EvolDir

July 1, 2013

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

Barcelona Systematics Sep25-27

Dear Friends and Colleagues:

You are kindly invited to attend the II Iberian Congress of Biological Systematics - CISA 2013 that will take place in Barcelona from September 25-27, 2013.

CISA2013 aims to provide an arena for presenting leading research in biosystematics, to encourage participation of young researchers and to stir up fruitful discussion in the field.

Registration and abstract submission is now open. Please, visit our website at http://www.CISA2013.org for registration and further information on the program, invited speakers, social events, fees and deadlines.

The CISA2013 Organizing Committee

j.gomez-zurita@ibe.upf-csic.es

Barcelona Systematics Sep25-27 Registration

Dear colleagues,

This is a friendly reminder that theREGISTRATIONandABSTRACT SUBMISSIONfor the/II IBERIAN CONGRESS OF BIOLOGICAL SYSTEMATICS - /CISA'2013will close in one week, on June 30th, 2013. We would also like to remind you that registration is limited to 150 participants and that registration and contributions will be accepted on first-come, first-served basis.

To register, pleasevisithttp://www.CISA2013.org[1] . Best regards, The Organizing Committee

Links:

[1] http://www.cisa2013.or[29 ˜ g/ “JESUS.GOMEZ-ZURITA.FRAU.592917” <j.gomez-zurita@ibe.upf-csic.es>

Cambridge HumanOrigins Jul5

Registration is now open for the conference

RELOCATING HUMAN ORIGINS - WHAT IF ADAM LIVED IN THE FOREST?

Homepage:

http://relocatingorigin.soc.srcf.net/ Registration:

http://relocatingorigin.soc.srcf.net/?page_id- Please note that the deadline for the call for papers has been extended till Sunday June 23rd.

CALL FOR PAPERS - RELOCATING HUMAN ORIGINS - WHAT IF ADAM LIVED IN THE FOREST?

LOCATION: University of Cambridge ORGANIZERS: Doctoral Students, Division of Biological Anthropology DATE: July 5, 2013

NOW ACCEPTING ABSTRACTS FOR: “ 15 Minute Oral Presentations Live at Conference Remotely Webcast Pre-Recorded and Archived on Conference Website ” Posters

THEME: Conventional scientific wisdom holds that modern humans evolved in the East African savannah. But what if the cradle of human evolution was actually the Central African forest, as hinted by new Y-chromosome results? How might this change our understanding of human evolution? This conference explores the implications of a forest origin for human population genetics, disease ecology, social systems, and cultural evolution.

KEYNOTE SPEAKERS: Prof Mark Thomas, University College London: Genetics of Forest Ancestry Dr Corey Fincher, University of Glasgow: Origins of cultural and biological diversity Dr Tom Currie, University College London: Habitat Productivity & Ethnolinguistic Diversity Dr Peter Walsh, University of Cambridge: Disease, Social Complexity & Innovation

Can’t make it to Cambridge? The entire conference will be webcast.

PLEASE SEND YOUR ABSTRACTS TILL 23/06/2013 TO:

bioanth-conference2013-abstracts@lists.cam.ac.uk

“C.E. Inchley” <cei23@cam.ac.uk>

Canberra Biogeography Jan7-10 CallAbstracts

CALL FOR ABSTRACTS

Abstract submission is now open for the 2014 INTERNATIONAL BIOGEOGRAPHY SOCIETY EARLY CAREER CONFERENCE, organised jointly by the International Biogeography Society (IBS) (http://www.biogeography.org/), the ANU Centre for Macroevolution and Macroecology (http://macroevoeco.com/) and the ANU-CSIRO Centre for Biodiversity Analysis (http://cba.anu.edu.au/).

The conference will take place in Canberra, ACT, Australia between the 7thand the 10 th of January 2014, and aims to bring together early career researchers, along with more experienced scientists, working on many aspects of biogeography.

ABSTRACT SUBMISSION DEADLINE IS JULY 30

To submit your abstract, please visit:

http://www.biogeography.org/html/Meetings/2014ECC/index.html CONFIRMED KEYNOTE SPEAKERS:

Prof Craig Moritz (ANU)

Dr Simon Ferrier (CSIRO)

Dr Michael Kearney (UniMelb)

For more information about the conference, please visit the conference website.

Student participation will be supported by awards offered by the IBS. To apply for a student award, please follow the instructions given on the website.

We look forward to welcoming you to Canberra in January 2014!

The ANU Organising Committee

Haris Saslis-Lagoudakis

Peter Cowman

Dan Warren

Dan Rosauer

Marcel Cardillo

Renee Catullo

ibsconference2014@gmail.com

@ibs2014

The local organising committee, IBS Early Career Conference 2014 @ibs2014

IBS Early Career Conference 2014 <ibsconference2014@gmail.com>

Chicago SMBE2013 Jul7-11 OnSiteChildcareSpecialOffer

SMBE on-site Childcare

2013 Annual Meeting of the Society for Molecular and Evolution

July 7-11, Chicago, USA

We are offering a special offer of half rate for the next 10 children to be registered.

Half rate per child, per session are:

US$ 15 Faculty US$ 12 Grad students and Post-docs

Childcare will be available from 8:00AM - 6:30 PM at the conference venue (Hyatt Regency Chicago), divided into morning and afternoon sessions, on July 8-11. Licensed childcare workers will provide fun activities for kids in a safe, caring environment.

Detailed information about rates and payments can be found on:

http://smbe2013.org/2013/Registration/Childcare-Information.aspx Space is limited, so register you child soon!

Questions about childcare and payment can be directed to cornellacademy4kids@gmail.com (please put 'SMBE 2013' in the subject line)

We look forward to meeting you and your children.

Maria D. Vibranovski Assistant Professor Department of Genetics and Evolutionary Biology University of São Paulo Rua do Matão 27, Cidade Universitária São Paulo, SP, 05508-090 Brazil

Phone : +55 (11) 3091-0952 e-mail : mdv@ib.usp.br

mdv@ib.usp.br

DalhousieU Endocytobiology Aug18-22 3

12th International Colloquium on Endocytobiology and Symbiosis

August 18th - 22nd, 2013 Dalhousie University, Halifax, Nova Scotia, CANADA

FIFTH CIRCULAR (13 June 2013)

Dear Colleagues,

There is still time to register for the 12th International Colloquium on Endocytobiology and Symbiosis of the International Society of Endocytobiology (ISE), which will be held August 18th to 22nd 2013 at Dalhousie University in Halifax, Nova Scotia, Canada.

There will be registration and an opening reception the evening of Sunday August 18. Talks will begin the morning of August 19th.

CONFERENCE WEBSITE

http://ices2013.biochem.dal.ca The colloquium will cover the latest research on all aspects of endosymbiosis and the biology of endosymbiotically-derived organelles. We look forward to seeing you in Halifax!

Best regards, John Archibald

John Archibald <jmarchib@Dal.Ca>

Fiji ONLINE BarcodingBiodiversity Jul8-12 2

The Consortium for the Barcode of Life (CBOL < http://www.barcodeoflife.org/content/about/what-cbol >) at the Smithsonian Institution and CSIRO < http://www.csiro.au/ > in Canberra, Australia, are the co-organizers of a full-day symposium/workshop on “Connecting Biodiversity Collections in the Pacific: Digitization through DNA Barcoding and Informatics”. The event will take place during the 12th Pacific Science Association Inter-Congress < http://www.psi2013.usp.ac.fj/ >, Suva, Fiji 8-12 July 2013.

To make the event as accessible as possible, it will be webcast as a GoToWebinar. Registrants will see and hear all presentations and discussions and will be able to pose questions to the presenters. The sessions are:

* Collection digitization, chaired by Beth Mantle, CSIRO: Wednesday afternoon from 14:20 to 17:30 (Fiji time, GMT +12 hours)

* DNA barcoding, chaired by David Schindel, CBOL, Smithsonian Institution: Thursday morning from 11:00-12:20 (Fiji time)

Information on the symposium/workshop and the webinar registration form can be found at http://connect.barcodeoflife.net/events/psa12 . Barcode of Wildlife Project now on Google+ < https://plus.google.com/u/0/b/107778383819228315340/107778383819228315340/posts/p/pub >

"Schindel, David" <schindeld@si.edu>

Fredericton VolvoxEvolution Jul31-Aug3 DeadlineExtended

The 2nd International Volvox Conference

EARLY REGISTRATION AND ABSTRACT SUBMISSION DEADLINE EXTENDED TO JUNE 15TH

Please join us for the 2nd International Volvox Conference (focused on the green alga Volvox and its close relatives) to be held July 31 V August 3, 2013, in Fredericton (New Brunswick, Canada). This is the second of what we hope to be a long series of Volvox meetings to be held every other year, alternating with the Chlamydomonas meetings. The first meeting, in 2011, was a great success (www.unbf.ca/vip/IVC/). Volvocine algae have become an important model system for the evolution of multicellularity, development and cellular differentiation, and lately have yielded important results in fields as diverse as genomics, hydrodynamics, and social evolution. We hope that the meeting will continue to foster exchange of ideas and expertise and will initiate new collaborations. We also wish to attract new people and to build a stronger Volvox community. The meeting (through contributed papers and posters) will highlight various aspects of the biology, taxonomy, ecology, development, genetics/genomics and evolution of Volvox and its relatives. For additional information and updates please visit the Conference page at http://www.unbf.ca/vip/IVC2013).

Aurora M. Nedelcu University of New Brunswick Department of Biology PO Box 4400 Fredericton, NB Canada E3B 5A3 phone: (506) 458-7463

Aurora Nedelcu <anedelcu@unb.ca>

Halifax PlantGenomics Aug12-15

The 9th Canadian Plant Genomics Workshop will be held August 12-15, 2013 in Halifax, Nova Scotia. Early bird registration rates are available until June 21st. We have a great line up of speakers, including:

Ed Buckler - Cornell University, USA Olivier Voinnet - ETH, Zurich, Switzerland Harry Klee - University of Florida, USA Ann Osbourn - John Innes Centre, UK John McKay, Laval University, Canada Robin Buell, Michigan State, USA Tim Sharbel, IPK Gatersleben, Germany Jeffrey Ross-Ibarra, UC Davis, USA

Register now at www.cpgw2013.org We hope to see you in Halifax this summer.

Sean Myles Lead Organizer Canadian Plant Genomics Workshop 2013 Canada Research Chair in Agricultural Genetic Diversity Dalhousie University www.cpgw2013.org sean.michael.myles@gmail.com

Heraklion MediterraneanMarineBiodiversity Oct7-9

Conference:"Mediterranean marine biodiversity in view of climate change and the invasion of alien species"

Heraklion, Crete, Greece

7^th to 9^th of October, 2013

The Institute of Marine Biology, Biotechnology and Aquaculture (*IMBBC*) of the Hellenic Centre for Marine Research (*HCMR*) announces the conference on *"/Mediterranean marine biodiversity in view of climate change and the invasion of alien species/"*to be held in the premises of "/Thalassocosmos/", Heraklion, Crete, Greece, from 7^th to 9^th October 2013. The conference will be organized in the context of the EU (FP7-REGPOT-2010-1) project "/Supporting Research Potential for Marine Biodiversity and Genomics in the Eastern Mediterranean/" (MARBIGEN, http://www.marbigen.org/).

The conference aims to bring together researchers of different fields in order to promote the multidisciplinary and integrated research regarding the response of biodiversity to the climatic change and the impact of the invasion of alien species in the Mediterranean and adjacent regions.

The European Commissioner for Maritime Affairs and Fisheries *Mrs. Maria Damanaki* will honor us giving the opening speech of the conference.

The tentative list of distinguished invited speakers who will give keynote lectures includes:

Dr. Alberto Garcia, Spanish Institute of Oceanography (IEO), Málaga Oceanographic Center, Spain

Professor Daniel Golani, Department of Evolution, Systematics and Ecology, The Hebrew University of Jerusalem, Israel

Professor Stephen Palumbi, Department of Biological Sciences, Stanford University, Director, Hopkins Marine Station, Stanford University, USA

Associate Professor Vassilis Zervakis, Department of Marine Sciences, University of the Aegean, Greece

Further information on registration, abstract submissions for oral and poster presentations and important dates will be announced soon.

We look forward to welcoming you in Heraklion, Crete for a scientifically stimulating and socially enjoyable meeting.

With best regards,

On behalf of the Organizing Committee

Dr. Antonios Magoulas

MARBIGEN Co-ordinator

Dr. Antoniou Aglaia (Cilia) Institute of Marine Biology and Genetics (IMBG) Hellenic Centre for Marine Research (HCMR) Gournes Pediados, P.O.Box 2214, 71003, Iraklio, Crete, Greece Tel.: +30 2810 337826 Fax: +30 2810 337820

Cilia Antoniou <antoniou@hcmr.gr>

Innsbruck Austria Wolbachia Jun6-11

Dear Wolbachia community,

One year and two days to go to the 8th International Wolbachia Conference which will be held from 6 to 11 June 2014 in Innsbruck, Austria.

Topics will include, inter alia, - ecology, evolution and development - phenotypes, diversity and distribution - cell biology - genetics & genomics - applications in pest control and disease management - other reproductive parasites than Wolbachia.

We are happy to announce that the conference website is now online: http://wolbachia2014.org Please also consider subscribing to our newsletter to be constantly informed about important news on the meeting: http://wolbachia2014.org/nl.php Looking forward to seeing you in Innsbruck next year, Wolfgang Arthofer in behalf of the WOLBACHIA 2014 Organising Committee

P. S.: Please apologize if you receive multiple copies of this mail. All further WOLBACHIA 2014 updates will be sent via the newsletter!

–

Dr. Wolfgang Arthofer

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

Tel +43 (0) 512 / 507 - 51751 Fax +43 (0) 512 / 507 - 6190 Mob +43 (0) 680 / 551 2814 wolfgang.arthofer@uibk.ac.at

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http://www.uibk.ac.at/ecology/forschung/molecular_ecology.html.en wolfgang.arthofer@uibk.ac.at

Ithaca AGA2013 Jul20-22 SpeciationContinuum

The AGA meeting is less than a month away. Did you know that, in addition to awesome speakers and a beautiful location, the very low registration fee includes a year's membership in AGA? That means receiving the Journal, having access to the +100 year archive, and being eligible to compete for generous awards. Plus, registration includes lunch! And there is very nice, inexpensive, on-campus housing. Students, this is an opportunity to meet your heroes at a small meeting where they will actually have time to engage with you.

Details and registration at: http://www.theaga.org/ Anjanette Baker Managing Editor Journal of Heredity agajoh@oregonstate.edu

AGAJOH@oregonstate.edu

Kuching Malaysia InsectEvolution Nov8-12

The next " Global conference of entomology" will take place from 8-12 November, 2013, at Kuching, Sarawak, Malaysia. The information is available on http://www.gce2013.com/ Theme: $B!H(BInsects and Humanity in the 21st Century$B!I(B

Technical Sessions:

Insect taxonomy and systematics including geography Insect ecology-population dynamics, climate change Insect toxicology: insecticide efficacy and resistance Insect behaviour and physiology Insect Molecular Genetics, Molecular biology and biotechnology Insect Biochemistry and physiology Insect Pathology and biological control Insects as vectors of crop diseases Public health, medical and veterinary entomology Forest entomology Useful and beneficial insects-sericulture, apiculture, resin culture Insects as bioresources-food, nutraceuticals, medicine and environmental health markers Acarology Insect Quarantine and SPS issues Insect pest management Biotechnological/Innovative Approaches in insect pest management. Deadline for abstract submission: June 30th 2013

Many thanks

Thierry Hance Member of the GCE2013 International organizing Committee

Earth and life Institute Biodiversity research Center UCL-17.07.04 Croix du Sud, 4-5 b-1348 Louvain-la-Neuve Belgium Phone # 32 10 47 34 93 Fax # 32 10 47 34 90 Thierry.Hance@uclouvain.be

Thierry Hance <Thierry.Hance@uclouvain.be>

Lausanne QuestForOrthologs3 Jul24-26

Dear colleagues,

We invite applications to the third Quest for Orthologs meeting, in Lausanne, Switzerland, July 24-26.

The QfO is an international scientific meeting that covers all aspects of orthology prediction, benchmarking, and application.

Further details at http://edu.isb-sib.ch/course/view.php?id=3D144 Marc

Marc Robinson-Rechavi Department of Ecology and Evolution Biophore 3219, University of Lausanne, 1015 Lausanne, Switzerland tel: +41 21 692 4220 fax: +41 21 692 4165 http://bioinfo.unil.ch/ Twitter: @marc_rr

Swiss Institute of Bioinformatics http://www.isb-sib.ch/groups/lausanne/eb-robinson-rechavi.html La liberte ne s'use que quand on ne s'en sert pas

Marc.Robinson-Rechavi@unil.ch

Lillehammer Norway AnimalGeneticResources Jan27-29

'Dear all,

We are pleased to announce that a conference on *"Genetic Resources for Food and Agriculture in a Changing Climate" *will take place at Lillehammer, Norway, 27^th – 29^th of January 2014.

The main aims of the conference are to:

* contribute to an understanding of climate change and its predicted impact on agriculture and forestry * increase our understanding of adaptive genetic diversity and adaptation * assess how genetic resources for food and agriculture are affected by the changing climate * discuss the consequences that climate change challenges bring upon the sustainable utilization of plant, animal and forest genetic resources

The conference aims at bringing together participants from all areas relevant to genetic resources for food and agriculture in a changing climate. The conference will focus on the scientific frontiers in this area as well as create a possibility for discussions from the political point of view.

The conference is organized by the Nordic Genetic Resource Center (NordGen, http://www.nordgen.org/index.php/en/content/view/full/2/) and four research networks under a program entitled "Climate ChangeImpacts, Adaptation and Mitigation in Nordic

Primary Industries" financed by the Nordic Council of Ministers and NordForsk. The results of three years network activity of the four networks will be presented during the conference.

The meeting is directed towards scientists, students, national genetic resource coordinators, breeding association representatives, government officials and other stakeholders with special interest in genetic resources for food and agriculture in a changing climate.

Please, follow the link below to the conference homepages for the preliminary scientific program, call for abstracts, and registration and practical information.

https://sites.google.com/a/nordgen.org/agricultural-genetic-resources-in-changing-climate/home Feel free to distribute this invitation amongst your colleagues and other institutions.

Best regards,

Anne Præbel'

Torsten Nygaard Kristensen <torsten.nygaard@nordgen.org>

Lyon ComparativeGenomics Oct17-19

Eleventh Annual RECOMB Satellite Workshop on Comparative Genomics

October 17-19, 2013, Lyon, France

Website: http://rcg2013.sciencesconf.org/ Contributions to the workshop are welcomed on any theoretical and/or empirical approach to genome-wide comparison. This includes genome evolution, algorithms for genome rearrangement, comparative tools for assembly, gene identification or annotation, comparison of functional networks, genomic variation in humans and model organisms, cancer genomics, duplication patterns of genes, segments and whole genomes, and comparative epigenetics. We encourage paper submissions that offer new biological findings or otherwise highlight their relevance to biology. Refereed papers will be published as open-access manuscripts in the journal BMC Bioinformatics.

