteban@icp.cat>

BarHarbor EvolutionMedicine Aug6-10

Evolutionary Foundations for Medicine and Public Health: Focus on Infection and Cancer

August 6-10 at the Mount Desert Island Biological Laboratory, Bar Harbor, Maine

Registration now open < http://www.mdibl.org/-courses/Evolution_and_Medicine/398/ >Initial admissions on March 15th. CME credit available

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.

Faculty

Randolph Nesse - University of Michigan (Course director) Douglas Brash Yale University Carlo Maley - University of California San Francisco Athena Aktipis – University of California San Francisco and Arizona State University Andrew Read - Pennsylvania State University Mark Schwartz New York University Stephen Stearns - 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 year's 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.

For more information on evolutionary applications in medicine and public health, see The Evolution & Medicine Review < http://evmedreview.com >

nesse@umich.edu

Basel MicrobiotaEvolution Sep12-14

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 (includes 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). Registration deadline is on June 30, 2012.

Confirmed Speakers:

Bioinformatics and Computational Tools

1. KNIGHT, Rob (University of Colorado Boulder, USA) - computational tools for understanding the evo-

lution of microbiota through time and space

2. CAPORASO Greg (Northern Arizona University, USA) - QIIME developer (Quantitative Insights Into Microbial Ecology) and microbiota dynamics

3. QI Weihong (ETH Zürich, CH) - Trends and applications of next- generation sequencing technologies

Microbial Diversity and Symbiosis

4. DUBILIER Nicole (Max Plank Institute, Bremen, DE) - Symbioses of bacteria and hydrothermal vent organisms

5. BRUNE, Andreas (Max Plank Institute, Marburg, DE) - Insect gut microbiology and symbiosis

6. EBERT Dieter (University of Basel, CH) - Daphnia parasites and microbiota

Microbiota Dynamics and Evolution

7. GILBERT Jack (University of Chicago, USA) - Microbial community dynamics and function

8. JANSSON, Janet (LNL, DOE-JGI, USA)- bacterial diversity in the environment

9. LEE Carol Eunmi (University of Wisconsin-Madison, USA) - Copepod microbiota and invasion success

10. Van der MEER Jan (University of Lausanne, CH) - Genetic adaptation and evolution of bacteria in the environment

Genomics of Health- and Nutrition-Associated Microorganisms

11. SVANBORG Catharina (University of Lund, SE) - Host imprints on human- associated bacterial genomes

12. VORHOLT Julia (ETH Zürich, CH) - Physiology of plant-associated microbes (metaproteomics)

Bacteria- host interactions and evolution

13. ROSENBERG Eugene and ZILBER-ROSENBERG, Ilana (University of Tel Aviv, IL) - Coral microbial communities and the hologenome theory

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)

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

Bologna Consanguinity May13-16

Course on Molecular and Statistical Genetics of Consanguinity < http://www.eurogene.org/?p=corsi&qc=920&cc=next&m=3&s=2 >

EuroMediterranean University Center of Ronzano, Bologna (Italy), 13-16 May,2012

For further info I am at your disposal, thank you

Serena

Serena Paterlini Training and Eu Projects European Genetics Foundation via di Gaibola, 16, Bologna (Italy) 0039-0512088414 www.eurogene.org Serena Paterlini <egf.serena.paterlini@gmail.com>

Edinburgh StatisticalGenetics Jun13-15 Jun25-29

European Institute in Statistical Genetics 13-15 June and 25-29 June 2012

The European Institute in Statistical Genetics will run in Edinburgh in June 2012, on either side of the 4th International Conference on Quantitative Genetics 2012. The Institute consists of a series of two-and-a-half day courses designed to introduce geneticists to modern methods of statistical analysis and to introduce statisticians to the statistical challenges posed by modern genetic data. Each course is taught by leading academics in the field, and prerequisites are minimal.

Courses are available in the following topics: 1. Genomic Prediction: Ben Hayes 2. Genetics of Competition: Peter Bijma and Bill Muir 3. Advanced R for Genetic Analysis: Thomas Lumley and Ken Rice 4. Population Genetic Data Analysis: Jérome Goudet and Bruce Weir 5. Gene Expression Profiling: Greg Gibson and John Storey 6. Mixed Models in Quantitative Genetics: Bill Muir and Bruce Walsh 7. MCMC for Genetics: Eric Anderson and Matthew Stephens 8. Plant and Animal Association Mapping: Peter Bradbury and Michel Georges 9. Inference of Relationships and Relatedness: Eric Anderson and Elizabeth Thompson