KEY DATES

Paper submission deadline June 21, 2013

Acceptance notification July 19, 2013

Workshop October 17-19, 2013 - Lyon, France

CONFIRMED KEYNOTE SPEAKERS

- Tal Dagan, Heinrich Heine Universität, Dusseldorf

- France Denoeud, Genoscope CEA, France

- Laurent Duret, Laboratoire de Biométrie et Biologie Ãvolutive, Lyon

- Nicolas Galtier, Institut des Sciences d'Evolution de Montpellier

- Ludovic Orlando, Centre for GeoGenetics, Natural History Museum of Denmark

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THEME AND SCOPE

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

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

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

Specific topics of interest include but are not limited to:

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

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CALL FOR PAPERS

Papers should be submitted via the EasyChair system:

Submissions must be received in electronic form by 11:59pm (Samoa time), June 21th, 2013.

https://www.easychair.org/conferences/?conf=recombcg2013 Papers submitted for review should represent original, previously unpublished work. At the time the paper is submitted to the conference, and for the entire review period, the paper should not be under review by any other conference or scientific journal.

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

Authors are encouraged to use the BMC document templates when preparing manuscripts. Templates are available in Microsoft and LaTeX formats. Otherwise, submissions should be typeset as double-spaced A4 pages with at least 1-inch margins all around in a minimum of 10 point font. Submissions should be limited to 16 pages, everything included (title, authors, addresses, abstract, references, figures, tables). Exceptions to this limit may be granted by consultation with the Program Committee Chairs. Submissions must include the corresponding author's email address.

When preparing your submission please follow the instructions for authors of BMC supplements: http://www.uff.br/recombcg/docs/Instructions-for-authors-BMC-Appendix-B.pdf . Submitted manuscripts must be rendered to PDF format prior to upload into EasyChair at the review stage.

Address any questions to the program committee chairs: Macha Nikolski macha (at) labri (dot) fr

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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

Madison Wisconsin SwitchgrassEvolution Sep10-12

Announcing SWITCHGRASS II, taking place in Madison, Wisconsin, USA, September 10-12 2013 at the Monona Terrace Convention Center. Registration, housing, and abstract submission information available at the following website: www.dfrc.wisc.edu/switchgrass . The conference will bring together scientists and students interested in switchgrass and other prairie grasses to discuss the state of the art of prairie grass research. It will be an excellent opportunity to meet and interact with researchers from a wide range of disciplines, including agronomy, physiology, ecology, soil science, pathology, entomology, genetics, genomics, and molecular biology. The conference will include a field tour, several plenary presentations, selected volunteered oral presentations, a poster session, and a community workshop.

Program Highlights:

All-day tour of prairie/savanna and bioenergy research. Eight topical areas, each with one invited speaker. One-day poster session, organized according to the eight topical areas.

A small group of abstracts from each topical area will be chosen, with the author's permission, for oral presentations. The committee will make this decision before the conference, so that authors have time to plan for an oral presentation.

Abstract submission deadline: 11:59pm Friday 16 August (Central Daylight Time USA)

Registration deadline: 1 September

For more information contact mdcasler@wisc.edu or jaraasch@tds.net.

John.Raasch@ARS.USDA.GOV

Marseilles 17thEvolBiol Sep17-20 Deadline2

Dear all

the dead line for the abstract submissions for the 17th EBM is june 30 We have also an latter dead line but based on the previous years no more spot available for oral presentations The program will be available the first week of July more info http://sites.univ-provence.fr/evol-cgr/ all the best

Pierre

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

Oslo 2013Galaxy Jun30-Jul2 2

This is the final registration reminder for the 2013 Galaxy Community Conference (GCC2013, http://galaxyproject.org/GCC2013), being held in Oslo, 30 June through July 2. GCC2013 is a great opportunity to share best practices and network with other researchers who are also facing the challenges of data-intensive biology.

Registration closes June 14. Register now and guarantee your spot in the Training Day sessions you want to take. Registration is still a bargain with the full 3-day registration starting at ˜ â¬165*forpost* − *docsandstudents*(*orjust*â¬55*perday*).

The program features

15 Training Day sessions in 5 tracks on 12 different topics, 25 Talks on topics ranging from Reproducibility to Exploiting Galaxy, 23 Posters (and counting), 2 Lightning Talk sessions, and a end-of-conference event at an historic venue high above Oslo.

Ser frem til Ã se deg i Oslo!

The GCC2013 Organizing Committee

– http://galaxyproject.org/GCC2013 http://galaxyproject.org/ http://getgalaxy.org/ http://usegalaxy.org/ http://wiki.galaxyproject.org/ Dave Clements <clements@galaxyproject.org>

Paris IMMEM-10 MicrobeEvolution Oct2-5 AbstractDeadline

IMMEM-10 conference: only a few days left to submit your abstract and for early registration fee

Dear Colleague,

We remind you that June 30th, 2013 will be the deadline for abstract submission and early registration fee at IMMEM-10, the 10th edition of the International Meeting on Microbial Epidemiological Markers (Paris, October 2 - 5, 2013).

A total of 33 abstracts will be selected for oral presentation. Please refer to the scientific programme for latest sessions and topics, available through the conference web site at http://www.immem-10.org . More than 250 abstracts have been submitted already. IMMEM-10 promises to be a very successful meeting.

We recommend all participants to arrange their accommodation in Paris as early as possible. Automn is a high season in Paris, and there are several medical congresses and sporting events in October, in particular, so hotels should be booked early.

Travel grants and free registration can be offered to a number of young scientists (< 36 years). Please see our website. Deadline is also June 30th.

Thank you for circulating the information among your colleagues.

Sylvain Brisse Institut Pasteur, Paris, France on behalf of the Organizing Committee http://www.immem-10.org IMMEM-10 topics The ability of microbes - bacteria, viruses, fungi and parasites - to mutate rapidly, disseminate and adapt to new hosts and environments, forces us to increase our capabilities for the early recognition of novel strains of pathogens, and to understand the factors that contribute to their diversity, evolution and dissemination. IMMEM-10 will address a variety of topics related to pathogen emergence, population-level diversity, evolution of virulence and antibiotic resistance, strain tracking, typing networks, public health and surveillance, novel typing approaches, high-throughput sequencing, genomics, and molecular epidemiology of infectious diseases. The meeting will take place at Institut Pasteur, in the heart of Paris.

Scientific Sessions Bioinformatics tools for genome-based microbial surveillance Outbreak genomics and epidemiology Population genetics, phylogenomics, emergence Molecular typing and epidemiology Novel typing methods for pathogen surveillance Practical use of typing methods in epidemiology Typing and surveillance networks in practice Round table: the Global Microbial Identifier initiative Phylodynamics of viral pathogens Molecular epidemiology of viral zoonoses Virulence: diagnostic and epidemiology Resistance: diagnostic and epidemiology Diagnostic by high-throughput sequencing Social networks and transmission modelling Molecular Epidemiology from Global Health to One Health

Confirmed speakers: Mark Achtman (Warwick University, UK) Andrea Ammon, European Center for Disease Control, Stockholm, Sweden Siv Andersson, Uppsala University, Sweden John Besser, CDC, Atlanta, USA Hervé Bourhy, Institut Pasteur, Paris, France Alessandra Carattoli, Institute of Public Health, Rome, Italy Stewart Cole, Global Health Institute, Lausanne, Switzerland Christian Drosten, Bonn University, Germany Pierre Formenty , World Health Organization, Genève, Switzerland Alex Friedrich, University Medical Center Groningen, The Netherlands Peter Gerner-Smidt, Center for Disease Control, Atlanta, USA Matthew Gilmour, Public Health Agency of Canada, Winnipeg, Canada Hajo Grundmann, National Institute for Public Health (RIVM), Bilthoven, The Netherlands Dag Harmsen, Universitätsklinikum Münster, Münster, Germany Alan Hay, MRC National Inst. for Medical Research, UK Rene Hendriksen, DTU, Denmark Keith Jolley, Oxford University, UK Philippe Lemey, Leuven, Belgium Martin Maiden, Oxford University, Oxford, UK Claudine Medigue, CEA-Genoscope, Evry, France Stephan Niemann, Borstel, Germany Julian Parkhill, Wellcome Trust Sanger Institute, Hinxton, UK Tim Peto, University of Oxford, UK Laurent Poirel, Univ. Paris Sud, Kremlin-Bicêtre, France Marc Struelens, European Center for Disease Control, Stockholm Anne-Mieke Vandamme, Katholieke Universiteit Leuven, Leuven, Belgium François-Xavier Weill, Institut Pasteur, Paris, France

Early fee registration: June 30, 2013 Standard fee: 400 euro - Student fee: 300 euro - Pasteur fee 100 euro Abstract submission deadline: June 30, 2013 How to register: www.immem-10.org Contact us: immem-10@pasteur.fr

Sylvain BRISSE <sylvain.brisse@pasteur.fr>

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Dear Colleague,

We remind you that the deadline is June 15th, 2013 for abstract submission at IMMEM-10, the 10th edition of the International Meeting on Microbial Epidemiological Markers. A total of 33 abstracts will be selected for oral presentation. Please refer to the scientific programme for latest sessions and topics, available through the conference web site at http://www.immem-10.org . We recommend all participants to arrange their accommodation in Paris as early as possible. Automn is a high season in Paris, and there are several medical congresses and sporting events in October, in particular, so hotels should be booked early.

Travel grants and free registration can be offered to a number of young scientists (< 36 years). Please see our website.

Sylvain Brisse Institut Pasteur, Paris, France on behalf of the Organizing Committee http://www.immem-10.org IMMEM-10 topics The ability of microbes - bacteria, viruses, fungi and parasites - to mutate rapidly, disseminate and adapt to new hosts and environments, forces us to increase our capabilities for the early recognition of novel strains of pathogens, and to understand the factors that contribute to their diversity, evolution and dissemination. IMMEM-10 will address a variety of topics related to pathogen emergence, population-level diversity, evolution of virulence and antibiotic resistance, strain tracking, typing networks, public health and surveillance, novel typing approaches, high-throughput sequencing, genomics, and molecular epidemiology of infectious diseases. The meeting will take place at Institut Pasteur, in the heart of Paris.

Scientific Sessions Bioinformatics tools for genome-based microbial surveillance Outbreak genomics and epidemiology Population genetics, phylogenomics, emergence Molecular typing and epidemiology Novel typing methods for pathogen surveillance Practical use of typing methods in epidemiology Typing and surveillance networks in practice Round table: the Global Microbial Identifier initiative Phylodynamics of viral pathogens Molecular epidemiology of viral zoonoses Virulence: diagnostic and epidemiology Resistance: diagnostic and epidemiology Diagnostic by high-throughput sequencing Social networks and transmission modelling Molecular Epidemiology from Global Health to One Health

Confirmed speakers: Mark Achtman (Warwick University, UK) Andrea Ammon, European Center for Disease Control, Stockholm, Sweden Siv Andersson, Uppsala University, Sweden John Besser, CDC, Atlanta, USA Hervé Bourhy, Institut Pasteur, Paris, France Alessandra Carattoli, Institute of Public Health, Rome, Italy Stewart Cole, Global Health Institute, Lausanne, Switzerland Christian Drosten, Bonn University, Germany Pierre Formenty , World Health Organization, Genève, Switzerland Alex Friedrich, University Medical Center Groningen, The Netherlands Peter Gerner-Smidt, Center for Disease Control, Atlanta, USA Matthew Gilmour, Public Health Agency of Canada, Winnipeg, Canada Hajo Grundmann, National Institute for Public Health (RIVM), Bilthoven, The Netherlands Jörg Hacker, Leopoldina Academia, Berlin, Germany Dag Harmsen, Universitätsklinikum Münster, Münster, Germany Alan Hay, MRC National Inst. for Medical Research, UK René Hendriksen, DTU, Denmark Keith Jolley, Oxford University, UK Philippe Lemey, Leuven, Belgium Martin Maiden, Oxford University, Oxford, UK Claudine Médigue, CEA-Genoscope, Evry, France Stephan Niemann, Borstel, Germany Julian Parkhill, Wellcome Trust Sanger Institute, Hinxton, UK Tim Peto, University of Oxford, UK Laurent Poirel, Univ. Paris Sud, Kremlin-Bicêtre, France Marc Struelens, European Center for Disease Control, Stockholm Anne-Mieke Vandamme, Katholieke Universiteit Leuven, Leuven, Belgium François-Xavier Weill, Institut Pasteur, Paris, France

Early fee registration: June 30, 2013 Standard fee: 400 â¬−*Studentfee* : 300â¬*Abstractsubmissiondeadline* : *June*15, 2013*Howtoregister* : *www.immem* − 10.*orgContactus* : *immem* − 10@*pasteur.fr*

Sylvain BRISSE <sylvain.brisse@pasteur.fr>

PoloniaCastle Poland ImmunoEvolution Sep23-28

This conference is of interest to evolutionary biologists, since it will bring together immunologists with evolutionary biologists. Evolutionary biologists find a rich source of open problems; vice versa, immunologists are keen to learn from evolutionary thinking. People interested in evolutionary and ecological immunology will find it a great oportunity to exchange ideas in a small setting. It focuses on invertebrates.

ESF-EMBO Symposium: Integrated Insect Immunology: From Basic Biology to Environmental Applications

23 - 28 September 2103 Polonia Castle in Pultusk, Poland Organised by: Dr. Dominique Ferrandonm CNRS Strasbourg, Prof. George Christophides, Imperial College London

The Forward Look Session will be chaired by Jules Hoffmann, CNRS, FR, who was awarded the 2011 Nobel Prize in Physiology or Medicine for his work on Insect Immunity.

For infomation and application: www.esf.org/-conferences/13423 Paul Schmid-Hempel <schmidhempel@me.com>

Roscoff EvolutionCancer Nov2-6

Registation open for Jacques Monod Conference "Ecological and Evolutionary Perspectives in Cancer" - Roscoff (Brittany), France, November 2-6, 2013

Cancer is a disease of opportunity, associated with clonal evolution, expansion and competition within the body. Specifically, somatic cellular selection and evolution are the fundamental processes leading to malignancy, metastasis and resistance to therapies. The Jacques Monod Conference "Ecological and Evolutionary Perspectives in Cancer" aims to promote this emerging discipline by addressing some of the most important questions about cancerogenesis. The conference will cover 3 themes:

Interspecific patterns and processes Progression Therapies

The first theme will address the observation that infectious agents can cause cancers. Persistent infections may promote cancer because long-term host defensive responses induce inflammation that subsequently increases mutation rates. Why human defensive mechanisms have not evolved to more efficiently control or eliminate invasive cell lineages, and why do some species with more somatic tissue show less than expected incidences of cancer? The second theme will evaluate the role of the tumor environment and natural selection in explaining cancer progression. To what extent are different cancers predictable and what are the key contributing variables? The third theme will tackle the daunting challenge of employing evolutionary theories to improve cancer therapies. It will seek how preventative, curative and management therapies can be improved and even optimized to slow or stop the emergence of resistance to chemotherapies.

Please note that participation at this conference is not limited to research on carcinogenesis: we will consider applications from scientists with affinities towards the themes of the conference, and working on related topics from ecology and the evolutionary sciences, including social evolution, evolution of multicellularity, resistance management, evolutionary medicine of diseases, and species invasions.

Jacques Monod Conferences organized by CNRS, are known for the high scientific quality of the talks and discussions, in a relaxed atmosphere.

Invited speakers:

AKTIPIS Athena (San Francisco, USA)

BEERENWINKEL Nico (Basel, Switzerland)

CICCARELLI Francesca (Milano, Italy)

CLAIRAMBAULT Jean (Paris, France)

CRESPI Bernard (Burnaby, Canada)

DELHOMMEAU François (Paris, France)

EWALD Paul (Louisville, USA)

FRIDMAN Hervé (Paris, France)

GATENBY Robert (Tampa, USA)

HAREL-BELLAN Annick (Gif-sur-Yvette, France)

HENG Henry (Detroit, USA)

HIBNER Urszula (Montpellier, France)

HOCHBERG Michael (Montpellier, France)

MAINI Philip (Oxford, United Kingdom)

MALEY Carlo (San Francisco, USA)

MORENO Eduardo (Bern, Switzerland)

OLIVIERI Isabelle (Montpellier, France)

PACHECO Jorge (Braga, Portugal)

PEPPER John (Bethesda, USA)

QUINTANA-MURCI Lluis (Paris, France)

RADMAN Miroslav (Paris,France)

SAVAGE Philip (London, United Kingdom)

SOLÃ Ricard (Barcelona, Spain)

SPROUFFSKE Kathleen (Zurich, Switzerland)

STRATTON Michael (Cambridge, United Kingdom)

THOMAS Frédéric (Montpellier, France)

TLSTY Thea (San Francisco, USA)

TOMLINSON Ian (Oxford, United Kingdom)

WEITZMAN Jonathan (Paris, France)

ZUR HAUSEN Harald, Nobel Prize in Medicine (Heidelberg, Germany)

Deadline for registration : August 1st, 2013

Registration fee (includes lodging, meals and conference banquet)

400 Âeuro for PhD students

520 Âeuro for other participants

Application for registration

The total number of participants is limited to 115 and all participants are expected to attend for the whole duration of the conference. Scientists and PhD Students interested in the meeting should send:

- their curriculum vitae

- the list of their main publications for the 3 last years

- the abstract of their presentation

to the Chairperson of the conference (mhochber@univ-montp2.fr) before August 1st. Except in some particular cases approved by the Chairperson, it is recommended that all selected participants present their work during the conference, either in poster form or by a brief in- session talk. The organizers choose the form in which the presentations are made. No payment will be sent with the application. Information on how and when to pay will be mailed in due time to those selected.

Michael Hochberg <mhochber@univ-montp2.fr>

Rostock WilliyHennigSociety Aug3-7

!!!!!Extended registration deadline 30.6.2013!!!!!

This is to remind you about our upcoming XXXII Meeting of the Willi Hennig Society in the beautiful city of Rostock, near the Baltic coast from August 3rd to 7th, 2013. This is also a special occasion to celebrate the 100th anniversary of Willi Hennig. Please, hurry up to register and submit your abstracts for one of the most exciting systematics meetings you could attend! The deadline for abstract submission has been extended until 30th of June.The conference will address the following topics and symposia:Morphology, Ontologies and SystematicsBiogeography, Phylogeny, ConservationPhylogenomicsand free topics from all fields of phylogeneticsRegistration fees are payable via the society's website (http://www.cladistics.org/-meetings.html) Please check our website http://-www.zoologie.uni-rostock.de/whs-xxxii/ frequently, as new information and details will be added regularly.For any additional questions, feel free to contact whs2013@uni-rostock.de.We are looking forward to seeing you in Rostock!

da_schwaentna@hotmail.com

Seville Adaptation Sep18-20

Adapting to Global Change in the Mediterranean

September 18-20, 2013

Estacion Biologica de Doñana, Seville, Spain

Dear Colleagues,

It is our pleasure to invite you to register for the international congress "Adapting to Global Change in the Mediterranean" in Seville September 18-20, 2013. This congress is sponsored by an EU Regpot grant, so registration is free. All talks will be presented by invited speakers. Abstracts for posters are welcome before July 17.

Please find more information on the conference website:

http://ebdecogenes.ebd.csic.es/ Sincerely, The Organizing Committee

Early Registration and Poster submission deadline: 17 July 2013

Late Registration Deadline: 6 September 2013

Congress sessions are:

- Phenotypic responses to global change
- Breakdown of species boundaries
- Emergent diseases in changing environments
- Responses to past global change
- Adaptation and speciation in response to changing environments
- Biological invasions: from species adaptation to ecosystem responses
- Monitoring ecosystems responses
- Consequences of global change in biotic interactions
- Population responses to global change

– Dr. Pim Edelaar

Dept. Molecular Biology and Biochemical Engineering University Pablo de Olavide, Sevilla, Spain tel (+34) 954 978 213 edelaar@upo.es

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Dept. Conservation Biology Estación Biológica de Doñana - CSIC, Sevilla, Spain tel (+34) 954 466738 (ext. 1042) edelaar@ebd.csic.es /http://www.researchgate.net/profile/Pim_Edelaar/ /http://scholar.google.com/citations?user=HJud5cEAAAAJ/ /http://www.ebd.csic.es/carnivoros/personal/edelaar/ edelaar <edelaar@upo.es>

Snowbird Utah Evolution2013 Jun21-25 Housing 2

Housing and Childcare Updates:

1. Housing for the conference is available at Crystal Inn, which is at the base of Little Cottonwood Canyon.Crystal Inn offers free airport shuttles. In the AM Crystal Inn will transport to a nearby bus stop for public transportation to Snowbirdand there will be complementary shuttle service from the meeting site back to the hotel late in the evening (10 PM).Rooms are still available at Snowbird from June 23^rd onwards.Call Snowbird accommodations for more information (1-800-232-9542).

2. Cabin rental (sleeps up to 14 with two bathrooms and kitchen) is available at Snowbird for the duration of the meeting.Call Snowbird accommodations for more information (1-800-232-9542).

3. Priority childcare registration ends June 3^rd .Contact Camp Snowbird for more information By email: campsnowbird@snowbird.com (please put 'Evolution 2013' in the subject line) By phone: (801) 933-2256

Evolution 2013 is the joint annual meeting of the Society for the Study of Evolution < http://www.evolutionsociety.org/ > (SSE), the Society of Systematic Biologists < http://systbiol.org/ > (SSB), and the American Society of Naturalists < http://www.amnat.org/ > (ASN), on June 21-25, 2013, at the Snowbird Alpine Village < http://www.snowbirdmeetings.com/?portfolio=snowbird-restaurants >.

This meeting is the premier annual opportunity for sharing scientific research related to evolution. Symposia presentations, concurrent contributed papers, and poster sessions will be presented by the 1,400 expected participants. Product and service providers will contribute to the meeting through their exhibits. Social activities will include an opening reception, mixers with each evening poster session, and a super-social/award ceremony - *all of these mixers and receptions are included with registration.*

Evolution 2013 meets jointly with the *iEvoBio < http://ievobio.org/ >* conference, which brings together biologists interested in evolution, systematics, biodiversity, software, and mathematics.

You can still register for the conference - for more information visit the conference web site: http://www.evolutionmeeting.org/index.html cruzan@pdx.edu

TahoeCity CA InvertMicrobeInteraction Jan26

Keystone Symposia Mechanisms and Consequences of Invertebrate-Microbe Interactions Granlibakken Resort, Tahoe City, California, USA January 26'30, 2014

Topics Advances in Understanding of Invertebrate Immunity Pathogens and Biocontrol Understanding the Function of Complex Host-Microbe Associated Microbial Communities Establishment of Host-Microbe Associations Ecology and Evolution of Host Immune Defense Host, Symbiont and Insect Vectors

Confirmed Speakers Takema Fukatsu Heidi Goodrich-Blair Frank Jiggins Brian Lazzaro

Margaret McFall-Ngai

Nancy Moran Todd Schlenke and many more

Important Dates Discounted Abstract Deadline: September 26, 2013 Student/Postdoc Scholarship Application Deadline: September 26, 2013 Abstract Deadline: October 30, 2013 Discounted Registration Deadline: November 25, 2013

For more information and to view the full program, visit www.keystonesymposia.org/14A7 Organizers: Bruno Lemaitre, Nicole M. Gerardo and Jason Rasgon

ngerard@emory.edu

UBirmingham DaphniaGenomics Jan19-22

"EARLY ANNOUNCEMENT: Daphnia Genomics Consortium Conference 2014, 19th - 22nd January 2014 at the University of Birmingham, UK." Please keep these dates free to attend the next in the series of these quasi-annual, exciting scientific meetings. A full announcement of the Conference details, the speakers and the scientific sessions will be released soon. This meeting will focus on combining the old and the new, from phenotypical variation, quantitative genetics and basic aquatic ecology and limnology, to novel techniques in bioinformatics, metabolomics and sequencing, eco-devo and functional and evolutionary genomics.

We hope to see you there! Best wishes The Organising Committee Dr Nadine Taylor Dr Leda Mirbahai Dr Kay Van Damme

dgc.birmingham@gmail.com

Many Thanks

Nadine

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Tel: +44 (0)121 4145409 Email: n.s.taylor@bham.ac.uk

Nadine Taylor <n.s.taylor@bham.ac.uk>

UCambridge HumanOrigins Jul5 3

Registration is now open for the conference

RELOCATING HUMAN ORIGINS - WHAT IF ADAM LIVED IN THE FOREST?

Join us for a day of discovery and excitement, challenging the way we do and communicate research. Come in person or follow us online.

Homepage:

http://relocatingorigin.soc.srcf.net/ Registration:

http://relocatingorigin.soc.srcf.net/?page_id- LOCATION: Sainsbury Laboratory, University of Cambridge ORGANIZERS: Doctoral Students, Division of Biological Anthropology DATE: July 5, 2013, 9.00 - 17.45

THEME: Conventional scientific wisdom holds that modern humans evolved in the East African savannah. But what if the cradle of human evolution was actually the Central African forest, as hinted by new Y-chromosome results? How might this change our understanding of human evolution? This conference explores the implications of a forest origin for human population genetics, disease ecology, social systems, and cultural evolution.

KEYNOTE SPEAKERS: Prof Mark Thomas, University College London: Genetics of Forest Ancestry Dr Corey Fincher, University of Glasgow: Origins of cultural and biological diversity Dr Tom Currie, University College London: Habitat Productivity & Ethnolinguistic Diversity Dr Peter Walsh, University of Cambridge: Disease, Social Complexity & Innovation

PANEL DISCUSSIONS: Spatialising research on genetic diversity 14.00 - 15.30 with Prof Mark Thomas, Prof Laurent Excoffier, Dr Anders Eriksson

Spatialising research on cultural diversity 16.00 - 17.30 with Dr William Banks, Dr Tom Currie, Dr Corey Fincher

Can't make it to Cambridge? The entire conference will be webcast.

Questions? Contact us on: bioanth-conference2013-enquiries@lists.cam.ac.uk

"C.E. Inchley" <cei23@cam.ac.uk>

UFlorida BarkBeetleEvolution May

Subject: Bark & Ambrosia Beetle Academy: mark the calendar!

TO ALL STUDENTS AND RESEARCHERS IN FOREST ENTOMOLOGY, ECOLOGY, AND RELATED FIELDS: The Forest Entomology and Symbiology Lab at the University of Florida is pleased to invite you to the first comprehensive, fun and nerdy workshop on bark and ambrosia beetles in May 2014.

Are you a researcher or a student interested in bark and ambrosia beetles? Do you need to know more about the beetle identification, classification, damage, or symbioses? Learn from international experts through hands-on labs, field demonstration, lectures, and fun socializing. Choose one or all three modules: Regional Applied Focus, Hardcore Identification, and Understanding the Bug.

See details at http://www.ambrosiasymbiosis.org/-academy/ . Sign up for updates - no spam, and you will be notified when the registration opens!

Jiri Hulcr, PhD School of Forest Resources and Conservation | University of Florida ph: 352-273-0299 | cell: 517-256-1894 | www.ambrosiasymbiosis.org "Hulcr,Jiri" <hulcr@ufl.edu>

UNewEngland Genomics Jul14-19

Please join us as we convene 10 years after the first GRC on Ecological & Evolutionary Genomics!

July 14-19, 2013 University of New England Biddeford, Maine

Speakers and Discussion Leaders will present cutting-edge genome-enabled approaches that are being used to further our understanding of how organisms adapt to changing environments. Specific topics to be addressed include critical research challenges in population genetics, the study of genome evolution, the evolution of complex phenotypes, and environmental and global change biology. We have made explicit emphasis on "ecogenomics", population genomics, and the bioinformatics required to understand the transition of genotype to phenotype.

We would like to invite you to attend this conference and join our community in discussing the frontiers and future challenges in this research area. Gordon Research Conferences are an ideal venue for informal and interactive discussions in beautiful locations in New England.

Speakers and Discussion Leaders: Julien Ayroles, Cornell University Rowan Barrett, Harvard University Holly Bik, UC Davis Mark Blaxter, The University of Edinburgh Justin Borevitz, The Australian National University Monica C. Muñoz-Torres, LBNL Sinead Collins, The University of Edinburgh Graham Coop, UC Davis Karel De Schamphelaere, Ghent University Maren Friesen, Michigan State University Omer Gokcumen, Harvard University Michael Hansen, Aarhus University Paul Hebert, University of Guelph Jessica Hellmann, University of Notre Dame Paul Hohenlohe, University of Idaho Chris Jiggins, University of Cambridge Felicity Jones, Max Planck Institute Ellen Ketterson, Indiana University Mikhail Matz, University of Texas, Austin Gos Micklem, University of Cambridge Stephen Palumbi, Stanford University Michael Pfrender, University of Notre Dame David Plachetzki, UC Davis John Quackenbush, Harvard University Christina Richards, University of South Florida Loren Rieseberg, University of British Columbia Emilie Snell-Rood, University of Minnesota Victoria Sork, UC Los Angeles Denis Tagu, INRA-RENNES Diethard Tautz, Max-Planck Institute Anne Todgham, San Francisco State University Thomas Turner, UC Santa Barbara Andrew Whitehead, UC Davis

For registration information and the speaker program, visit the GRC website: http://www.grc.org/programs.aspx?year=2013&program=ecolevol Best wishes, Gretchen E. Hofmann & John Colbourne, Mike Herman & Jack Werren

Michael Herman <mherman@ksu.edu>

UNewEngland Genomics Jul14-19 2

Limited space still available for the 10 year celebration of Ecological & Evolutionary Genomics at the Gordon Research Conference! Applications for this meeting must be submitted by June 16, 2013. Please apply now.

July 14-19, 2013 University of New England Biddeford, Maine

Speakers and Discussion Leaders will present cutting-edge genome-enabled approaches that are being used to further our understanding of how organisms adapt to changing environments. We hope to see a great representation of the Daphnia Genomics community at this meeting, already including invited speakers and discussion leaders. Specific topics to be addressed include critical research challenges in population genetics, the study of genome evolution, the evolution of complex phenotypes, and environmental and global change biology. We have made explicit emphasis on "ecogenomics", population genomics, and the bioinformatics required to understand the transition of genotype to phenotype.

We would like to invite you to attend this conference and join our community in discussing the frontiers and future challenges in this research area. Gordon Research Conferences are an ideal venue for informal and interactive discussions in beautiful locations in New England.

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For registration information and the speaker program, visit the GRC website: http://www.grc.org/programs.aspx?year=2013&program=ecolevol Best wishes, Gretchen E. Hofmann & John Colbourne, Mike Herman & Jack Werren

Michael Herman <mherman@ksu.edu>

Vienna PopGenetics Nov1-2

Announcement: Conference: Vienna, Mind the Gap 4, 1st and 2nd of November, 2013

MIND THE GAP 4 Conference Vienna, Austria 1st and 2nd of November, 2013

Bridging the gap between theoretical and empirical population genetics

The Vienna Graduate School of Population Genetics, Vienna, Austria, and the DFG Priority Programme "Probabilistic Structures in Evolution", Bielefeld, Germany, are proud to announce the fourth MIND THE GAP conference to be held the 1st and 2nd of November 2013 in Vienna, Austria.

MIND THE GAP aims at bringing together theoretical and empirical population geneticists.

This conference is the 4th meeting in a series of conferences held in Freiburg 2009, Plön 2010, and Cologne 2011.

As in these past meetings, there are different main topics for this conference. This year's themes are:

1. Viral and Predictive Evolution
2. Experimental Evolution
3. Signatures of Complex Selection

4. Introgression, Hybrid Zones, and Clines

The current list of invited speakers includes:

Nicolas Bierne, University II of Montpellier Simon Boitard, INRA, Toulouse Luis-Miguel Chevin, Centre for Functional and Evolutionary Ecology, CNRS, Montpellier Michael Desai, Harvard University Philip Gerrish, University of New Mexico Toni Gossmann, University of Sussex Joachim Krug, University of Cologne Michael Lässig, University of Cologne Henrique Teotónio, University of Lisbon Jarle Tufto, Norwegian University of Science and Technology Anton Wakolbinger, Goethe-Universtität Frankfurt

Attendance is free of charge. There are a few remaining speaker positions for the conference and we invite you to apply. All attendees are welcome to bring a poster. Registration details for the conference and application for a speaker position, along with further information, can be found at the following website: http://www.popgen-vienna.at/news/mindthegap.html The deadline for application is Sunday, 14th July, 2013. We strongly advise participants to arrive at latest on the evening of Thursday, 30th October, 2013 and to stay at least until Sunday, 3rd November 2013.

http://www.popgen-vienna.at/ http://www.dfg-spp1590.de Ilse Hoellinger <ilse.hoellinger@univie.ac.at>

GradStudentPositions

Lille France PopulationGenetics

A PhD position in population genetics and evolutionary ecology of two threatened amphibian species is available for three years in the GEPV lab., UMR CNRS 8198 at the University of Lille 1 - Sciences & Technologies (France).

This project deals with the management and protection of biodiversity in one of the most fragmented landscape in France, mostly constituted of man-made habitats: the coal basin of northern France. This area has been highly disturbed from the start of the last industrial revolution till the cessation of mining activities in the late eighties. This PhD thesis project will focus on a comparative analysis of population genetic structure in two amphibian species classified as endangered in northern France and recolonising the mining area: the natterjack toad (Bufo calamita) and the Parsley frog (Pelodytes punctatus). The patterns of gene flow and connectivity among populations in these two amphibian species will be investigated to identify relevant conservation priorities. This project as well as the PhD position is fully founded by the "Région Nord-Pas-De-Calais" (administrative district of the North of France) and the "Fondation pour la recherche sur la Biodiversité" (Foundation for Research on Biodiversity).

Applications from highly motivated and outstanding students with a strong background in empirical and theoretical population genetics and good skills in molecular biology will be considered. The position would suit an enthusiastic, motivated, and independent graduate with interest in field sampling and ecological characterization of habitats, and whose degree has a solid component in evolutionary biology. Given the extensive sampling planned over all the north of France, the PhD candidate should have a driving license. The candidate will also have to make the link between a scientific institution (University of Lille 1) and various NGOs (Regional natural reserves and local naturalist societies. Finally, the candidate should have the ability to coordinate the diverse project managers in charge of the extensive sampling that will be carried out during this project.

Only complete applications (CV, motivation letter - max. 1 page-, university certificates with official grades in a single pdf) received by 01 July 2013 will be considered. Contact details and/or recommendation letters from two referees are also required. The selection criteria will be the excellence of the curriculum vitae and the adequacy between the professional project of the candidate and the thesis subject. Candidates will be short listed before the 15th of July. Final decision will be made after auditions by the end of July. Applications should be sent to Jean-François Arnaud (jean-francois.arnaud@univ-lille1.fr) and Cédric Vanappelghem (cedric.vanappelghem@espaces-naturels.fr). The selected candidate will obtain the PhD grant for three years (1684,93 EUR brut salary per month for a full-time PhD researcher). The advisor will be Jean-François Arnaud (Professor, Université Lille 1) and the co-advisor will be Cédric Vanappelghem (Conservation manager, Université Lille 1 and Conservatory of natural areas of Nord of France). The city of Lille is located in the north of France and is an attractive and vibrant cultural city with a high quality of life. Lille is a city with a central location in Europe, just 35 minutes from Bruxelles, one hour from Paris and two hours from London by high-speed train. More information about the department is available at the following website: http://gepv.univ-lille1.fr/ and general information about the city of Lille can be found at the following website: http://www.lilletourism.com/ . PhD's summary: This PhD's project focuses on a comparative analysis of population genetic structure in two amphibian species that are classified as endangered in northern France and that are recolonizing the mining area: the natterjack toad and the Parsley frog. The aims of this project are the following: (1) In a first step, the candidate will attempt to compare the levels of genetic diversity and the patterns of genetic differentiation within and among native coastal and inland populations and sites recently colonized in the coal basin of northern France. Using neutral microsatellite loci and mitochondrial polymorphism, a number of questions can be put forward. Is there a critical level of fragmentation beyond which the two species respond differently in term of mean levels of genetic differentiation? Where do the mining area populations come from? Do they originate from founder individuals coming from native populations? If so, are there signatures of bottlenecks within the mining area? Are the patterns of inbreeding and/or level of genetic diversity contrasted between these two areas? Have these populations been founded by

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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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MaxPlanckInst Leipzig 3 ComputationalBiol

The Max Planck Institute for Evolutionary Anthropology (http://www.eva.mpg.de) is spear-heading the research in the evolution of modern humans. The institute encompasses five departments working towards this goal by studying genetics, language, psychology, anthropology and primate behavior. It is located in Leipzig, Germany, one of the most livable cities in the world.