For more details and registration: http://

www.eisg2012.org.uk/ . Loeske Kruuk

Professor Loeske Kruuk Institute of Evolutionary Biology School of Biological Sciences University of Edinburgh Edinburgh, EH9 3JT, UK Tel. 0131 650 5515 http://wildevolution.biology.ed.ac.uk/lkruuk Fourth International Conference on Quantitative Genetics http://www.icqg4.org.uk/ and European Institute in Statistical Genetics http://www.eisg2012.org.uk/ Edinburgh June 2012

Loeske Kruuk <Loeske.Kruuk@ed.ac.uk>

Florence AncientDNA Mar22 Deadline

Dear Colleague and Friends ,

Deadline o of The workshop "A day with.ancient DNA" is approaching (on March 9th); few places are still available, if you are interested please register ASAP at ://www.unifi.it/dbalan/CMpro-v-p-166.html where you will find all other information (venue, talk title, time table)

Speakers:

Michael Hofreiter

Johannes Krause

Carles Lalueza-Fox

Tomas Marques Bonet

Ludovic Orlando

Ermanno Rizzi

See you in Florence,

David Caramelli, Martina Lari, Carles Lalueza-Fox.

The workshop is FREE and open to any interested participants. Participation by graduate students and post-docs is particularly encouraged. Limited space is available at the Aula Magna of DBE so we ask to register asap @ http://www.unifi.it/dbalan/CMpro-v-p-166.html where you will find all other information (venue, talk title, time table and registration form).

The application deadline is on March 9th.

See you in Florence,

David Caramelli, Martina Lari, Carles Lalueza-Fox.

David Caramelli Department of Evolutionary Biology Laboratory of Anthropology Molecular Anthropology/Paleogenetics Unit University of Florence Via del Proconsolo 12 50122 Florence- Italy

tel +390552743021 fax+390552743038

David Caramelli <david.caramelli@unifi.it>

Germany SummerSchoolWorkshop ProteinEvolution July

Summerschool and Workshop on Protein Evolution - Germany, July 2012

Dear colleagues,

On behalf of the Organizing Committee, it is my great pleasure to draw your attention to two interesting meetings on "Protein Evolution" taking place this year in July in Germany. Both events are jointly organized by the University of Munich (LMU) and the University of Muenster (WWU). Official language of both events will be English.

First, we are organizing a summer school for late Master/early PhD students. The summerschool will once again - for the 6th time - be held at the Abtei Frauenwörth (Lake Chiemsee, close to Munich and the Bavarian alps) from July 22nd till July 27th, 2012. Several international senior scientists will give general lectures and hands-on sessions on their topics within the field of protein evolution. Around 20 students (Master and early PhD level) will have the opportunity to join the summerschool and present their work in short oral presentations. In addition, there will be plenty of time for discussion with senior scientists about the students' projects and other questions. Deadline for application is May 1st, 2012. More information on the summerschool can be found on our website: http://www.eeslmu.de/eeswiki/Summer_school_2012 Second, for more senior scientists (advanced PhD level onwards), we are organizing a workshop taking place at the University of Munich from July 27th till July 29th, 2012. The workshop comprises four main topics: Evolution of new Proteins Protein Modelling Systems Biology Evolutionary and Functional Genomics For each main session, we invited 2-3 international scientists who will present their work in 45min talks. Short oral contributions will be selected from submitted poster abstracts. Overall, we aim for around 50 participants.

This meeting provides an opportunity for experts to share their knowledge, present new results, and forge new networks to develop new ideas in the field of protein evolution. We kindly invite you to register and submit your abstract. Deadline for registration and abstract submission is May 18th, 2012. More information on the workshop can be found on our website: http://ieb.uni-muenster.de/protein-evolution-workshop-2012 I would also like to ask for your assistance in forwarding the information to your colleagues who may be interested in joining the meetings.

Do not hesitate to contact me in case you have any further questions.

With kind regards,

Sonja Grath

Dr. Sonja Grath Westfalian Wilhelms University Evolutionary Bioinformatics Institute for Evolution and Biodiversity Huefferstrasse 1, D-48149 Muenster, Germany http://ieb.uni-muenster.de/bioinf/people/Sonja-Grath.html Sonja Grath <s.grath@uni-muenster.de>

Helsinki SpeciationTheory Aug19-26

As the application deadline is getting near, we would like to remind you of

The Helsinki Summer School on Mathematical Ecology and Evolution 2012: THEORY OF SPECIATION

Dear Colleagues,

We are pleased to invite students and young researchers to the summer school Theory of Speciation to be held between 19 and 26 August 2012 in Turku, Finland. The core program of the school consists of five series of lectures,

Sergey Gavrilets: Population genetics of speciation Nick Barton: Multilocus models of speciation Sander van Doorn: The role of sexual selection in speciation Eva Kisdi: The ecology of speciation Daniel Bolnick: Theory and empirical speciation research

All young researchers working in mathematical ecology/evolution can apply from all countries, especially from Europe and the Mediterranean. The school is aimed at PhD students of biology with sufficient theoretical background and at PhD students of mathematics with interest in ecology and evolution, but we also welcome advanced undergraduates and postdocs.