As part of the Department of Evolutionary Genetics, the groups for Bioinformatics and Genome Analysis are seeking

3 PhD candidates in Computational Biology (available immediately).

The groups are interested in the development of computational methods and software for the analysis of next generation sequence data. A particular area of interest is the analysis of modern human, archaic human and primate genomes. The successful applicant will work in close collaboration with experimental biologists, statisticians and population geneticists to address questions about recent human evolution. Specific projects will be dependent on the skills and interests of the candidate. The position includes a stipend to cover living expenses.

Potential topics include: - Analysis of candidate genes for human traits - Comparative gene expression analysis - Metagenome assembly from archaic samples - Development and analysis of sequence alignment and genotyping algorithms - Methods for identifying positive selection - Population genomics analyses

The candidate should have experience with at least one programming language (preferably perl, python or C++). Previous experience with large biological datasets and advanced statistical analyses would be an advantage. We seek individuals that are highly self-motivated, able to work independently and to collaborate closely and effectively with other members in a research team.

Candidates with experience in molecular evolution, genetics, computation biology or computer science are invited to apply with: - Statement of interest - CV - At least 1 reference - Masters degree

Questions and applications please by email to: kelso@eva.mpg.de or pruefer@eva.mpg.de

Bioinformatics Group: http://www.eva.mpg.de/-genetics/bioinformatics/overview.html Genomes Group: http://www.eva.mpg.de/genetics/genomes/-overview.html Kay Pruefer <pruefer@eva.mpg.de> Kay Pruefer <pruefer@eva.mpg.de>

MonashU MitochondrialEvolution

PhD top-up scholarship available for project in mitochondrial evolutionary ecology / genomics.

An opportunity - and top-up scholarship paid over three years - is available for a PhD position in the research group of Dr Damian Dowling at Monash University, to work on the evolutionary processes shaping mitochondrial genome evolution and mitochondrial-nuclear coadaptation.

Energy production - life's most important biological process - is encoded by genes dispersed over two obligate genomes - mitochondrial and nuclear. These genes must interact closely to ensure mitochondrial, hence organismal functionality. Hence, we expect strong selection to optimize mitochondrial-nuclear coadaptation. However, due to fundamental genetic differences between the mitochondrial and nuclear genomes, there is considerable scope for evolutionary conflicts to arise between the two genomes, the dynamics of which could modify the evolution of life histories.

The project is inter-disciplinary, and grounded in fundamental principles of evolutionary ecology and genomics. The successful applicant will be familiar with basic evolutionary concepts, understand the core tenets of experimental design, and have strong quantitative skills. Some expertise in evolutionary genomics is desirable, but not essential.

The top-up scholarship will supplement a scholarship for doctoral study, which the successful applicant must apply for through Monash (Australian Postgraduate Award or Monash University PhD scholarship). Outstanding Australian or international students who have completed a four year undergraduate degree have an excellent chance of obtaining such scholarships. The tax-free 2013 rate of a scholarship is A$24 653, and the top up will add an extra $5,000 to this amount).

The position includes funding for international and national conference visits, and for all research costs.

The deadline for scholarship applications at Monash University is 31st October 2013.

Interested students should contact damian.dowling@monash.edu and attach a CV, academic transcript, contact details of two academic referees, and a brief description of their research interests.

For further information on these scholarships and Monash application procedures, please visit http://monash.edu/science/about/schools/-biological-sciences/postgrad/ For further information on the research group of Damian Dowling, visit http://www.damiandowlinglab.com damian.dowling@monash.edu

SalfordU EvolutionaryBiol

We would like to draw attention to the initiative that academics at Salford University's School of Environment & Life Sciences have set up for the "Science without Borders" program of the Brazilian government.

We have tailored over 50 PhD projects, across the broad spectrum of our School's research areas, many of which have a strong evolutionary and conservation biology slant.

For detailed information, please visit the page: http://www.salford.ac.uk/environment-life-sciences/research/postgraduate-research thank you.

Stefano.

http://www.salford.ac.uk/environment-life-sciences/els-academics/stefano-mariani http://hub.salford.ac.uk/bicome/2013/01/22/stefano-mariani/ Researcher.ID: A-2964-2012

Mariani Stefano <S.Mariani@salford.ac.uk>

Tulsa Oklahoma EvolutionBedBugs

Graduate research opportunity to study the molecular ecology of bed bugs. Department of Biological Sciences - University of Tulsa

A graduate student at the M.S/Ph.D level (3 year) is sought to work with Dr. Warren Booth in the Department of Biological Sciences at The University of Tulsa, Oklahoma. The successful applicant will develop a thesis research project focused on the evolutionary dynamics and population structure of the bed bug (Cimex lectularius) in the South Central U.S.

The study aims to examine the following objectives: infestation dynamics, population genetic structure, dispersal patterns, inbreeding dynamics, population differentiation, and patterns of insecticide resistance in bed bugs. Research will primarily focus on populations within Oklahoma and its 6 adjacent states. This research will be addressed using microsatellite markers, previously developed by the P.I., mtDNA and nDNA sequencing, and potentially RADseq.

Applicants for this position should have a strong background in population genetics, molecular ecology, evolutionary biology, or ecology, be willing to undertake field research to collect samples (if required), and meet the admission requirements for the Department of Biological Sciences graduate program. (http://www.utulsa.edu/academics/colleges/college-of-engineering-and-natural-sciences/departments-and-schools/Department-of-Biological-Science.aspx). Previous lab experience would be beneficial.

Applications should include the following: 1) A letter of interest (not exceeding two pages). 2) A curriculum vitae. 3) Names and email addresses for at least two academics/researchers willing to provide a letter of recommendation 4) Copies of undergraduate/graduate transcripts 5) Electronic copies of published manuscripts, if any.

For more information about this opportunity, contact Dr. Booth (warren-booth@utulsa.edu). Anticipated start date is mid-August 2013, however this may be delayed if required. Anticipated annual stipend is $19,000 and includes tuition and medical

Additional information regarding our research can be found at my current departmental webpage: Booth - http://www.utulsa.edu/academics/colleges/college-of-engineering-and-natural-sciences/departments-and-schools/Department-of-Biological-Science/Our-Faculty-and-Staff/B/Warren%20Booth.aspx Dr. Warren Booth Assistant Professor of Molecular Ecology Department of Biological Sciences University of Tulsa 315 Oliphant Hall Tulsa, OK 74104

Tel. (918) 631-3421 - Office (918) 631-3136 - Lab Web site < http://www.utulsa.edu/academics/colleges/college-of-engineering-and-natural-sciences/departments-and-schools/Department-of-Biological-Science/Our-Faculty-and-Staff/B/Warren%20Booth.aspx >

"Booth, Warren" <warren-booth@utulsa.edu>

UAberdeen ReproductiveSuccess

PhD position in evolutionary ecology at the UNiversity of Aberdeen Title:?Individual variation in age-specific reproductive success and survival in wild yellow-bellied marmots?

Understanding the causes and consequences of senescence, defined as declines in reproductive success and survival in old age, is a key but challenging aim in evolutionary ecology. It has recently been realised that the magnitude and relative timing of senescence can vary among individual population members, and that quantifying such individual variation is key to understanding the ecological and evolutionary causes and consequences of senescence.

This project will use 52 years of data from a wild population of yellow bellied marmots, where individuals have been marked, weighed and observed from birth to death, to quantify individual variation in survival and reproduction during late life, and to explore the quantitative genetic basis of and life-history consequences of this variation.

The student will be based within the dynamic Ecology research group at the University of Aberdeen. They will contribute to data collection through 2 summers of fieldwork at the Rocky Mountain Biological Laboratory, Colorado, USA, and then apply sophisticated statistical analyses to the long-term data. Full training in fieldwork and data analysis will be provided, providing a broad range of necessary skills for ecological research.

The PhD will be supervised by Dr Julien Martin (www.abdn.ac.uk/staffpages/julienmartin), Dr Jane Reid (www.abdn.ac.uk/staffpages/jane.reid) and Dr Daniel Blumstein (www.eeb.ucla.edu/Faculty/-Blumstein/).

The PhD will start in October 2013 (but later starting would be considered). It will be funded by a NERC studentship (limited to UK nationals and UK residents) for 3.5 years.

For further enquiries about the project, please email me at julienmartin@abdn.ac.uk

To apply, apply online on the university website (http:/-/www.abdn.ac.uk/postgraduate/apply.php) and send me an email. You should select a Degree of Doctor of Philosophy in Marine Biology, to ensure that your application is passed to the correct College for processing.

The closing date for applications is 17 July 2013.

Dr. Julien Martin University of Aberdeen School of Biological Sciences julienmartin@abdn.ac.uk

“Martin, Julien” <julienmartin@abdn.ac.uk>

UCanberra 2 InvasiveFish

eDNA surveillance for multiple high risk invasive fish; 2 PhD scholarships

Invasive fishes are a major threat to native species and ecological communities, nationally and internationally. Early detection of such fishes while they are still rare is the key to eradication success but is problematic using conventional sampling.

We seek two PhD students with molecular skills to use advanced genomic approaches, such as next generation sequencing, to develop species-specific markers for key aquatic pest species. eDNA techniques will be developed to determine low-density detection probabilities and to evaluate DNA degradation under varying conditions (e.g. changes in temperature or UV exposure) with the aim of improving the technology^{1}s management application. eDNA detection will be utilised in the field to identify low-density populations of invasives to identify invasion fronts and to confirm recent eradication efforts.

The overall project is funded via the multi-agency Invasive Animal Cooperative Research Centre (www.invasiveanimals.com). The PhD students would be based within the Wildlife Genetics Laboratory, Institute of Applied Ecology, University of Canberra, Canberra ACT, Australia For more details contact either: Dr Dianne Gleeson: Dianne.Gleeson@canberra.edu.au Dr Elise Furlan: Elise.Furlan@canberra.edu.au

Applications & further information on PhD scholarships: www.invasiveanimals.com/phd-scholarship-applications Dianne Gleeson PhD| Population Genetics | Phone: +61 2 62012237| Cell: +61 424221214| Institute for Applied Ecology| University of Canberra | Bruce ACT AUSTRALIA | email: Dianne.Gleeson@canberra.edu.au

“Dianne.Gleeson” <Dianne.Gleeson@canberra.edu.au>

UCollegeLondon Bioinformatics Genomics

PhD opportunity: Comparative Genomics of Xenoturbella and the Acoelomorph flatworms.

Application Deadline: 30 June 2013

The Telford Lab in the Department of Genetics Evolution and Environment, University College London is seeking a PhD student to join a team funded by an ERC Advanced Award.

The project aims to study the morphology, embryology and genetics of the Xenacoelomorpha (Xenoturbellida and Acoelomorpha) - a newly identified phylum of worms that have (contentiously) been linked to the deuterostomes.

The Doctoral Student will contribute to an analysis of the genomes and transcriptomes of several species of Xenacoelomorpha and will integrate their findings with parallel studies of the morphology, ultrastructure and embryology of these animals.

The successful applicant will be exposed to a vivid, collaborative scientific environment and a broad range of advanced bioinformatics techniques. The project will involve sequencing and assembly of genomes/transcriptomes, automatic gene prediction and genome annotation and comparative/evolutionary analyses of animal genomes

Applicants are required to have a strong background in computing/ bioinformatics and an interest in evolutionary biology. The position is available from September 2013.

For further information regarding the position and scientific content of the project please contact the Group Leader, Prof. Max Telford (email m.telford@ucl.ac.uk).

Written applications in English should include a C.V., summary of educational and work experience, statement describing your scientific interests and contact information for two references. Applications can be mailed to: Prof Max Telford, Dept GEE, University College London, Gower Street, London WC1E 6BT, UK. Application deadline 30 June 2013.

Applications by e-mail only will NOT be considered.

Apologies for cross-posting

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

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

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

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

Xenoturbella You Tube video < http://uk.youtube.com/watch?v=3DyJXNcoxL2Xs >

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

m.telford@ucl.ac.uk

UCollege London MadagascarChameleons

Institution: University College London

Dept/School/Faculty: Department of Genetics, Evolution and Environment

PhD Supervisors: Dr. Richard Pearson (UCL) and Dr Mark Wilkinson (NHM)

Application Deadline: 15 July 2013

Funding Availability: Funded PhD Project (European/UK Students Only)

This PhD project will be jointly funded by UCL and the Natural History Museum.

PhD opportunity in Biodiversity, Ecology & Evolution Project title: Niche conservatism among chameleons in Madagascar

UCLs Centre for Biodiversity and Environment Research, and the Natural History Museum, invite applicants for a PhD studentship to study ecological niche conservatism among chameleons in Madagascar. Niche conservatism (NC) can be defined as the retention of niche-related ecological traits over time. NC has been shown to be of fundamental importance for addressing a wide range of questions, including concerning species richness patterns, invasive species, speciation processes, ecosystem function, and responses to global climate change. Despite this, there remains much debate as to how frequently and under what circumstances NC occurs, a problem confounded by uncertainty over which of several recently proposed computational methods are most appropriate for testing for conservatism. This PhD project will focus on the development and testing of methods for assessing NC, including GIS-based ecological niche models, and will undertake a detailed study of phylogenetic niche conservatism among chameleons in Madagascar, for which novel datasets are becoming available.

The project will be primarily desk-based (no fieldwork) and will provide advanced training in the use of Geographic Information Systems, ecological modeling, and remote sensing to address fundamental questions in ecology, evolution, and biodiversity conservation, as well as a grounding in reptile taxonomy. The project will best suit a student with keen interest and proficiency in computational approaches (including programming/scripting) and training in ecological and evolutionary theory. The project is part of an exciting collaboration between UCLs Centre for Biodiversity and Environment Research and the Natural History Museum, and the successful candidate will benefit from training and research opportunities at both institutions. The student will also benefit from the input of international collaborator Dr. Chris Raxworthy of the American Museum of Natural History.

Applicants must be UK/EU nationals and have at least a 2:1 (Hons) degree. Start date is September 2013 or up to six months after.

Application procedure: Please send a full academic CV, contact details for two referees, and a covering letter (up to 2 pages) electronically by email to CBER@ucl.ac.uk no later than 15 July 2013. Please also send any informal enquiries to this address.

Mark Wilkinson <M.Wilkinson@nhm.ac.uk>

UHelsinki EvolutionButterflyImmunity

PHD STUDENT POSITION IN ECOLOGY AND EVOLUTION OF IMMUNE DEFENCE IN A BUTTERFLY METAPOPULATION AT THE UNIVERSITY OF HELSINKI

Applications are invited for a PhD fellowship to study the interplay between ecology and genetics in shaping immune defence in natural butterfly (meta)population. The project is funded by the Kone Foundation (http://www.koneensaatio.fi/fi/tiivistelmaet/#Saastamoinen: in Finnish only) Motivated students with a MSc degree in ecology, evolutionary biology or molecular biology (or other related fields) are encouraged to apply. Prior expertise in experimental design, statistical analysis or laboratory work are a bonus but your most important assets are enthusiasm for research, motivation to learn new things, and ability to work independently while being an active member of a research team.

The project is centered within a larger study of the ecological processes and the underlying genetic mechanisms that allow the Glanville fritillary butterfly (Melitaea cinxia) to cope with environmental challenges in the wild. This particular project will focus on the immune defence. In your project you will ask what are the significance of encapsulation response in terms of disease and parasitism resistance, how does it relate to other immunological assays, and if between individual variation influenced by population dynamics? In practice, you will carry out field work in the Ãland Islands archipelago (SW Finland) and conduct experimental work in the laboratory and under semi natural field conditions. There is also potential to use recently developed genomic tools to identify genes involved in immune defence. You are expected to present your findings in scientific meetings and workshops, as well as prepare publications for international scientific journals.

The research group of Dr Marjo Saastamoinen is part of the Metapopulation Research Group, Centre of Excellence appointed by the Academy of Finland, where you'll find a wide range of expertise in ecological and evolutionary questions within a spatial framework.

Please send your application to marjo.saastamoinen@helsinki.fi by 7 June 2013. Attach a CV (with publications included), a copy of your transcript records (= printout of the courses you've completed during your MSc), contact details of two references (e.g. MSc thesis supervisor), and a letter (MAX 1 page) with a description of your researcher interests and why you would be a suitable candidate for the project.

The work is scheduled to start in August 2013. The Phd student will receive a personal researcher grant (2100 per month, 25200 annually). The Kone Foundation grants funding one year at the time, so funding for the successive years need to be applied.

For more information, please contact Dr Marjo Saastamoinen (marjo.saastamoinen@helsinki.fi) and visit the website at (https://tuhat.halvi.helsinki.fi/portal/en/persons/marjo-anna-kaarina-%280d792de9-7077-4683-8e2b-4e15b5e9620d%29.htm). For information on the University of Helsinki, please visit: http://www.helsinki.fi/university/index.html Marjo Saastamoinen, PhD Metapopulation Research Group Department of Biological Sciences PO Box 65 (Viikinkaari 1) FI-00014 University of Helsinki FINLAND

Phone +358 9 191 57741

marjo.saastamoinen@helsinki.fi

UHelsinki InsectImmuneEvolution

PhD position in ecological and evolutionary immunology, Jyväskylä Finland

We are looking for a doctoral candidate to work on ecological and evolutionary immunology of insects.

We study the mechanistic trade-offs between various stress responses, and how environmental variation affects an organism's capacity to fight off infections. Maternal and paternal effects on trans-generational priming of immunity are of special interest. There is increasing evidence that epigenetic mechanisms mediate between environmental factors and phenotypic adaptations. Trans-generational epigenetic inheritance, although still poorly understood, is of great importance as it may help to understand how environment affects innate immunity against pathogens. It can be predicted that organisms can cope better with local, "familiar" stressors and are therefore also better able to fight off the diseases caused by "familiar" pathogens. At the same time, organisms should be less well adapted to foreign, novel pathogens even if those are closely related to the local pathogens.

As a part of this research project the candidate will use the wood tiger moth Parasemia plantaginis to study the host-parasite interaction focusing on how the immune system performs against local pathogens and against cross-infections with novel microorganisms. The position suits an enthusiastic, motivated, and independent graduate whose degree has strong components of entomology, molecular biology and ecology. Experience with molecular techniques (e.g. qPCR, enzyme assays), experimental evolution, and different insect species and microbes is an advantage. The candidate will work as part of a team developing new techniques, carrying out experiments and collecting and analyzing data. The candidate will also be able to work independently, and s/he will have the option to lead small projects which could involve supervising undergraduate students.

The position is based at the Centre of Excellence in Biological Interactions at the University of Jyväskylä, a cutting-edge research community with many opportunities for collaborations world-wide. The candidate will be supervised by Dr. Dalial Freitak and Prof. Johanna Mappes. For additional information please contact Dalial.Freitak@helsinki.fi Applications including a CV, a letter of motivation and contact details of two references should be addressed and sent to Dr. Dalial Freitak, Dalial.Freitak@helsinki.fi. The closing date is 19 July 2013. The position is available immediately.

Dr. Dalial Freitak Postdoctoral researcher University of Helsinki Centre of Excellence in Biological interactions Department of Biosciences Antzz Viikinkaari 1, Biocenter 3 P.O.Box 65, FI-00014 Helsinki. Finland phone: +358-(0)9 191 57812 email: dalial.freitak (at) helsinki.fi web site: www.helsinki.fi/science/ants dfreitak@mappi.helsinki.fi

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ULausanne EvolutionSocialInsects

PhD position: communication and decision-making in social insects, University of Lausanne (Switzerland)

We invite applications for a 3-year SNSF (Swiss National Science Foundation) funded PhD position at the University of Lausanne, Switzerland. We are looking for a highly motivated student to study communication, learning and decision-making in ants and bees. In many social insect species, workers communicate about profitable food sources or nest-sites. Honeybees, for example, use the waggle dance to direct nest-mates to profitable resources. Many ants and tropical bees use pheromone trails. However, not all species communicate about foraging sites and even in species with communication foragers often search for food independently. The project investigates the circumstances that favour different information-use strategies and explores the relationship between flexible individual foraging strategies and colony fitness. The research will include experimental work in and around Lausanne, with a possibility to perform field work in Brazil and/or develop simulation models. The main study animals are honeybees, ants and stingless bees.

We are looking for a candidate with a Masters degree (or equivalent) in Biology and a strong background in behaviour, ecology or evolution. Good English skills and an ability to work independently are important. Experience with social insects, statistical or modelling methods and a basic knowledge of French are helpful but not a requirement.

Supervisors and laboratory: Dr. Christoph Grüter (principal supervisor) & Prof. Laurent Keller, Laboratory of Evolutionary Genetics and Ecology of Social Life, University of Lausanne, Switzerland.

Web Sites: www.socialinsect-research.com, www.unil.ch/dee/page6763.html How to apply: applications include (1) a one-page cover letter describing your motivation, previous research activities and current research interests, (2) a CV, (3) two reference letters and (4) publications (if existing; e.g. MSc thesis). Send all documents except the publications in a single pdf file. Applications must be written in English and should be sent to christophgrueter77@gmail.com before the 15th July 2013. Earliest possible start date is the 1st of September 2013.

Informal enquiries: christophgrueter77@gmail.com

Dr. Christoph Grueter University of São Paulo Faculdade de Filosofia Ciências e Letras de Ribeirão Preto Departamento de Biologia Av. Bandeirantes, 3900 14040-901 - Ribeirao Preto, SP, Brazil Tel: 0055 16 3602 3815 Website: www.socialinsect-research.com Christoph Grueter <C.Grueter@sussex.ac.uk>

ULausanne PhenotypicVariation

University of Lausanne, Department of Ecology and Evolution, Building Biophore, 1015 Lausanne, Switzerland

Supervisor: Prof. Alexandre Roulin Email: Alexandre.Roulin@unil.ch

The evolution and maintenance of phenotypic variation is a central question in evolutionary biology. A commonly suggested mechanism is local adaptation, whereby different phenotypes are adapted to alternative environmental conditions. Ecological parameters vary in space, and the resulting heterogeneity of selective forces can drive adaptive population divergence. Because at the scale of a population variation in ecological factors is usually limited, the study of adaptive phenotypic evolution would be easier if organisms can be studied at a much larger scale. In the present PhD project, we propose to investigate the evolution of a highly variable phenotypic trait (pigmentation) in the barn owl (Tyto alba). This cosmopolite species is found in North, Central and South America, Africa, Europe, Asia and Oceania including many islands. We count 36 barn owl subspecies and 6 species. The aim is to examine the population genetics of this species at the worldwide scale in order to understand how this species spread and examine the relative role of neutral and adaptive processes involved in the evolution of phenotypic diversity within and between populations/subspecies/species. This project has the potential to help understand the build-up of reproductive isolation and the processes leading to speciation.

Prof. Alexandre Roulin Department of Ecology & Evolution Building Biophore University of Lausanne CH-1015 Lausanne Switzerland

Desk 3202 Tel: 0041 21 692 41 89 Mobile: 0041 79 686 08 64 Fax: 0041 21 692 41 65 Website: http://www.unil.ch/dee/page7006.html alexandre.roulin@unil.ch

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ULausanne SocialEvolution

1 PhD position: Sibling negotiation, communication network, social rules University of Lausanne, Department of Ecology and Evolution

We are looking for one PhD student to work on sibling negotiation. Animal communication is often studied by averaging the performance of each participant of a social network, while we expect that individuals adjust their investment in signalling at each moment according to their counterparts and to their likelihood of winning the contest. Using the barn owl as a model species, we want to tackle this issue and study experimentally the dynamics of animal communication. How individual siblings that vocally negotiate prey items invest in the vocal contest: with which sibling do they interact, how, and do the ways they interact with siblings affect their ability to monopolise the food resource? To go further, as social rules that ultimately determine food share have been found, what happens if some siblings do not follow these rules? Is there a social control that prevents cheaters to emerge?

The student will take part in natural population monitoring, setting up and follow up of experiments in laboratory, behavioural observations, acoustic analyses, and elaboration of acoustic tools in collaboration with acousticians.

Eligibility: Dynamic and motivated student holding a master in ecology and or related disciplines. The applicant is expected to have a good knowledge (spoken and written) of the English language. Driving license is needed. The duration of the PhD training period is three full years.

Applications should comprise a CV, a letter explaining the motivation and one or two letters of reference The position will be filled as soon as a suitable candidate is found.

The Department of Ecology and Evolution is a well-funded institution, one of the largest and most reputed departments in this field. We have a dynamic doctoral school and a doctoral program for the different Swiss universities.

Contact: University of Lausanne, Department of Ecology and Evolution, Building Biophore, 1015 Lausanne, Switzerland

Supervisors Prof. Alexandre Roulin, Alexandre.Roulin@unil.ch Dr. Amélie Dreiss, Amelie.Dreiss@unil.ch

Prof. Alexandre Roulin Department of Ecology & Evolution Building Biophore University of Lausanne CH-1015 Lausanne Switzerland

Desk 3202 Tel: 0041 21 692 41 89 Mobile: 0041 79 686 08 64 Fax: 0041 21 692 41 65 Website: http://www.unil.ch/dee/page7006.html alexandre.roulin@unil.ch

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ULaval GenomicsBehaviouralManipulation

PHD POSITION: GENOMIC AND PROTEOMIC MECHANISMS OF BEHAVIOURAL TAKE-OVER OF STICKLEBACKS BY A PARASITIC FLATWORM

We are looking for a motivated student to join our team to work on the ecological genomics of host-parasite interactions at UNIVERSITÉ LAVAL, Quebec City, Canada. Our labs are part of the Biology Department and are located in the INSTITUTE OF INTEGRATIVE AND SYSTEMS BIOLOGY. The PhD position offered is part of a FRQNT-Équipe project (Quebec, Canada) to study the interaction between the genomes of the threespine stickleback (Gasterosteus aculeatus) and of its flatworm parasite (Schistocephalus solidus). The project leaders are Dr. Nadia AUBIN-HORTH (behavioural genomics and neuroendocrinology) & Dr. Christian LANDRY (bioinformatics, evolutionary genomics and proteomics). We work in collaboration with Dr. Iain BARBER (evolution of host-parasite interactions and their consequences) from University of Leicester.

PROJECT: Sticklebacks parasitized by the cestod flatworm do not show the normal behavioural response to predation risk and, as a consequence, are more frequently captured by their bird predator. These behaviour modifications are often presented as adaptations of the parasite to enhance transmission rates to its final bird host in order to complete its life cycle, as the changes in stickleback behaviour occur specifically when the flatworm is ready to mature in its final host, suggesting a stage-specific active manipulation by the parasite. However, we know very little about the molecular mechanisms that underlie this host-parasite interaction. Our team aims to answer questions about the molecular changes happening in the host and the parasite and how their genomes interact.

Motivated students with a MSc degree in life sciences (ecology, evolution, molecular biology or other related fields) are encouraged to apply. A strong interest for an INTEGRATIVE APPROACH, combining novel tools in GENOMICS, PROTEOMICS and BIOINFORMATICS with BEHAVIOURAL ASSAYS and pharmacological manipulation and working actively in a team is a must. Prior experience in animal behaviour, endocrinology, molecular biology, genomics, proteomics, bioinformatics or statistical analysis is an advantage. A PhD fellowship is available for 3 years for the chosen candidate.

To apply, please send an email including a CV, a letter describing your research experience in link with the project and your research interest, your diplomas and transcripts, and the names and email addresses of 3 references (including your M.Sc. Advisor). Applications will be accepted until July 15, 2013 or until a candidate is selected. The position will start in September 2013. For more information about the position, please feel free to contact the head of the team, Dr. Nadia Aubin-Horth (Nadia.Aubin-Horth@bio.ulaval.ca). For more information about the labs, see: http://wikiaubinhorth.ibis.ulaval.ca/Main_Page http://www.bio.ulaval.ca/landrylab/en/pmwiki.php Nadia Aubin-Horth Associate professor Biology Department Institute of Integrative and Systems Biology Laval University Quebec City (QC) G1V 0A6 Canada

Aubin-Horth Nadia <Nadia.Aubin-Horth@bio.ulaval.ca>

ULeuven MarineEvolution

University of Leuven - PhD studentship in Biological Sciences on Connectivity in marine flatfish populations

The Laboratory of Biodiversity and Evolutionary Genomics (LBEG: http://bio.kuleuven.be/eeb/lbeg), Department of Biology, University of Leuven, Leuven, B invites applications for a 4-year PhD studentship recently awarded by the Research Foundation Vlaanderen and linked to the project FISHCONNECT.

Background: The primary focus of the research project FISHCONNECT is to disentangle the influence of regulatory (oceanographic) and adaptive (biological) factors on connectivity in flatfish through an integrated empirical and modeling approach.

Aims and objectives: The aim of the PhD project is to trace back the postlarval stages of four flatfishes to the spawning grounds with genetic and demographic tracing methods. At the moment a first PhD fellow has started work on the ecology and demography of postlarval flatfish. A third PhD fellow who will further develop an integrated hydrodynamical-biological model is also being recruited (see www.mumm.ac.be). We are looking for a multidisciplinary fellow with a background and interest in field and lab-based fish(eries) biology and genetics combining at least two of the following topics (evolution, population genomics, fish biology, modeling). The successful candidate will be involved with ship and shore based fieldwork, data collection, molecular/genetic methodology, morphometric and genetic data analysis and manuscript writing.

Requirements and elegibility: Applicants are required to hold a MSc in Biological sciences, bio-engineering or related fields and excellent study records. The PhD fellow will work collaboratively with two other PhD fellows, exchanging ideas and skills during the course of the project. The PhD fellow will work in team with a senior scientist, a postdoc and graduate students at the KU Leuven. The project requires skills in (molecular) biology, biostatistics, modeling, data banking and IT. In addition to the primary research responsibilities, duties will include assisting and mentoring undergraduate students, some teaching in Bachelor courses and the organization and management of large datasets.

Host details: Leuven is a pleasant and high-quality medium-sized town. The KU Leuven, founded in 1425 is the largest and most research intensive university of Belgium. LBEG focuses on the neutral and adaptive evolution of fish and their parasites.

Relevant papers include

Lacroix G., Maes G.E., Bolle L.J., Volckaert F.A.M. (2013) Modelling dispersal dynamics of the early life stages of a marine flatfish (Solea solea L.). Journal of Sea Research 75: 00-00;

Nielsen E.E., Cariani A. Mac Aoidh E., Maes G.E., ... , Diopere E., Volckaert F.A.M. Waples R.S., FishPopTrace consortium, Carvalho G.R., (2012) Gene-associated markers provide tools for tackling IUU fishing and false eco-certification. Nature Communications 3:851;

Volckaert F.A.M. (2012) (Flat)fish stocks in an ecosystem and evolutionary perspective. Journal of Sea Research 75: 19-32;

Cuveliers E.L., Volckaert F.A.M., Rijnsdorp A.D., Larmuseau M.H.D., Maes G.E. (2011). Temporal genetic stability and high effective population size despite fisheries-induced life-history trait evolution in the North Sea sole. Molecular Ecology 20: 3555-3568.

Interested candidates should e-mail Prof. Filip Volckaert (filip.volckaert@bio.kuleuven.be) for informal inquiries. Please apply formally at the KU Leuven Arenberg Doctoral School https://phd.kuleuven.be/set with a motivation letter (past research projects and interests), study transcript, two letters of reference and CV by 08 July 2013. Interviews are scheduled in the week of 15 July 2013. The expected start is 1 September 2013.

Filip Volckaert <Filip.Volckaert@bio.kuleuven.be>

UMuenster EvolutionGeneTranscription

PhD position Evolution of gene transcription in Arabidopsis , Lab Juliette de Meaux, Münster, Germany

I am looking for a highly motivated PhD student to study the evolution of cis-regulatory DNA in the genus Arabidopsis.

Our research seeks to reconstruct the recent history of adaptive molecular variation in the genus Arabidopsis. We are especially interested in the accurate characterization of adaptively relevant variation. Our ultimate goal is to understand the molecular basis of adaptation in plants. In this framework, the project of the PhD student will be to determine the role of regulatory evolution in phenotypic adaptation, via the combined analysis of functional and nucleotide variation in gene expression in the Arabidopsis genus. The project will entail bioinformatics and genomics approach and the outcome will be experimentally validated.

Applicants must hold a Diploma/Master degree and prove advanced education in genomics, bioinformatics or population genetics. Proficiency in English is required. Applications of women are specially invited; in the case of similar qualifications, competence and specific achievements, women will be considered on preferential terms, within the framework of the legal possibilities. Handicapped candidates with equivalent qualifications will be given preference. Applications (CV, letter of motivation, and contact of two referees) should be sent to juliette.de.meaux@uni-muenster.de. The examination of applications will begin immediately until the position is filled. The position is for three years. Starting date can be adjusted to your availability.

For more information on our research, refer to our website (http://ieb.uni-muenster.de/plantmolevol).

The IEB in Münster is unique in Germany (http://ieb.uni-muenster.de/). It runs the Münster Graduate School of Evolution which is at the forefront of education and research in diverse sectors of evolutionary biology, from evolutionary ecology to phylogenetics, population genetics and evolutionary bioinformatics (http://ieb.uni-muenster.de/mgse/). This interdisciplinary environment promises to bring you a highly interactive environment in which both your theoretical and experimental skills can be harmoniously developed.

Münster is a multi-faceted city. It is a city of science and learning. Münster, Westphalia's longstanding regional capital, is a young city; one of 7 of its inhabitants is either studying or employed by university and half of its inhabitants are below 30 years of age. Münster is a forerunner in the field of environment and climate protection. It is Germany's bicycle metropolis with more bikes than inhabitants, more than 250 kilometres of bicycle paths and an underground bicycle parking area in front of the main train station. High-tech and traditional trade coexist in this city, as well as baroque noble residences and modern architecture, with a historical city centre and progressive urban development. Münster guarantees you the highest quality of life!

juliette.de.meaux@uni-muenster.de

UNorthernBritishColumbia FrogEvolution

Graduate Opportunity (PhD)

Distribution Ecology and Landscape Genetics of Coastal Tailed Frog

We are recruiting a PhD student to investigate the distribution ecology of post-metamorphic tailed frogs in northwestern, British Columbia, Canada. The work will be conducted in a landscape containing four experimental watersheds, each with three replicated treatments representing forest harvest and retention. We anticipate methods that incorporate both observational and genetic data and explain the connectivity of populations of tailed frog within and across watersheds. Each treatment site has a permanent installation of directional pitfall traps and we are successful in using radiotelemetry to locate this species. Given the breadth of this project and the paucity of research on the ecology of post-metamorphic tailed frog, there will be considerable opportunities for students to direct specific research questions and methods. Results of this study will improve our understanding of the ecology of tailed frog and provide guidance for the protection, management, and restoration of headwater forests. We expect direct application of findings to the development or improvement of best management practices to mitigate the impacts of forest harvesting and linear corridors.

The qualified student will attend classes at the Prince George campus of the University of Northern BC. UNBC is a small, but dynamic research intensive university (www.unbc.ca). The Prince George area offers abundant outdoor recreation activities. Please see our website for more information on the Natural Resources and Environmental Studies Graduate Program including degree requirements and expectations (www.unbc.ca/nres/). Research activities will be conducted at permanent study sites near Terrace, BC. The the student will be expected to live in Terrace (http://www.visitterrace.com/) when collecting field data (May to September).

Qualifications: This is a challenging, but rewarding project requiring a range of interests and aptitudes. Preferably, the successful applicant will have a degree in biology or ecology. The student should be willing to work in a collaborative environment with multiple research partners coming from both government and industry. This study requires intensive field work throughout the summer and early fall. Demonstration of field-based competencies (e.g., GPS operation, compassing, backcountry safety/skills) is an asset as well as a desire to get dirty and potentially work long hours. Also, the student should have an interest or experience in field ecology, landscape genetics, and GIS.

The successful student should be prepared to spend a portion of this summer (2013) working at the study sites with a program start date of September 2013. Research funding for the first two years of the project will be confirmed within the next month. We anticipate a competitive stipend ($25,000) and funding to support field and lab activities.

For further information please contact Dr. Chris Johnson, (johnsoch@unbc.ca; 1-250-960-5357;

http://web.unbc.ca/˜johnsoch) or Dr. Brent Murray (murrayb@unbc.ca; 1-250-960-5638;

http://web.unbc.ca/˜murrayb).

Brent Murray <Brent.Murray@unbc.ca>

UQueensland TheoreticalEvolutionaryBiol

The newly established evolutionary genetics group of Jan Engelstädter at The University of Queensland (Brisbane, Australia) invites applications for a PhD position in theoretical evolutionary biology. We are interested in the evolution of sex and recombination, host-parasite coevolution and the evolution of antibiotic resistance. Different PhD projects from these research areas involving mathematical modelling are available or can be developed together with the successful candidate. For details about our research, see our website at http://engelstaedterlab.org/ . We are looking for a motivated student with either a strong background in evolutionary biology or strong quantitative skills. Applicants should possess a Bachelor's degree with Honours, Master of Science, MPhil or equivalent. Candidates with a non-biology degree (mathematics, physics, computer science) are especially encouraged to apply. Good communication skills, scientific curiosity and enthusiasm for research in evolutionary biology are essential.

Funding can be obtained through a competitive international PhD scholarship scheme for overseas students interested in undertaking PhDs in the School of Biological Sciences at The University of Queensland. For more information about this scholarship scheme as well as formal requirements for PhD students and The School of Biological Sciences at UQ, see below.

Interested candidates should send a cover letter describing their motivation and research interests, CV, copy of degrees, and contact information for two academic references to: j.engelstaedter@uq.edu.au.