The deadline for applications is 15 April 2012 and there is no fee for registration. The school is financially supported by the ESF network Frontiers of Speciation Research, the Finnish Doctoral Programme in Computational Sciences and the Academy of Finland, and is endorsed by ESMTB and EMS.

For more details and application, see http://wiki.helsinki.fi/display/huippu/mathbio2012 . Eva Kisdi and Tadeas Priklopil

kisdi@mappi.helsinki.fi

Hinxton HumanGenomeAnalysis Jul11-17

Deadline for applications approaching: 5 April 2012 Human Genome Analysis: Genetic Analysis of Multifactorial Diseases 11-17 July 2012 Wellcome Trust Genome Campus, Hinxton, Cambridge

http://www.wellcome.ac.uk/Education-resources/Courses-and-conferences/Advanced-Courses-and-Scientific-Conferences/Advanced-Courses/WTX026851.htm Course summary An intensive, residential, computer-based course aimed at scientists actively involved in genetic analysis of multifactorial traits.

Course organisers * Daniel Weeks (University of Pittsburgh, USA) * Mark Lathrop (Centre National de Genotypage, Evry, France)

Course instructors * Heather Cordell (Institute of Human Genetics, University of Newcastle upon Tyne, UK) * Janet Sinsheimer (University of California, Los Angeles, USA) * Eric Sobel (University of California, Los Angeles, USA) * Joe Terwilliger (Columbia University, New York, USA) * Chad Garner (University of California, Irvine, USA) * Simon Heath (Centre Nacional d'Anàlisi Genòmica (CNAG), Barcelona, Spain)

Guest speakers

Yurii Aulchenko (Independent researcher and consultant) Hakon Hakonarson (Children's Hospital of Philadelphia, USA) Bertram Müller-Myhsok (Max Planck Institute of Psychiatry, Germany) Stephen S. Rich (Univeristy of Virginia, USA) H.-Hilger Ropers (Max Planck Institute of Medical Genetics, Germany)

Feedback from previous years "The course was highly relevant for my current work and I am sure it will shape my next steps in my career."

"I wish to thank the course instructors and the Wellcome trust for providing me the opportunity [to] gain knowledge and share thoughts."

"Thanks a lot for this great course and the great time we have spent here!"

Programme This advanced course covers statistical methods currently used to map disease susceptibility genes, with an emphasis on (but not limited to) methods that can analyse family data or a combination of families and individuals. Discussions of the latest statistical methodology are complemented by practical hands-on computer exercises using state-of-the-art software. The statistical basics behind each method will be carefully explained so that participants with a non-statistical background can understand.

With a focus on family data, we will discuss fundamental issues needed to increase success in gene mapping studies including: optimal study design, power to detect linkage and association, determining the most appropriate statistical methods and software, interpretation of statistical results and trouble shooting. We will also cover the basic principles of statistical inference, hypothesis testing, population and quantitative genetics and Mendelian inheritance. Our interactive and intensive educational program will enable one to better carry out sophisticated statistical analyses of genetic data, and will also improve one's interpretation and understanding of the results. All the software used is freely available, so that skills learned can be easily applied after the course.

JanetS@mednet.ucla.edu

Lima ConservationMarineMammals Jun30-Jul9

The Center for Environmental Sustainability (CSA - Centro para la Sostenibilidad Ambiental) and Universidad Peruana Cayetano Heredias (UPCH) Life Sciences Field School are pleased to announce the course:

*** Ecology & Conservation of Marine Mammals of the Humboldt Upwelling Ecosystem Dates: June 30th - July 9th 2012 Location: Punta San Juan, Peru ***

This is a residential field-based course in Peru on the biology, anatomy, physiology, ecology, evolution, behavior, population biology, management and conservation of marine mammals, explaining why this group is so important, controversial and interesting.

Students will be provided with comprehensive knowledge on marine mammal ecology with special emphasis on species inhabiting the Humboldt Current Upwelling Ecosystem off the coast of Peru a developing country with the largest single species fishery in the world.

This is a university-accredited course and is intended for students in the summer vacation of 2012 and for enthusiastic individuals with keen interest in the marine environment. This course is suitable for M.Sc., undergraduate students in the last 3 years of study and individuals who want to learn from experts about sea lions, fur seals, dolphins, whales, marine otters of the south Pacific Ocean.

For more information, please visit: http://upch-fieldschool.edu.pe/front/-course_information_marine_mammals Or email us at: info@upch-fieldschool.edu.pe

Best regards, Mónica Muelbert, Susana Cárdenas, Patrica Majluf

UPCH's Life Sciences Field School Av. Armendáriz 445 Lima 18, Miraflores Perú

Telephone: +51-1-626-9401

Web: http://upch-fieldschool.edu.pe -

Susana Cárdenas Alayza <scardenasalayza@yahoo.com>

juandiegos@hotmail.com

Montreal PopulationGenomics May28-Jun1 Reminder

Montreal Spring School of Population Genomics and Genetic Epidemiology

May 28 - June 1, 2012

The objective of the School is to provide training in genetic epidemiology, human evolutionary genetics, population genomics and bioinformatics.

The School consists of five days of lectures and computer labs. Days 1 and 2 will cover introductory concepts in human population, medical genomics, and genetic epidemiology. Days 3 to 5 will consist of concurrent sessions in advanced concepts in population genomics/statistical genetics and in genetic epidemiology (see detailed program below).

If you wish to participate in the workshop, please visit our website for instructions and to download the application form. All applications should be submitted no later than Friday, March 23, 2012. Because of a limited number of places, participants will be selected based on their academic and scientific background.

See www.montrealspringschool.ca < http://www.montrealspringschool.ca > for details

Program

Day 1 - May 28th Introductory Concepts in Human Populations and Medical Genomics Instructor: Laurent Excoffier Time: 8:00 - 12:00 Place: Room 1

§Principles of population genetics: This lecture will cover some of the major concepts in human population genetics including random genetic drift and the derivation and properties of the basic coalescence model.

o Random Genetic Drift

Â§The Hardy-Weinberg equilibrium law

Â§The Wright-Fisher Model of random genetic drift

Â§Effective population size

o Gene trees and the basic coalescence model

Â§Coalescence under different demographic scenarios (e.g. population growth)

Introductory Concepts in Genetic Epidemiology Instructors: Alexandre Alcaïs and Hélène Vézina Time: 13:00 - 17:00 Place: Room 1

§We will first briefly introduce concepts and designs to study familial aggregation followed by basic principles of linkage and association analysis for qualitative traits. Topics covered will include designs and analytical methods used to study genetic linkage. Both parametric and non-parametric linkage analysis will be covered.

§Presentation of the concepts will be followed by a computer lab application using real data an durrently availabe software such as MLB.

§Finally, a brief introduction to the BALSAC genealogical resource and presentation of existing tools for their analysis will be presented.

Day 2 - May 29th Introductory Concepts in Human Populations and Medical Genomics Instructors: Luis B. Barreiro and Lluis Quintana-Murci Time: 8:00 - 12:00 Place: Room 1

§Human population genomics: This lecture will introduce the students to the most recent genomic datasets on human genome diversity. We will discuss the contribution of HapMap and the 1000 Genomes Project to the better understanding of human evolution and the development of genome- wide association studies. The following concepts will be presented:

o Mutation and recombination

o Recombination at pedigree level - concept of linkage disequilibrium (LD)

o Measures of LD and its decay

o Tagging SNPs

o Population mutation parameter, population recombination rate

The lab will introduce methods of analyzing data from the HapMap project.

§Demography of human populations: This lecture will introduce the different models to explain human evolution. It will give an overview of the most recent genetic data explaining the human origins and migration patterns. It will concentrate on phylogeographic studies, mostly concerning uniparentally-inherited genomes.

Introductory Concepts in Genetic Epidemiology Instructor: Alexandre Alcaïs Time: 13:00 - 16:15 Place: Room 1

§This lecture will cover designs and analytic methods for genetic association studies. Methods to investigate direct (candidate locus) and indirect (linkage disequilibrium mapping) associations with human disease will be introduced. Both family-based and population-based designs will be presented.

§Presentation of the concepts will be followed by a computer lab application using real data and currently available software such as FBAT.

Invited Lecture Speaker: Ellen Wijsman Time: 16:30 - 18:00 Place: Albert-Royer Auditorium at CHU Sainte-Justine (3175 Côte-Ste-Catherine Road)

Day 3 -May 30th (Concurrent Sessions - lectures and computer labs, except for the first session)

Presentation of current research by a Faculty member in Population Genomics Speaker: Laurent Excoffier Title: The complex making of humans: relationships with archaic hominins Time: 8:00 - 8:40 Place: Room 1

Advanced Concepts in Population Genomics Instructors: Laurent Excoffier, Nicolas Lartillot, and Luis B. Barreiro Time: 8:45 - 17:00 Place: Room 1

§Extension of the coalescence theory: this lecture will cover the following topics:

o Probabilistic modeling in population genetics: principles of

— / —

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mcmaster.ca/˜brian/evoldir.html

Roscoff MarineGenomics Jun4-15

>From June 4th - 15th, 2012 the 8th Summer Course on Marine Evolutionary & Ecological Genomics will take place at the Station Biologique de Roscoff, Roscoff, France.