Jan Engelstädter School of Biological Sciences The University of Queensland Brisbane QLD 4072 Australia

phone: +61 7 336 57959 fax: +61 7 336 51655 http://engelstaedterlab.org/ International PhD Scholarships in Biology at UQ

The School of Biological Sciences is a large and research intensive unit at the University of Queensland, one of Australia's most prestigious Universities. The School has broad expertise across the disciplines of ecology and evolution, molecular and quantitative genetics, developmental biology, behaviour, plant and animal physiology, and conservation biology. Our research programs span all scales of biological organisation, from molecules and cells, to organisms, populations, species and communities, and take advantage of study animal and plant systems in a large variety of habitats (see http://www.biology.uq.edu.au/ for detailed information on our research programs). The School is very pleased to announce a new initiative that has made available a number of PhD scholarships for talented International students who enroll in our PhD program in 2013.

Qualifications Applicants should possess a Bachelor's degree with Honours, Master of Science, MPhil or equivalent, and must be accepted into the PhD program at the University of Queensland. The UQ Graduate School website provides further information on the entry requirements for admission to the PhD program (http://www.uq.edu.au/grad-school/our-research-degrees).

Remuneration Living stipend (scholarship) of $24,653 per annum for 3 years which is tax free, with the possibility of a 6 month extension. International students normally pay international student fees of $32,200 per year, however individuals successful in gaining one of these scholarships will also be granted a full tuition-fee waiver.

The Application Process Interested students should identify potential supervisors within their research area of interest (http://www.biology.uq.edu.au/academic-staff) and contact them to discuss potential projects. Strong candidates will be invited to apply for entry to the PhD program, and if accepted into the program will be considered for the School of Biological Sciences International Scholarships on a competitive basis.

Enquiries For further information on the application process please contact the Postgraduate Administration Officer Gail Walter gj.walter@uq.edu.au

j.engelstaedter@uq.edu.au

UWesternOntario 2 EvolutionaryPhysiology

Evolutionary Physiology in the cold: 2 PhD studentships

Several PhD positions available in the Sinclair lab, Department of Biology, University of Western Ontario.

1.Evolutionary physiology of insect freeze tolerance.This project will use a combination of transcriptomics and physiology to determine the common factors that allow some insects to withstand internal ice formation.

2.Overwintering adaptations associated with the northward spread of the invasive land snail /Cepaea nemoralis/.This project will use a combination of physiology and population genetics to examine evolutionary change in cold tolerance of an invasive snail whose geographic range is expanding beyond that predicted from its native distribution in Europe.In collaboration with Dr. Annegret Nicolai.

The Sinclair lab is a vibrant, social and diverse group of individuals dedicated to understanding how winter drives natural processes.We are question-driven, and use a wide range of techniques, and interact with a broad range of collaborators in Canada and abroad.The Sinclair lab provides an exceptional training environment, and members have enjoyed success, winning scholarships, awards... and occasionally even jobs!

The Department of Biology has a large graduate programme that provides competitive stipends, flexible start dates, excellent training and sensible times-to-completion.The University of Western Ontario is located in London, Ontario, Canada, and has over 5000 graduate students on a beautiful urban campus.London, situated mid-way between Detroit and Toronto, has a population of 450,000, a thriving arts scene, and all amenities expected for a city its size.

Exceptional students from any nationality are encouraged to apply, however, applications from Canadian citizens and permanent residents are especially encouraged.For more information, visit publish.uwo.ca~bsincla7, or contact Dr. Brent Sinclair, bsincla7@uwo.ca. Applications should include a cover letter, CV and unofficial copy of an academic transcript (a scanned version is fine) and should be received by August 31, 2013.

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Dr Brent Sinclair Associate Professor, Department of Biology Biological & Geological Sciences Room 2078 (Lab: Room 2056) University of Western Ontario, 1151 Richmond St N, London, Ontario N6A 5B7

bsincla7@uwo.ca tel: 519-661-2111 ext 83138; Fax 519-661-3935 http://publish.uwo.ca/~bsincla7/ Come to ISEPEP5! 12-16 August, 2013, London, ONtario, Canada http://www.uwo.ca/biology/ISEPEP5/ Brent Sinclair <bsincla7@uwo.ca>

UWisconsin Madison EvolutionaryGenomics

Ph.D. Positions in Evolutionary Genomics

The research group of John Pool at the University of Wisconsin - Madison is seeking one or two Ph.D. students to start in the Fall 2014 academic year.

A brief summary of our research can be found here: http://www.genetics.wisc.edu/user/338 More information about the lab is at: http://johnpool.net/ Our work offers the opportunity to study genetic variation at the scale of whole genomes. We also use population genomic data to identify the genetic basis of adaptive phenotypic evolution within the genetics model species, Drosophila melanogaster. The Pool lab currently includes four postdoctoral researchers and six undergraduates. I can offer training in some of the most sought-after scientific skills in modern evolutionary genomics, and I can devote ample time to each student's scientific development.

Interested students should apply (by December 1) to the UW Genetics Ph.D.program: http://www.genetics.wisc.edu/node/15 Students typically rotate in three labs during their first semester before choosing an advisor. The Genetics program has an especially strong contingent of faculty with evolutionary interests, including:

David Baum http://www.genetics.wisc.edu/user/14 Karl Broman http://www.genetics.wisc.edu/user/333 Cameron Currie http://www.genetics.wisc.edu/user/80 Sean Carroll http://www.genetics.wisc.edu/user/22 John Doebley http://www.genetics.wisc.edu/user/28 Bill Engels http://www.genetics.wisc.edu/user/33 Audrey Gasch http://www.genetics.wisc.edu/user/37 Chris Hittinger http://www.genetics.wisc.edu/user/329 Carol Lee http://www.genetics.wisc.edu/user/56 Laurence Loewe http://www.genetics.wisc.edu/user/316 Bret Payseur http://www.genetics.wisc.edu/user/63 Caitlin Pepperell http://www.genetics.wisc.edu/user/372 Nicole Perna http://www.genetics.wisc.edu/user/65 John Pool http://www.genetics.wisc.edu/user/338 Sushmita Roy http://www.genetics.wisc.edu/user/373 Don Waller http://www.genetics.wisc.edu/user/74 A more complete list of evolution faculty at UW Madison is available through the J. F. Crow Institute for the

Study of Evolution: http://www.evolution.wisc.edu/ Financial support for Genetics PhD students is available from training grants, research assistantships, and teaching assistantships (one semester of teaching is required).

Madison offers an exceptional quality of life in a beautiful natural setting. Downtown and campus are bordered by lakes, and the area includes a number of long distance bike trails. Madison features diverse art, music, and cultural offerings. A great farmers market and a focus on local food are complemented by a wide range of international restaurants.

Students with a particular interest in my lab are encouraged to contact me before applying: jpool@wisc.edu

John Pool Assistant Professor Laboratory of Genetics University of Wisconsin-Madison

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UppsalaU SexualConflict

PHD POSITION IN EVOLUTIONARY BIOLOGY: Sex, genes and conflict in novel environments

Uppsala University hereby invites applications for a Postgraduate PhD position in Animal Ecology at the Department of Ecology and Genetics, Evolutionary Biology Centre (EBC) with a tentative starting date being October 1st, 2013, or as soon as possible after this date.

BACKGROUND: Males and females have distinct life styles and experience different selection pressures. These differences in selection have likely given rise to many of the striking sexual dimorphisms in life history, morphology and behaviour observed across animal taxa. There are however good reasons to believe that, typically, the evolution of pronounced sex-differences is severely constrained by the fact that males and females share most of their genome. Genes that have net benefits to one sex therefore often inflict costs when expressed in the other. The result is a genetic conflict over optimal male and female phenotypes, with potentially grave and wide-ranging evolutionary consequences. This form of sexual conflict is a key focus of current evolutionary research and is predicted to be a crucial mechanism maintaining genetic variation within populations, imposing demographic costs to natural populations, and setting limits to rates of adaptation.

OBJECTIVE: The focus of this project is to understand how new mutations and cryptic genetic variation affect male and female phenotypes, and how adaptation from these sources of genetic variation influence male and female evolution and the importance of sexual conflict in novel environments. The successful candidate will utilize insect model systems to perform quantitative genetic breeding designs and/or laboratory evolution experiments, to estimate genetic architecture and selection on important fitness traits in males and females. It will also be possible to combine quantitative genetic data with genome sequence data, to link variation in male and female phenotypes to variation at the molecular level. This PhD position forms a part of a new project on genetic conflict, funded by the European Research Council and the Swedish Research Council. The entire project employs some 7-8 PhD students and postdocs, as well as a full time research engineer, a research professor and a se nior PI, and strongly encourages interactions and collaborations within the group. Dr. David Berger and Prof. Göran Arnqvist will act as supervisors for the successful applicant.

WORKING PLACE: The Evolutionary Biology Centre hosts one of the world's largest aggregations of evolutionary biologists, and is a prime research environment for a wide range of fields in evolutionary biology (see "http://www.ebc.uu.se/" for more information). The working atmosphere is very international with English as our operational language. Our graduate school offers a creative and stimulating environment and offers a rich variety of seminars, journal clubs, courses and many possibilities to interact with other scholars and students (see "http://www.ebc.uu.se/education/-"). Graduate students recently ranked Uppsala University in first place among all institutions in Europe in the subject of biology (CHE European ranking). Uppsala University is the oldest university in Scandinavia and the city of Uppsala is a vibrant college town with beautiful surroundings conveniently situated 40 minutes by train from Stockholm.

ELIGABILITY: The successful candidate should have a relevant MSc/BSc degree (or equivalent) in biology/genetics/ecology.

QUALIFICATIONS: We seek highly motivated candidates with a broad interest in evolutionary biology. Experience in quantitative and/or population genetics or in life-history- and sexual selection theory is an advantage. Experience in using statistical software (e.g. R, SAS, Genstat) is a merit. Because the holder of this position will collaborate and interact closely with other members of the group, we will put emphasis on both independence and ability to collaborate. The applicant is expected to have a good knowledge (spoken and written) of the English language.

SALARY AND APPOINTMENT: The duration of the PhD training period is four full years. The successful candidate will be employed on a postgraduate PhD position (following current agreements, salary is starting at 23.100 and ending at 27.500 SEK/month) which entitles the holder to full social benefits.

FURTHER INFORMATION: please contact Dr. David Berger (tel. 018-471 6428, email: david.berger@ebc.uu.se). Union representatives are Anders Grundström, Saco-rådet, phone. +46-18-4715380; Carin Söderhäll, TCO/ST, phone. +46-18-4711996, Stefan Djurström, Seko, phone. +46-18-4713315.

See also:

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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

UppsalaU SexualConflict CorrectLink

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SALARY AND APPOINTMENT: The duration of the PhD training period is four full years. The successful candidate will be employed on a postgraduate PhD position (following current agreements, salary is starting at 23.100 and ending at 27.500 SEK/month) which entitles the holder to full social benefits.

FURTHER INFORMATION: please contact Dr. David Berger (tel. 018-471 6428, email:david.berger@ebc.uu.se). Union representatives are Anders Grundström, Saco-rÃdet, phone. +46-18-4715380; Carin Söderhäll, TCO/ST, phone. +46-18-4711996, Stefan Djurström, Seko, phone. +46-18-4713315.

See also:

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Vigo Spain EvolutionaryBiol

Master in Biological Sciences (MBS) at the University of Vigo, Spain

We are pleased to announce the launch of the *Master in Biological Sciences (MBS) of the University of Vigo (Spain)* for the *academic year 2013-2014*. The MBS aims to provide future professionals in biology with the knowledge, skills and insights they will need to take on top science-based positions around the world (academic, research, environmental and biomedical applications, bioinformatics).

The* official language of the MBS is English*. Non-English speaking students must demonstrate that they have acquired the minimum language skills to study the Master. No additional proof is required, although holding a B1 or equivalent title would be desirable. In addition, personal interviews with members of the Academic Commission might be required before admission.

The staff teaching in this master cover a wide range of areas giving students contact with renowned researchers, specialists in developing professional skills and practitioners from industry. They all have long-term teaching experience.

For those students interested in doing a PhD, there are two Doctorate Programmes linked to the MBS, and rated as excellent from the Spanish Education Ministry

* *

Master outline

The MSc programme comprises *120 ECTS in total distributed between 2 academic years *(60 ECTS each one). During the 1st year, students will follow 4 general courses (*Basic Module, 12 ECTS)* on basic tools for designing and performing experimental tasks, analysing results and elaborating conclusions. This will be followed by the *Elective Component (42 ECTS) *where students will have the chance to follow specific tracks:

1. Molecular Biology for Health and Life Sciences 2. Environmental Sciences 3. Bioinformatics and Computational Biology 4. Green-Industries Management

The main part of the second year consists of a major project (*Mandatory Major Project 48 ECTS*), in which students will acquire advanced knowledge on different methodologies and techniques under the guidance of experienced experts to fulfil your professional requirements and possibly to gain a better position on the job market.

Finally, all students need to carry out a *Master's thesis (12 credits).*

APPLICATION for academic year 2013-14

- First pre-registration period: 28 June to 4 July 2013

- Second pre-registration period: 27 August to 3 September 2013

* *

DOCUMENTS that must accompany the application form:

- DNI, NIE or Passport

- Bachelor's degree diploma

- Brief CV

CONTACT

María JesÃºs Iglesias Briones (coordinator)

mbriones@uvigo.es

Master in Biological Sciences

Facultad de Biología Campus Lagoas-Marcosende Universidad de Vigo 36310 Vigo, Spain.

FURTHER INFORMATION

http://biology.uvigo.es Armando Caballero

<armando@uvigo.es>

iDiv Germany PlantAntagonism

The German Centre for Integrative Biodiversity Research (iDiv) is one of the seven National Research Centres funded by the German Research Foundation (DFG). It is located in the city of Leipzig and jointly hosted by the Martin Luther University Halle-Wittenberg (MLU), the Friedrich Schiller University Jena (FSU), the University of Leipzig (UL) and the Helmholtz Centre for Environmental Research (UFZ). It is supported by the Max Planck Society, the Leibniz Association, the Klaus Tschira Foundation and the Free State of Saxony. Its central mission is to promote theory-driven synthesis and data-driven theory in this emerging field. The concept of iDiv encompasses the detection of biodiversity, understanding its emergence, exploring its consequences for ecosystem functions and services, and developing strategies to safeguard biodiversity under global change. Embedded in the active research environment of iDiv, the Young BioDiversity Research Training Group (yDiv) will be established. Its goal is to educate a new generation of scientists in transdisciplinary biodiversity research, who will have gained expertise both in experimental as well as theoretical fields of research.

The University of Leipzig offers the following position:

Doctoral fellowship (initially limited to 3 years, 65 percent of a full-time employment) Salary: Entgeltgruppe 13 TV-L on“The importance of antagonistic interactions for plant species coexistence and ecosystem functioning”

Topic/job description:

*conduct ecological field experiments in grassland ecosystems (manipulate plant species abundance, insect herbivory, and pathogen attack) to study mechanisms of plant species coexistence * carry out greenhouse experiments, e. g. to investigate competition-defense tradeoffs and negative feedbacks with pathogens * apply advanced molecular techniques to identify fungal taxa

Requirements / expected profile:

* an excellent Master’s or Diploma degree in a relevant field of research * experience in experimental ecology, including the design and statistical analysis of ecological experiments * strong interest in conceptual issues in ecology * good use of spoken and written English and ambition to publish in international journals * experience in sequencing techniques is advantageous

We offer you a PhD position, affiliated with the University of Leipzig and supervised by Prof. Christian Wilhelm, department of Plant Physiology, Institute of Biology/University of Leipzig (http://www.uni-leipzig.de/~ pflaphys < http://www.uni-leipzig.de/%7Epflaphys >).

Applications are accepted until July 01, 2013.

All applications should include:

- filled application form (download under http://www.idiv-biodiversity.de/ydiv/positionsjobs - cover letter describing research interests & relevant experience - curriculum vitae - one letter of recommendation - MA/BA/Diploma certificates

Applications should be directed to the yDiv coordinator Dr. Jula Zimmermann (ydiv@idiv-biodiversity.de <mailto:ydiv@idiv-biodiversity.de>) in a single PDF file with reference file number (106/2013) in the subject line.

We prefer applications in electronic form (hard copy applications can be sent to Dr. J. Zimmermann; German Centre for Integrative Biodiversity Research - iDiv; Deutscher Platz 5e; 04103 Leipzig)

For queries on the application process please contact ydiv@idiv-biodiversity.de <mailto:ydiv@idiv-biodiversity.de>

–

*Dr. Jula Zimmermann *

/Scientific Coordinator of the Graduate School - yDiv / Wissenschaftliche Koordinatorin der Graduiertenschule - yDiv German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig/

//iDiv_Logo

Phone +49(0)341-97-33125 Fax +49(0)341-97-31264 Email jula.zimmermann@idiv-biodiversity.de<mailto:friederike.heinze@idiv-biodiversity.de>

German Centre for Integrative Biodiversity Research(iDiv) Halle-Jena-Leipzig Deutscher Platz 5d 04103 Leipzig Germany

iDiv ist ein Forschungszentrum der Deutschen Forschungsgemeinschaft (DFG). Es ist eine zentrale Einrichtung der Universität Leipzig im Sinne des §92 Abs. 1 SächsHSFG und wird zusammen mit der Martin-Luther-Universität Halle-Wittenberg, der Friedrich-Schiller-Universität Jena sowie dem

Helmholtz-Zentrum für Umweltforschung (UFZ) betrieben. Sieben außeruniversitäre Einrichtungen unterstützen iDiv finanziell sowie durch ihre Expertise: das Max-Planck-Institut für Biogeochemie (MPI BGC), das Max-Planck-Institut für chemische Ökologie (MPI CE), das Max-Planck-Institut für evolutionäre Anthropologie (MPI EVA), das Leibniz-Institut Deutsche Sammlung von Mikroorganismen und Zellkulturen (DSMZ), das Leibniz-Institut für Pflanzenbiochemie (IPB), das Leibnitz-Institut für

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Jobs

BarnardC NY Teaching 2013-2014

Adjunct or Term Assistant Professor

The Barnard College Department of Biology seeks a visiting Assistant Professor for the 2013-14 academic year. Teaching duties in the fall semester include a course in animal behavior, a senior seminar on a topic in the candidates area of specialty, and instructional support in running a large Introductory Biology lab that focuses on physiology and ecology. Highly qualified individuals will be considered for a one-year full-time Term Assistant Professor appointment that requires the candidate to teach two additional courses in Spring 2014 on topics to be determined. A Ph.D. and teaching experience are required. Applicants should send curriculum vitae, a teaching statement, and three letters of recommendation to: biologyjob@barnard.edu. Review of applications will begin on 15 July 2013. Barnard College is an Equal Opportunity Employer and encourages applications from women and individuals from underrepresented groups.