First announcement

Aims: The course, which consists of lectures, tutorials and computer based exercises, aims to highlight the crucial role of marine genomics for the understanding of the marine environment and for an efficient use of its resources. Advanced PhD students and junior postdocs are encouraged to apply.

The course consists of the following topics. - Phylogeny & tree of life - sequence analyses, phylogenetic techniques (clustering, Bayesian statistics), molecular clock, case studies - Phylogeography - molecular evolution through networks, phylogeographical techniques, coalescence, population dynamics, case studies - Population genetics - structure, connectivity and gene flow, assignment, effective size and population dynamics, case studies - Genomics - next generation sequencing, database searching, basic skills in data handling and bioinformatics - Functional genomics - genome structure, molecular evolution at the functional level - Comparative genomics - whole genome comparisons, concatenated phylogeny, genome organization, annotating genomic information, co-evolution - Environmental genomics - methods for detecting diversity; detecting adaptive variation; NGS: why and how; case studies. Applications in aquaculture, blue biotech, conservation, fisheries, nutrigenomics and the like will be discussed.

Target group PhD students (at least in their second year) and junior post docs with a solid knowledge in phylogenetics and/or population genetics. Students with an applied background (e.g. aquaculture, blue biotech, fisheries, nutrigenomics) are encouraged to apply.

16 participants will be selected on the following criteria: 1. Relevance of the course for their PhD or post-doc project 2. Background and experience 3. We aim at mixing people with different research backgrounds; not more than one person per institute will be considered. We aim at an equal gender distribution.

The selected persons will be notified at the end of April and have to confirm attendance within 7 days. We will have a waiting list in case of non-confirmations and cancellations.

Teachers Sandie Baldauf, U. Uppsala, SE Jonas Collén, U Paris 6, FR Simon Creer, U Bangor, UK Yves Desdevises, U ParisVI, FR Jakob Hemmer-Hansen, DTU-Aqua, DK Jeanine Olsen, U Groningen, NL Frédéric Partensky, SB-Roscoff, FR Filip Volckaert, KU Leuven, BE Mathias Wegner, GEOMAR, Kiel and AWI-Sylt, GE

Organizing committee Jonas Collén, SB-Roscoff, FR Damien Guiffant, SB-Roscoff, FR Matthias Obst, Univ. Gothenburg, SW Jeanine Olsen, Univ Groningen, NL Filip Volckaert, KU Leuven, BE

For information and application please consult http://meeg2012.sciencesconf.org . The application deadline is April 9th 2012.

Filip Volckaert <Filip.Volckaert@bio.kuleuven.be>

SaoPaulo Evolution Aug19-31

Greetings colleagues,

My apologies for cross-posting.

We are pleased to announce the São Paulo School of Advanced Sciences - Evolution (SPSAS-evo) to be held in August 19-31, 2012, in Ilhabela, São Paulo, Brazil. This is the 6th edition of an ambitious initiative by the Fundação de Amparo à Pesquisa do Estado de São Paulo (FAPESP), whose main purpose is to bring together leading experts and outstanding students/post-docs from all over the world in order to advance areas considered strategic for Brazilian science.

SPSAS-evo will be a two-week course centered on a range of topics in Evolutionary Biology taught by a host of world class experts conducting cutting-edge research in Evolution. The main goals are to generate authoritative outreach material focused on Evolution and to showcase ongoing research in São Paulo, aiming at attracting the most promising students, post-docs and young faculty to the state of São

Paulo.

There are 80 spots available, the target applicants are graduate students, but a few spots will be filled by outstanding post-docs and undergraduate students. People from all nationalities and backgrounds conducting research in Evolutionary Biology are encouraged to apply. Applications will be evaluated on a competitive basis and selected applicants will have expenses fully covered by FAPESP (except students who already receive FAPESP funding). Application deadline is April 9th. To apply, follow instructions at:

http://www.ib.usp.br/zoologia/evolution Please direct any questions you may have to evolution@ib.usp.br

Invited Speakers: Michael Alfaro (University of California at Los Angeles), André V. L. Freitas (Universidade Estadual de Campinas), Gonzalo Giribet (Harvard University), Alexander W. A. Kellner (Universidade Federal do Rio de Janeiro), Andrew Knoll (Harvard University), Antonio Carlos Marques (Universidade de São Paulo), Mark Q. Martindale (University of Hawai'i), Nancy Moran (Yale University), Howard Ochman (Yale University), Tiago B. Quental (Universidade de São Paulo), Gregory Rouse (Scripps Institution of Oceanography), Marcello G. Simões (UNESP - Botucatu), Antonio M. Solé-Cava (Universidade Federal do Rio de Janeiro), Günter Wagner (Yale University)