Hilary Callahan Associate Professor, Department Chair Department of Biological Sciences 1007 Altschul Barnard College, Columbia University 3009 Broadway New York, NY 10027 212-854-5405

Heredity is nothing but stored environment. < http://www.searchquotes.com/quotation/Heredity_is_nothing_but_stored_environment./96519/ >

Luther Burbank

Hilary Callahan <hcallaha@barnard.edu>

MaxPlanck FishTechnician

Stickleback Fish Husbandry Technician, Jones Lab, Friedrich Miescher Laboratory of the Max Planck Society, Tuebingen Germany.

The research group of Felicity Jones at the Friedrich Miescher Laboratory of the Max Planck Society is looking for a motivated Animal Husbandry Technician - Fish (Full time).

Our lab investigates the molecular mechanisms of adaptation and speciation in threespine stickleback fish. Using functional genetics and genomics we aim to understand the molecular changes that contribute to phenotypic differences, affect individual fitness and play a role in adaptive divergence.

Your responsibilities: You will be responsible for the feeding, care, husbandry and maintenance of threespine stickleback fish in a new aquarium facility. You will be actively involved in the day-to-day running of the facility including the administering of food, monitoring of animal health, water chemistry changes, aquarium cleaning, and record keeping in a husbandry database. Basic knowledge and experience working with fish husbandry would be advantageous. As we study natural populations of sticklebacks, your help and participation in field collections may occasionally be required.

Our requirements: We are looking for a reliable, enthusiastic and motivated individual with training in animal husbandry, biological sciences or similar qualification. Prior experience with fish husbandry and technical running of aquatic facilities (handling, crossing, breeding, care, and water chemistry) would be advantageous but not required. The ability to carry out clean and physically demanding work is an absolute requirement. Willingness to learn and troubleshoot new techniques is important. Experience or understanding of basic genetics would be helpful, but is not necessarily a requirement. We expect from you interest and enjoyment in basic research, goal-oriented and self-motivated work ethic, flexibility and the readiness to learn new skills. English communication skills would be useful, as English is the working language in our lab.

We offer: interesting work in an interdisciplinary team with young scientists, and international atmosphere and excellent lab working conditions. We will provide comprehensive on-the-job training. We offer remuneration in accordance to the TVöD standard based on qualification and previous experience. The position is initially limited to 2 years, with the possibility of extension. The Max Planck Society is committed to employing more women in the various jurisdictions in which they are underrepresented. Qualified women are therefore particularly being encouraged to apply. The Max Planck Society is committed to the employment of disabled people. With equal qualifications preference will be given to those with a disability.

Application deadline: 07 July 2013. Please send your applications with CV and contact details of at least two referees by post or e-mail to:

Dr. Felicity Jones Friedrich Miescher Laboratory of the Max Planck Society Spemannstrasse 39 72076 Tübingen Germany fcjones@tuebingen.mpg.de http://www.fml.tuebingen.mpg.de/jones-group.html jones.floss@gmail.com

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Norway AnimalGenetics

NordGen is seeking a senior advisor/scientist for NordGen Farm Animals

NordGen offers an interesting position with variable and challenging work in conservation and sustainable management of farm animal genetic resources in the Nordic and international arena.

NordGen is seeking a person with a strong interest in farm animal genetic resources, with higher academic education (MSc or PhD) in population genetics, conservation genetics, quantitative genetics and/or animal breeding or related disciplines. Working experience obtained from research and development, animal breeding organizations, conservation organisations, international processes and networking and/or public administration is appreciated. Strong English communication skills are required as well as knowledge of one of the Scandinavian languages.

Main responsibilities:

- Knowledge and capacity building within sustainable use and conservation of farm animal genetic resources in collaboration with universities, international organizations, conservation and breeding organizations. - Project development and initiation - Project participation, management and communication. - Contribution to the development of networks with Nordic and international stakeholders and promotion of current networks through workshops, seminars and meetings. - Participation in the information and communication tasks (presentations, publications) and production of information materials for NordGen's website Acting as coordinator and secretary of NordGen Farm Animals projects and working groups. - Contribution to meetings, seminars and the daily team-based work of NordGen Farm Animals and at NordGen's headquarters.

The position requires some travelling.

NordGen offers:

- An exciting position in a professional and international working environment.

Employment contract according to the regulations of the Nordic Council of Ministers. The employment contract will be signed first for 4 years with the possibility for an additional 4 years.

- Salary according to individual agreement, other working conditions are given by the regulation of the employment agreements of the State of Sweden. - Possibilities to develop personal competence.

The post is located at the Norwegian Forest and Landscape Institute, Ås, Norway. The number of employees of NordGen-Farm Animals is three persons. The senior advisor will report directly to Head of NordGen Farm Animals.

Information about the position can be obtained from Director Árni Bragason, +46738171215 or +4640536644 or Head of NordGen Farm Animals, Dr. Peer Berg, +47 6494 9790 or +47 4062 4469

Applications, including CV and references should be sent *no later than August 2, 2013 *to Nordic Genetic Resource Center, jobb@nordgen.org or to the mailing address: NordGen, Arni Bragason, P.O. Box 41, SE-23053 Alnarp, Sweden.

See also:

http://www.nordgen.org/index.php/en/Innehaall/-About-NordGen/Job-vacancies/Senior-Advisor-NordGen-Animal Kind Regards

Peer Berg Section Leader NordGen Farm Animals *NordGen - Nordic Genetic Resource Center* www.NordGen.org E-mail: Peer.Berg@nordgen.org Phone: +47 6494 9790 Mobile: +47 4062 4469

peer.berg@nordgen.org

R-programming animations

Job: R-programming and Flash Animations

Programming needed for animation of figures for the online version of an advanced text on phenotypic evolution. Rough programs in R will be provided for original, static figures. The task is to modify these programs so that the figures are animated in particular ways and those animations can be posted on a text website. Contracts can be let and work conducted at a distance. Contractor must not be an employee of Oregon State University. Funding is in place for about 1,000 hours of programming work. For additional detail contact Stevan J Arnold at

arnolds@science.oregonstate.edu

with "Animation programming" in subject line.

Stevan J Arnold Department of Zoology Oregon State University Corvallis, OR 97331

website: http://people.oregonstate.edu/ ~ arnoldst/ Stevan J Arnold <arnolds@science.oregonstate.edu>

ReedCollege LabAssistant

Please post or distribute to people who may be interested in applying for the job below. Experience in particular areas of biology or with particular equipment/tools (for example, microscopy, working with live animal/plant systems, cell culture experience, etc.) should be indicated in the application. The position provides many opportunities to interact closely with faculty and students in the department. Also, the ad indicates only a bachelor's is required, but applicants with advanced degrees are strongly encouraged to apply. * *

*About Reed: *Reed College, located in Portland, Oregon, was founded in 1908 as an independent, coeducational, nonsectarian college of the liberal arts and sciences. Devoted to the intrinsic value of intellectual pursuit and governed by the highest standards of scholarly practice, critical thought, and creativity, Reed has served for over a hundred years as an exemplar of the liberal arts while consistently providing one of the best academic experiences in the United States. In support of this mission, we are seeking a dynamic *Laboratory Stockroom Assistant* to join our team.

*Position Summary: *The Laboratory Stockroom Assistant is responsible for setting up equipment, reagents, supplies and organisms required for classroom laboratory exercises.This is a full-time, 12-month exempt position, (1.00 FTE), working 37.5 hours a week, beginning August 1, 2013. Reed College offers a benefits package that is unparalleled. Benefits include comprehensive medical and dental insurance, 403(b) retirement plan with 10% employer contribution, retiree medical plan, college tuition assistance for employees' children, paid holidays, paid vacation and many other campus amenities, such as membership to the campus fitness center for employee and spouse and discounted TriMet bus passes.

Essential functions

Setting up equipment and organisms for experiments

Preparation of media and buffers

Working knowledge of modern, molecular biology techniques

Assisting students with independent research projects

Supervising student workers

Maintaining common equipment

Knowledge, Skills and Abilities

Knowledge of laboratory and safety techniques, practices and procedures

Specific knowledge of techniques such as PCR, quantitative PCR, and Western Blotting, in situ hybridization a plus

Knowledge of aseptic technique and troubleshooting a plus

Education and Experience

Bachelor's degree in Biology or related field

Directly related laboratory experience

Or any combination of experience and education that provides the applicant with the desired skills, knowledge and ability required to perform the job.

To Apply Email a Letter of Introduction discussing your qualifications and interests, a Reed Application for Employment< http://www.reed.edu/human_resources/assets/pdfs/2011HR_app_form_fillable.pdf >and your resume to employment@reed.edu.

Review of applications will begin immediately, deadline to apply is June 30, 2013.

The Reed Application for Employment is located at: http://www.reed.edu/human_resources/staffsearch/index.html Reed College is an Equal Opportunity Employer, Reed values diversity and encourages applications from underrepresented groups.

Sarah Schaack, PhD Reed College Assistant Professor Department of Biology, B106 3203 Southeast Woodstock Boulevard Portland, OR 97202 office: 503-517-7948 lab: 503-517-7976

Email: schaackmobile@gmail.com, schaack@reed.edu Website: https://sites.google.com/site/schaackwork/ Office hours, Spring 2013: Thursdays, 10:30 am to 12:30 pm

schaackmobile@gmail.com

Repsol Madrid DirectedEvolution

Seeking a Protein Engineer with experience in directed evolution and enzymology.

The Repsol Technology Center seeks a biochemist with at least two years postdoctoral experience in protein engineering and directed evolution of enzymes. Industry experience is not a must, however we seek demonstrated ability in designing methodologies for approaching problems in biocatalysis. This experience should include laboratory automation and the implementation of state of the art genetic and evolutionary approaches towards enzyme catalysis.

The protein engineer will be integrated within a growing team of highly qualified scientists within the Bioenergy Group at Repsol. The aim of this group is to develop the technological and scientific tools necessary for meeting the energy challenges of the twenty first century. This is an exciting and demanding work environment requiring intellectual creativity and the capacity to work with scientists and engineers from diverse disciplines.

The Repsol Technology Center is the flagship R&D facility of Repsol, which is a leading multinational oil and gas company with operations across the globe. The technology center is located in the outskirts of Madrid, a vibrant and diverse metropolitan area with a high standard of living and quality of life.

Applicants should send their CV including a list of publications, a cover letter, and a one to two page summary of their past experience and how they can contribute to projects focusing on bioenergy. Please send application material to seleccion10@repsol.com. The application deadline is 15th July 2013.

seleccion10@repsol.com

RyersonU GenomicBigData

Hello folks,

The Dean of the Faculty of Science has just announced that Ryerson University is conducting an external search for a Teir II NSERC Canada Research Chair in the area of Big data (broadly defined). If you are aware of any young (within 10 years of PhD) research stars in this area, please alert them to this opportunity. We are very excited to have an opportunity to recruit another excellent researcher in the area of Big Data to the Faculty of Science (if the successful candidate chooses us as their home).

Our ability to secure one and possibly two new CRCs is a testament to the tremendous research activities and efforts of our new and growing Faculty of Science. The Tier II Canada Research Chairs that will come available within the Faculty in 2014.

If interested folks email me, I will send them contact information to express their interest to the appropriate people at Ryerson. It would be really great to have Eco-informatics or Genome Informatics folks considered in this competition. BEST, LC

lesley.g.campbell@ryerson.ca

SW Australia FieldAssist Wrens

Field assistant job fairy-wrens

I am looking for a field assistant to monitor a population of red-winged fairy-wrens in south-west Australia for a 15 week period (9 October 2013 - 22 January 2014) as part of an on-going study on cooperation and competition. The study is based at Smithbrook Nature Reserve in one of the 35 biodiversity hotspots of the world. Duties include searching for nests, monitoring colour-ringed birds, behavioural observations, mist netting and data entry. Working days are long, start early and consist of lots of hiking through dense forest with occasional encounters with venomous snakes. Applicants must be physically fit and have outstanding hearing and vision, be able to work independently, get along well with others in remote field setting and tolerate hot weather conditions. Enthusiasm, self-motivation, and a strong work ethic are a must. Qualifications: experience monitoring colour-ringed birds, nest-searching, mist netting and current drivers licence. Field assistant will be appointed as a research assistant at the Australian National University (total gross salary for 15 weeks $13,907 AUD). Onsite accommodation is provided, but candidate must pay their own flight to Perth, Australia. To apply, please email a letter outlining previous relevant field research experience, and a resume including names and contact information for 3 referees to Lyanne Brouwer (lyanne.brouwer@anu.edu.au). Applicants will be considered as they apply until the position is filled.

Lyanne Brouwer <lyanne.brouwer@anu.edu.au>

TreeViewingApp programmer

I am a biologist currently working with a team of App developers to build a tree viewing App for exploring the tree of life.

So long, we have managed to develop the main functions of the App, but we have had many troubles with the last features.

We want to hire someone with experience in programming tree-viewing software to finish the App, so I was wondering if you know someone that could be interested in the job.

I would greatly appreciate your help.

Best regards,

Andres

Enviado con Correo de Windows

Andrés Del Risco <andres_delrisco@hotmail.com>

UAlabama LabTech SuccessionDynamics

Research Technician in Community Ecology at The University of Alabama

The Howeth Laboratory at the University of Alabama invites applications for a full-time research technician in community ecology beginning August 15, 2013. The technician will be involved in projects which aim to understand (1) succession in pond metacommunities and (2) the role of metacommunity dynamics in affecting the establishment, spread, and impact of non-native species, using freshwater plankton communities as a model system. The position is for 12 months, with responsibilities divided equally between field and laboratory work. Field work may include out-of-state travel for several weeks, and mesocosm experiments at the University of Alabama Tanglewood Biological Station. Laboratory work may include identification and enumeration of zooplankton, culturing of zooplankton, water chemistry analyses, and microsatellite DNA analyses.

Required qualifications: BS or MS in Biology, Ecology, or related science. Ability to tolerate harsh field conditions when necessary. Basic computer skills and familiarity with major software programs (word processing and database management). Ability to interact congenially with students.

Preferred qualifications: Previous experience in freshwater ecology and/or molecular ecology.

Relevant Links:

Department of Biological Sciences: http://bsc.ua.edu/ Center for Freshwater Studies: http://as.ua.edu/cfs/ University of Alabama: www.ua.edu Tuscaloosa, Alabama is a vibrant university community with numerous cultural and recreational opportunities available. The newly constructed Tuscaloosa Amphitheater, located on the banks of the Black Warrior River and just minutes from the UA campus, brings a variety of shows and musicians to the city. Recreational activities such as canoeing and hiking are quite popular in the nearby Black Warrior and Sipsey River natural areas, and the Talladega National Forest.

Salary is commensurate with experience. Visit UA's staff employment website at http://jobs.ua.edu for more information and to apply. All applicants should submit a cover letter, a statement detailing relevant research experience, contact information for three references, and a CV. Job close date 05/30/2013. EOE/AA

–

Jennifer Howeth, PhD Assistant Professor Department of Biological Sciences Program in Ecology, Evolution, and Systematics

University of Alabama Box 870206 1106 Bevill Building, 201 7th Ave. Tuscaloosa, AL 35487-0206

http://bsc.ua.edu/jennifer-howeth/
jghoweth@as.ua.edu

UAlaska Fairbanks GeneticLabTech

Genetics Laboratory Technician needed at the University of Alaska Fairbanks

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Job Description:

The Prugh lab at the University of Alaska Fairbanks is seeking an experienced genetics lab technician to conduct microsatellite and mitochondrial DNA analyses for a non-invasive genetics study of carnivores in Alaska. We are studying the population dynamics of coyotes and other small furbearers (foxes, lynx, and marten) to examine the relative importance of predation, food supply, and climate in the dynamics of mid-sized furbearers. The technician will help to set up a new genetics lab in a new building (the Margaret Murie Life Sciences Building), extract DNA, optimize PCR protocols, run mtDNA and microsatellite analyses, and use software to analyze results. Other duties will include purchasing, training undergraduate and graduate students, and possible assistance with manuscript preparation (with potential co-authorship).

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Specific Duties:

* Extract DNA from hair and feces * Amplify mtDNA and nuclear DNA using PCR * Run and analyze agarose gels (for species ID and sex) * Prepare amplified DNA for microsatellite analyses on ABR sequencers * Analyze microsatellite images using standard software to obtain genotypes * Error check data for signs of allelic dropout, false alleles, and contamination * Optimize protocols for amplifying DNA

Dates and hours:

The position is full-time from July through December 2013, with the possibility of extension for 6 additional months.

Compensation:

$23.95 per hour

Knowledge, skills and abilities:

Proficiency at conducting microsatellite and mtDNA analyses is required (extraction, PCR, genotyping). Successful applicants will be able to conduct analyses and optimize protocols with little training or supervision. Applicants must be highly organized, detail-oriented, and possess a strong work ethic.

Education or training:

A bachelor's degree in the biological sciences is required, emphasis on molecular biology and genetics is preferred. MSc degree in wildlife genetics or related field is preferred. At least 1 year of experience conducting genetic analyses in a research lab is required, 2+ years of experience is preferred. Previous experience and coursework in wildlife ecology and conservation genetics is preferred.

To Apply:

Visit**https://www.uakjobs.com/applicants/Central?quickFind=81163 Deadline 6/15/13

For questions, please email Laura Prugh at lprugh@alaska.edu**

– Laura Prugh Assistant Professor of Wildlife Ecology 311 Irving I University of Alaska Fairbanks Fairbanks, AK 99775 lprugh@alaska.edu office: 401 Irving I phone: 907-474-5965 fax: 907-474-7666 http://sites.google.com/site/laurarprugh/ Laura Prugh <lprugh@alaska.edu>

UBritishColumbia ResAssist Bioinformatics

JOB SUMMARY Will provide bioinformatics support for a large scale genomics project. The primary focus of this research is to generate a reference sequence for sunflowers using next generation sequencing technology, and to make this data and related resources publicly available

ORGANIZATIONAL STATUS Employed by Dr. Loren Rieseberg (Principle Investigator). Reports directly to L. Rieseberg. Works together with and provides technical assistance to other members of the research group including postdoctoral fellows and graduate students. For administrative matters, reports to the Botany Administrative Manager.

WORK PERFORMED Designs and implements algorithms and pipelines for plant genome assembly and population genetics data analysis. Develops pipelines for processing next generation sequence data. Writes reports, presents research results at lab meetings and conferences , and assists with writing grant applications and publications. Organizes large data sets for evolutionary studies and distributes data to collaborators as needed. Automates submission to NCBI and other public data repositories. Maintains a Laboratory Information Management System for biological samples, and sequencing and phenotype data. Complete web and database development for a data repository website, integrating search and bioinformatic tools for online analysis. Performs Linux administration, data backup, and hardware maintenance of high performance servers. Other related tasks in support of the research project.