Daniel J. G. Lahr, PhD Post-Doctoral Research Associate, Dept. of Zoology University of Sao Paulo, Brazil

daniel.lahr@gmail.com

Seattle StatGenetics Jul9-27

The 17th Summer Institute in Statistical Genetics will be held in Seattle, July 9-27. Some modules are filling rapidly. Scholarship applications are due on April 13. Details at http://www.biostat.washington.edu/SISG/ Some of the SISG courses (Genomic Prediction, Genetics of Competition, Advanced R for Genetic Analysis, Population Genetic Data Analysis, Gene Expression Profiling, Mixed Models in Quantitative Genetics, MCMC for Genetics, Plant and Animal Association Mapping, Inference of Relationships and Relstedness) will be offered in Edinburgh, before and after the 4th International Conference on Quantitative Genetics, June 13-15, 25-29. Details at http://www.icqg4.org.uk/EISG/

Bruce Weir

Bruce Weir <bsweir@u.washington.edu>

Smithsonian ConsGeneticTechniques May19-25

Limited number of spots still available. Application deadline has been extended

Graduate and Professional Course Non-Invasive Genetic Techniques in Wildlife Conservation May 19-25, 2012 Smithsonian-Mason School of Conservation At the Smithsonian Conservation Biology Institute, Front Royal, VA, USA Visit http://conservationtraining.si.edu or contact SCBItraining@si.edu for more information.

This course is an introduction for graduate students and professionals to the applications, benefits, and drawbacks of non-invasive genetic techniques to wildlife conservation. The course will concentrate on the use of non-invasive techniques to answer questions in animal behavior, population biology, and population management, with a particular focus on the conservation of mammalian populations. Participants gain hands-on experience relating to all stages of a research project utilizing modern non-invasive methods by working with expert researchers through a combination of field, laboratory and computer-based modules.

Throughout the course participants work through directed research projects, progressing from study design through field data collection, sampling protocols, and DNA extraction and amplification, to analysis of microsatellite and sequence data using the most effective and accessible software packages. The course focuses on relatedness, population size estimation and population dynamics; additional lectures address genotype reliability, research applications for ancient DNA, and applications of next-generation pyrosequencing.

Many of these groundbreaking non-invasive genetic techniques were initially developed at the Smithsonian's National Zoo and its Center for Conservation and Evolutionary Genetics (CCEG). Course instructors include scientists from CCEG (Drs. Jesus Maldonado and Rob Fleischer) and George Mason University (Dr. Christine Bozarth) and several expert visiting instructors including Drs. Mike Schwartz, Elizabeth Archie, and Lori Eggert. While most instruction takes place in Front Royal, the course also includes laboratory work at the National Zoo's new state-of-the-art genetics lab in Washington, DC.

The course fee is $1,500, which includes instruction and course materials as well as all meals, lodging, and transport to/from Washington-Dulles International Airport (IAD). All other travel costs and incidental expenses are the participant's responsibility. Participants earn Continuing Education Units; graduate course credit (1) is available for qualified applicants through George Mason University (total fee: $1600 in-state (VA), $1850 out-of-state). Participants should have previously completed a college-level genetics and basic ecology/evolution course.

Additional Upcoming Courses:

For more information on each of these, see: http://conservationtraining.si.edu * Species Monitoring & Conservation: Amphibians (March 26- April 6, 2012)

* Species Monitoring & Conservation: Terrestrial Mammals (April 16-27, 2012)

* Adaptive Management for Conservation Success (June 11-22, 2012)

* Applied Climate Change (October 15-26, 2012)

* Spatial Ecology, Geospatial Analysis, and Remote Sensing for Conservation (October 29-November 9, 2012)

* Effective Conservation Leadership (November 4-10, 2012)

Joe Kolowski, Ph.D.| Graduate and Professional Training Manager Smithsonian Conservation Biology Institute Center for Conservation Education and Sustainability National Zoological Park 1500 Remount Road, Front Royal, VA 22630 T 540.635.0205| F 540.635.6506| Email kolowskij@si.edu

"Kolowski, Joseph" <kolowskij@si.edu>

Switzerland BioinformaticsPopGenomics Jun17-22

*** Announcement ***

The SIB and the Doctoral Program in Population Genomics will be organising a Joint Summer School in June 17-22, 2012 in Adelboden, a small and charming village in the Swiss Alps.

Further information and registration can be found at:

http://www.isb-sib.ch/education/sib-phd-training-network/phd-summer-school-2012.html

Applications are open until April 17, but can be closed earlier according to the level of demand.

For the organisers,

Patricia M. Palagi, Ph.D. Swiss Institute of Bioinformatics CMU, 1 Michel-Servet CH-1211 Geneva 4 - Switzerland

Tel.: (+41 22) 379 5831 Email: Patricia.Palagi@isb-sib.ch Fax.: (+41 22) 379 5858 http://www.isb-sib.ch/education Patricia Palagi <Patricia.Palagi@isb-sib.ch>

Tubingen MoralityEvolution Jun12-16 2

As the application deadline is getting near, we would like to remind you of

International Interdisciplinary Summer School with Frans de Waal (Emory University in Atlanta, USA.

"The Evolution of Morality"

Tuebingen, June 12th - 16th

It is a well known saying that "nothing in Biology makes sense except in the light of evolution" (Dobzhansky). Thus, what kind of new perspectives and implications can be drawn from insights of the theory of evolution for the understanding of the morality of human beings?

Therefore, this year's Unseld summer school will focus on the evolutionary fundaments of morality presenting as lecturer the primatologist Frans de Waal. De Waal brings forward the argument that the core concept of morality has already been present in the pre-social tendencies of nonhuman primates. As a consequence he attacks what he calls the "Veneer Theory", which holds that human ethics and morality - established as a cultural innovation - would only be a thin crust masking our Hobbesian brutish nature.

We are looking forward to reaching all prospective participants of a wide range of scientific disciplines and fields of specialization.

The deadline for applications Application procedure is March 30th.

There is no program fee. The Forum Scientiarum seeks to facilitate the participation of competent students from all over the world - limited financial resources should not affect your decision to apply. We therefore provide participants grants for covering part of their travel expenses, awarded by the Udo Keller Foundation Forum Humanum. Also, the Forum Scientiarum will assist participants finding inexpensive accommodation.

Thank you in advance and best regards Yanti Hölzchen and Michael Herrmann

Michael Herrmann <michael.herrmann@fsci.uni-tuebingen.de>

UNewSouthWales ShapeAnalysis Sep3-7

WORKSHOP IN VIRTUAL RECONSTRUCTION, SHAPE ANALYSIS & BIOMECHANICAL MODELLING

Computer-based Virtual Reconstruction, Biomechanical Modelling and Shape Analysis are powerful, fast developing tools for the analysis of form & function in evolutionary biology, paleontology, physical anthropology and biomedicine. The Computational Biomechanics Research Group (CBRG) based at UNSW and Univ. Newcastle (Australia) is at the forefront of these fields.

Current team members working on projects ranging from Virtual Reconstruction and modelling of extinct hominids and giant bears to the development of improved surgical techniques and vertebral disc and ankle bone prosthetics.

This year the CBRG is running a workshop in the application of Finite Element Analysis, Shape Analysis and Virtual Reconstruction at the University of New South Wales - September 3rd to 7th 2012.

Attendees will be given a solid grounding in the skills required to assemble and analyse 3D mechanical models from serial x-ray (CT or microCT) data of biological specimens. The very latest approaches to model generation and analysis for use in form-function studies will be covered.

CT data is available for a wide range of taxa V including fossil species such as the Haarsts eagle of New Zealand, South American glyptodonts, giant short-faced kangaroos and extinct members of the human family tree, as well as a wide range of living vertebrate species.

Where possible attendees are encouraged to bring their own CT data or nominate the species or taxa of interest to them so that we can help them generate and analyse their models.

The workshop is structured to accommodate biologists, paleontologists and physical anthropologists with no formal background in engineering; or engineers with no formal training in biosciences.

We aim to get people up and running on their own projects. We will maintain assistance beyond the workshop to bring projects to completion.

The workshop will be run by Stephen Wroe (Senior Research Fellow, UNSW), Prof. Philip Clausen, (Head of Discipline, Mechanical Engineering, Univ. of Newcastle) and Dr William Parr (Endeavour Fellow, UNSW). Technical experts from the two primary software companies involved (Materialise and Strand7) will offer further assistance, as will other members of the CBRG team, including postgraduate students.

Guest lectures will also be presented by experts in related areas including Computational Fluid Dynamics and Occlusal Fingerprint Analysis.

The workshop is free for postgraduates and undergraduates. A nominal fee of AUD $200.00 will be charged for professionals. The number of places available is limited.

Please contact Stephen Wroe for further details: s.wroe@unsw.edu.au

Publications and examples of models and methods generated/applied by the CBRG are available at: http://compbiomechblog.blogspot.com.au/ Dr Stephen Wroe Director - Computational Biomechanics Research Group School of Biological Earth & Environmental Sciences, UNSW Conjoint Associate Professor School of Engineering, University of Newcastle

Webpages: http://compbiomechblog.blogspot.com/ http://www.compbiomech.com http://unsw.academia.edu/StephenWroe http://www.bees.unsw.edu.au/staff/stephen-wroe School of Biological, Earth and Environmental Sciences University of New South Wales, Kensington, NSW, 2052 Email: s.wroe@unsw.edu.au Ph: 61 2 9385 3866; 61 2 4969 3006 Mobile 04323 49049

Stephen Wroe <s.wroe@unsw.edu.au>

Yunnan China Biodiversity

Workshop on Tropical Biodiversity and Genomics *Time and Venue* June 4-7 2012 Xishuangbanna Tropical Botanical Garden Menglun, Yunnan, China

This small workshop will be organized in two sessions: a series of lectures and discussions with all participants, followed by two days of focused analysis of participant data. The Ecological Evolution group at XTBG has whole genome Illumina sequence data from numerous species of tropical tree, primarily in the genus *Ficus *(figs) and the family Fagaceae (oaks, stone oaks, chestnuts and beeches) and has several analyses and collaborations in progress. The group has primarily been developing reference-free analyses of this data from comparative and phylogenetic purposes. The following participants have been confirmed:

Confirmed participants and their expertise Chuck CANNON, XTBG and Texas Tech University - Reference-free analytical approaches - Tropical biodiversity and forests Graham STONE, Edinburgh - gall wasps - transcriptomics RUAN Jue, Beijing Institute of Genomics - *de novo* analysis of next-gen data SHI Su-Hua, San Yat Sen University, Guangzhou - comparative genomics of mangrove species WU Chung-I, Beijing Institute of Genomics, Beijing - population genetics and diversification Yann SURGET-GROBA, University of California, Santa Cruz and XTBG - transcriptomes and biodiversity YU Jun, Beijing Institute of Genomics - biotechnology and next-gen sequencing

Registration At the moment, we can still accept 4-5 additional participants but you must contact us before April 21st, 2011, when the participant list will be finalized. Please contact Chai-Shian KUA (*kuacs@xtbg.ac.cn*) or Chuck CANNON (*chuck@ <chuck.cannon@gmail.com>xtbg.ac.cn*) to register.

Fees, due upon arrival 950 RMB for scientists from China and 550 USD for foreign scientists 500 RMB for students from China and 250 USD for foreign students

Accommodation: 200 RMB per night at the XTBG garden hotel. Other accommodation options are also available around XTBG

Field Trip : 200 RMB

Visit our website for more details, including a draft agenda and research topics: www.ecologicalevolution.org/training chuck.cannon@gmail.com

Instructions

Instructions: To be added to the EvolDir mailing list please send an email message to Golding@McMaster.CA. At this time provide a binary six letter code that determines which messages will be mailed to you. These are listed in the same order as presented here — Conferences; Graduate Student Positions; Jobs; Other; Post-doctoral positions; WorkshopsCourses. For example to receive the listings that concern conferences and post-doctoral positions this would be 100010. Messages are categorized on the basis of their subject headings. If this subject heading is not successfully parsed, the message will be sent to me at Golding@McMaster.CA. In addition, if it originates from 'blackballed' addresses it will be sent to me at Golding@McMaster.CA. These messages will only be read and dealt with when I have time. The code 000000 has all channels turned off and hence gets only a once monthly notifcation of the availability of a monthly review pdf file.

To be removed from the EvolDir mailing list please send an email message to Golding@McMaster.CA. Note that 'on vacation', etc, style messages are automatically filtered and should not be transmitted to the list (I hope), but should you wish to avoid the e-mail's your code can be temporarily changed to 000000.

To send messages to the EvolDir direct them to the email evoldir@evol.biology.McMaster.CA. Do not include encoded attachments and do not send it as Word files, as HTML files, as LaTeX files, Excel files, etc. . . . plain old ASCII will work great and can be read by everyone. Add a subject header that contains the correct category "Conference:, Graduate position:, Job:, Other:, Postdoc:, Workshop:" and then the message stands a better chance of being correctly parsed. Note that the colon is mandatory.

The message will be stored until the middle of the night (local time). At a predetermined time, the collected messages will be captured and then processed by programs and filters. If the message is caught by one of the filters (e.g. a subject header is not correctly formated) the message will be send to me at Golding@McMaster.CA and processed later. In either case, please do not expect an instant response.

Afterword

This program is an attempt to automatically process a broad variety of e-mail messages. Most preformating is collapsed to save space. At the current time, many features may be incorrectly handled and some email messages may be positively mauled. Although this is being produced by LaTeX do not try to embed LaTeX or TeX in your message (or other formats) since my program will strip these from the message.