QUALIFICATIONS Undergraduate degree in Biology or Computer Science required. Minimum of 4 years of related experience or the equivalent combination of education and experience. Two years relevant experience with bioinformatics tools required. Proficiency in at least one scripting language, such as Perl or Python, is required. Experience with statistical analysis, cluster computing, IT support, and development of web applications is highly desirable. Working knowledge of C/C++, Java, Javascript, R, SQL is an asset. Completion of courses in evolutionary biology, statistics, molecular biology and computer science an asset. Must demonstrate strong skills in programming, a good understanding of high performance computing and knowledge of probability theory. Ability to learn new software; Ability to troubleshoot; Ability to exercise initiative, tact and discretion; Ability to participate in and contribute to a multidisciplinary team; a high degree of motivation, enthusiasm and initiative; Strong problem solving and decision making skills; Ability to prioritize workload and meet deadlines; Attentive to detail, with the ability to work quickly and accurately.

CONSEQUENCE OF ERROR Work will be clearly defined and tasks and duties will often follow existing protocols. However, there is considerable room for innovative thinking to improve upon existing approaches, as well as to provide novel solutions for the assembly of very large and complex genomes. In most cases errors would require troubleshooting and then repeating the procedure.

SUPERVISION RECEIVED Receives instructions during orientation, thereafter on new assignments or changes in procedures. Work is subject to check by the Principle Investigator (PI) and PDFs. Errors will be followed up by discussions and troubleshooting with the PDFs and the PI.

SUPERVISION GIVEN Supervises more junior bioinformatician in L. Rieseberg's group (Tech 2).

POSITION DESCRIPTION #00033735 BUSINESS TITLE: Research Asst/Tech 4 EMPLOYMENT GROUP: CUPE 116(Service/Techs/Trades) JOB FAMILY: Research/Technical - CUPE 116 JOB CODE: 251406 - Research Asst/Tech 4 VP/FACULTY: Faculty of Science DEPARTMENT: Botany Desired Start Date: September 2013 Funding Type: Grant Funded

apply directly on UBCs HR site: http://www.hr.ubc.ca/careers-postings/staff.php Closing Date: 2013/06/28

Sebastien Renaut <srenaut@interchange.ubc.ca>

sebastien.renaut@gmail.com

UCBerkeley LabManager Adaptation

The Rosenblum Lab at UC Berkeley is looking for a new lab member to serve as a staff scientist and laboratory manager, ideally joining the lab in late summer 2013. The scientist will join a dynamic research group and will be affiliated with the Department of Environmental Science, Policy and Management, the UC Berkeley Museum of Vertebrate Zoology, and the Berkeley Initiative for Global Change Biology. The scientist will be responsible for day-to-day lab operations including laboratory administration, regulatory compliance, budgetary accounting, and mentoring undergraduate researchers. The scientist will also be actively involved in research on the genomics of adaptation and speciation and can be engaged in project coordination, wet lab research, data analysis, and manuscript preparation. The scientist must have excellent organizational and interpersonal skills. Expertise in molecular biology or bioinformatics is desired. The opportunity can be tailored to a scientist at the MA/MS or PhD level. More information about research activities in the Rosenblum Lab is available at http://nature.berkeley.edu/rosenblum. If interested, please send a CV and letter of interest (no more than 2 pages on prior experience, current interests, career goals, fit for the position, and any timing constraints) to rosenblum@berkeley.edu by June 17th 2013.

rosenblum@berkeley.edu

UCDavis LabManager PlantEvolutionaryGenetics

Lab Manager: Plant evolutionary geneticist at University of California Davis

Job summary:

The Schmitt Lab at the University of California Davis (plantgxe.ucdavis.edu) is seeking an experienced plant evolutionary geneticist as a lab manager. Under general supervision, the lab manager will assist in the set up and management of a new research lab and help launch and coordinate new research projects focused on quantitative genetics and genomics of plant adaptation in Arabidopsis thaliana and other species. He/she will apply understanding of basic laboratory operations to conduct current molecular biology work and have the resources required to run a lab, including strong management and organizational ability, good communication skills and strong data base and computer analysis skills. He/she will support experimental work in the greenhouse, growth chambers and/or a field environment. The candidate is expected to be an intellectual contributor to the lab by: reading, understanding and assimilating the scientific literature relevant to ongoing projects; independently working on his/her own research and supervising others on the project; writing or contributing to research publications.

Minimum qualifications:

- Masters degree in biology, genetics, or related fields or equivalent education and experience. - Skill to exact and organize lab and field work. - Background in working with plants in the field. - Experience in a plant evolutionary biology or molecular biology lab. - Proficiency in common laboratory skills and knowledge (e.g., pipetting, preparing reagents, standard calculations.) - Proficiency in genetics. - Experience with gel electrophoresis, PCR, DNA and RNA hybridization. - Computer skills for raw data file and results data file handling, entry into database from sheets, record keeping of quality control charts. - Knowledge to interpret and follow protocols in the scientific literature. - Knowledge of chemicals and requirements for safe handling procedures. - Experience demonstrating excellent communications skills to, speak on a one-to-one basis, and interact effectively with others. - Skills to listen to and follow verbal and written instructions. - Experience to independently follow through with projects, learn specific laboratory Standard Operating Procedures and safety requirements.

Start Date:

August/September 2013

Please see the UC Davis job posting for more information, additional qualifications and how to apply:

www.employment.ucdavis.edu/applicants/-Central?quickFinde466

All applicants must submit through the UC Davis website, however if there are additional questions please email Amanda Gorton at ajgorton@ucdavis.edu

Amanda J. Gorton, MSc Schmitt Lab plantgxe.ucdavis.edu Department of Evolution and Ecology UC Davis One Shields Ave Davis, CA 95616

ajgorton.work@gmail.com

UConnecticut Bioinformatics

Research Scientist Position in Genomics

A research scientist position in bioinformatics and computational biology is available in the Malone Laboratory of Gene Dosage and Evolution in the Department of Molecular and Cell Biology at the University of Connecticut. The laboratory will address questions of gene dosage, aneuploidy, sex chromosome evolution, and sex determination using frogs and flies to ultimately understand the relationship between gene dose, genome balance, and phenotype.

The research scientist will take part in de novo assembly analyses of several frog species and analyze a variety of high-throughput sequencing datasets to address questions of dose, dosage compensation, and gene evolution. Proficiency with multiple scripting languages, experience with de novo assembly algorithms, high-throughput sequencing analysis, and tools for computational, comparative, and evolutionary genomic analysis are required. The research scientist will help train undergraduate and graduate students in genome analyses and organize workflows and databases for data storage and management. Excellent communication skills are necessary.

The intellectual environment for genomic research at the University of Connecticut is rich and vibrant, including the Institute of Systems Genomics, University of Connecticut Health Center, Jackson Laboratory for Genomic Medicine, Center for Applied Genetics and Technology, and a 1.5+ billion dollar investment in STEM fields by the state of Connecticut. The laboratory will interact closely with these centers and resources and these interactions promise exciting new avenues to address fundamental and applied questions in genome biology. Candidates should expect to engage with the genome analysis community at the University of Connecticut, develop and pursue their own research ideas, and receive mentoring and guidance from the PI.

Applicants should send a single PDF file that contains a cover letter describing your research interests and experience (maximum 2 pages), C.V., and contact information for three references to john.malone@uconn.edu. Review of applications will begin on 22 July and continue until the position is filled. Start period: fall 2013.

Applications for either a research scientist or postdoctoral role and informal inquires from candidates with other backgrounds in genomics and evolutionary biology are welcome.

The University of Connecticut is an EEO/AA employer

John H. Malone Assistant Professor Department of Molecular and Cell Biology University of Connecticut http://scholar.google.com/citations?user=-3D09eqGzIAAAAJ&hl=3Den john.malone@uconn.edu

jmalone@bio.fsu.edu

UMississippi FreshwaterBiology

Doherty Chair in Freshwater Biology Department of Biology and Center for Water and Wetland Resources, The University of Mississippi

The University of Mississippi's Department of Biology and Center for Water and Wetland Resources (CWWR) seek an exceptional individual to expand research programs in freshwater biology. The successful candidate will hold the title of Doherty Chair and will be a tenured faculty member hired at the full Professor level with office and laboratory space at the CWWR located at the UM Field Station. We seek a model mentor, teacher and internationally recognized researcher with an established, extramurally funded research program in any discipline within freshwater/wetlands biology. The Doherty Chair will be expected to 1) ensure excellence in scholarship, teaching and service; 2) increase the level and scope of extramural funding that supports academic and research initiatives in the Department of Biology and the CWWR; 3) provide leadership in developing a national reputation in freshwater/wetlands biology at the University of Mississippi; and 4) enhance outreach efforts in the com munity and the region. It is expected that the Chair's research will be conducted at least in part at the CWWR. Teaching will be commensurate with the Chair's research commitment and interests. The position offers a competitive salary, benefits, and funded graduate assistantships.

The Department of Biology consists of 18 faculty and annually educates approximately 1200 undergraduate biology majors and 35 graduate students (M.S. and Ph.D.). Departmental research spans all levels of organization from the cell to the ecosystem. More detailed information concerning the department is available at http://www.olemiss.edu/depts/biology. The Center for Water and Wetland Resources is a specialized research unit located at the 740-acre UM Field Station, approximately 12 miles from the main campus, which includes natural and constructed wetlands, 200 constructed ponds, and several natural springs and small streams. More information concerning the CWWR and field station is available at http://www.baysprings.olemiss.edu/ . Founded in 1848 as the state's first public university, the main campus of The University of Mississippi is located in Oxford, Mississippi, a community known for its many outstanding educational and cultural opportunities. More detailed information on Oxford is available at http://www.oxfordms.net/. The University is a growing, vibrant institution that offers nationally ranked academic and research programs, and has been cited by Forbes Magazine as one of the nation's 20 Best College Buys and by the Chronicle of Higher Education as one of the 10 top "Great Colleges to Work For". Within the last 12 years, the University has produced eight Goldwater Scholars, two Rhodes Scholars, six Truman Scholars, seven Fulbright Scholars, one Marshall Scholar, one Udall Scholar and one Gates Cambridge Scholar.

To apply, please visit our Online Employment Service at jobs.olemiss.edu. Applications should include: (1) cover letter outlining interest and suitability for the position, (2) curriculum vitae, (3) statement of research interests, (4) reprints of up to five recent publications, and (5) a list of five references. Letters of nomination should be addressed to; Chair, Search Committee for Doherty Chair in Freshwater Biology, Department of Biology, University of Mississippi, University, MS 38677.

Consideration of applications will begin immediately and continue until the position is filled. The University of Mississippi is an EEO/AA/TITLE IX/SECTION 504/ADA/ADEA EMPLOYER.

Ryan Garrick Department of Biology 508 Shoemaker Hall University of Mississippi University, MS 38677-1848, USA

webpage: http://www.rcgarrick.org< http://www.rcgarrick.org/ >

rgarrick@olemiss.edu

UPennsylvania Bioinformatics

Assistant Professor, Penn Institute for Biomedical Informatics

Posting Department:

Posted Date: 05/07/2013

Expire Date: 05/07/2015

To apply: http://www.med.upenn.edu/apps/faculty_ad/index.php/d3300

The Penn Institute for Biomedical Informatics at the Perelman School of Medicine at the University of Pennsylvania seeks candidates for an Assistant Professor position in the tenure track. The successful applicant will have experience in the field of bioinformatics research. Applicants must have an M.D. and/or Ph.D degree and have demonstrated excellent qualifications in research and education.

The faculty appointments will be at the Assistant Professor level in the tenure track in an appropriate department in the School of Medicine. Applicants are expected to establish robust independent funding for their research program.

This Institute is enabled by a recent multi-million dollar gift and focused on the science of biomedical informatics. The Institute will integrate informatics disciplines from bioinformatics, to translational, clinical, and public health informatics.

The University of Pennsylvania, founded by Benjamin Franklin, is a world-class research institution located near the center of Philadelphia. All of Penn's twelve schools are located within walking distance of one another. The Perelman School of Medicine at the University of Pennsylvania is one of the top ranked medical schools in the nation for research and NIH funding.

We seek candidates who embrace and reflect diversity in the broadest sense.

The University of Pennsylvania is an equal opportunity, affirmative action employer.

Sarah Tishkoff, Ph.D. David and Lyn Silfen University Professor Departments of Genetics and Biology University of Pennsylvania Tel: 215-746-2670 tishkoff@mail.med.upenn.edu http://www.med.upenn.edu/tishkoff/

tishkoff@mail.med.upenn.edu

UPennsylvania LabTech MicrobeEvolution

Job: Laboratory Technician Department of Biology, University of Pennsylvania

A laboratory technician position is available in the evolution of infectious microbes lab led by Dustin Brisson at the University of Pennsylvania. The main focus of the projects involves the bacterial cause of Lyme disease, Borrelia burgdorferi. The position requires both laboratory skills to collect data as well as intellectual skills to integrate ideas across multiple scales of biological complexity (i.e. molecular-level, organism-level, and population-level).

We are seeking a highly motivated, enthusiastic, and enquiring individual with a background in evolutionary biology or ecology. Strong molecular genetic skills are highly advantageous. The successful candidate will conduct both molecular biology and animal husbandry and will contribute to formulation of experiments, data collection and data analysis.

A Bachelor's degree in biology (or a related science) OR 2 years of experience or equivalent combination of education and experience is required.

The University of Pennsylvania has a strong group of evolutionary biologists and ecologists in the biology department that frequently interact with each other and with an accomplished group of microbiologists in the Medical and Veterinary schools.

Starting dates are flexible and and can start as early as August 2013. Salary is commensurate with experience.

Please send enquiries to dbrisson@sas.upenn.edu

dbrisson@sas.upenn.edu

USheffield Bioinformatics

University of Sheffield Department of Animal & Plant Sciences Lecturer (= Assistant Professor) in Bioinformatics

The University is advertising four academic posts in Bioinformatics, including one in the Department of Animal and Plant Sciences (APS).

APS (http://www.shef.ac.uk/aps) is renowned for its work on behavioural ecology, evolutionary ecology, population genetics and plant ecophysiology, and supports multiple major field and lab studies of adaptation and speciation. This work is increasingly dependent on whole-genome sequencing and comparative genome analysis. We wish to appoint a talented genome biologist who complements our current strengths and who has a track record in, for example, genome assembly and analysis, environmental epigenomics, or using genomic data to test evolutionary or mechanistic hypotheses. Computational/ statistical biologists who have a strong interest in creating computational or analytical tools (e.g. new algorithms, statistical methods) for wider community use are also encouraged to apply.

The successful candidate will have a strong track record of research in a bioinformatics-led subject area relevant to the expertise in APS, and should have experience of delivering teaching to undergraduates.

For further details of the post see Job Reference Number: UOS006629 APS http://www.jobs.ac.uk/job/AGQ577/lecturer-in-bioinformatics/ Closing date: 1 July 2013.

The Bioinformatics Centre, with links to the other posts, is described at http://www.shef.ac.uk/faculty/science/bioinformatics Informal enquiries about the post in APS can be addressed to Terry Burke (t.a.burke@sheffield.ac.uk; +44 114 222 0096).

t.a.burke@sheffield.ac.uk

USussex ResearchTech SocialWasps

RESEARCH TECHNICIAN IN MOLECULAR/BEHAVIOURAL ECOLOGY OF SOCIAL

SYSTEMS

Full time, 29 months fixed term Closing date for applications: 17 July 2013 Start date: 1 October 2013 Salary range: starting at £27,047 and rising to £30,424 per annum. It is normal to appoint at the first point of the salary scale.

We seek a self-motivated person with an interest in behavioural ecology/entomology for a 29-month NERC-funded full-time post in the research group of Professor Jeremy Field at Sussex University, UK (http://www.sussex.ac.uk/lifesci/fieldlab/). The aim of the project is to understand group formation in primitively eusocial insects, using Polistes paper wasps as a model. The major part of the work will be microsatellite genotyping, with initial training provided as required. There will also be a range of other labwork, and there may be an opportunity to take part in fieldwork in Spain.

The successful applicant will have a degree or equivalent in a relevant subject and an interest in animal behaviour/entomology. Experience with animal social systems (especially social insects), and experience of molecular techniques, behavioural ecology/entomology and fieldwork would be useful, but it is not necessary to have experience in all of these areas.

The Evolution, Behaviour and Environment (EBE) Subject Group in the School of Life Sciences at Sussex (http://www.sussex.ac.uk/lifesci/ebe/research) is a thriving research environment with an exceptional concentration of research expertise that focusses on social evolution in insects. Jeremy Field, Francis Ratnieks, Bill Hughes, Dave Goulson, Tom Collett and Paul Graham all lead well-established research groups in the area.

As well as the standard University of Sussex application form, applications should include a statement of the earliest date on which the applicant would be available to start work; a CV and a covering letter explaining their suitability for the post; and contact details (including email addresses) of 2-3 referees who would be available to provide references before interview.

Informal enquiries may be made to Professor Jeremy Field (j.field@sussex.ac.uk).

Closing date for applications: 17 July 2013

Interviews will be held between 7 and 16 August 2013

For full details and how to apply see http://www.sussex.ac.uk/aboutus/jobs/204 The University of Sussex is committed to equality of opportunity

J.Field@sussex.ac.uk

UTexas Austin LabTech HostParasiteEvolution

HHMI & Univ. of Texas at Austin: laboratory technician position in host-parasite interactions

The laboratory of Dr. Daniel Bolnick at UT Austin, supported by the Howard Hughes Medical Institute, seeks an organized and experienced individual to fill a laboratory technician position studying host-parasite interactions. The technician will be expected to work with lab members to carry out assays of three-spine stickleback (Gasterosteus aculeatus) resistance/tolerance to a tapeworm parasite. This is part of a study of the genetic basis of parasite resistance. The technician will also be asked to assist with dissecting specimens, flow cytometry assays of immune function, ELISAs, and RNAseq and SNP genotyping using RADseq genotyping. Applicants should have lab experience with molecular genetics, including DNA extraction, quantitation, PCR, and sequencing, and familiarity with sterile techniques. Preference is given to applicants who also have some laboratory experience with flow cytometry or ELISAs, RNAseq, or bioinformatics. Strong organizational skills are a necessity, as are a strong work ethic and the ability to work well with others.

The Bolnick lab's research focuses on evolutionary ecology of trait variation within populations, including variation in diet, courtship traits, and immune function. More information on research in the lab can be found at https://webspace.utexas.edu/dib73/Bolnicklab/Bolnicklab.htm?uniq=3D5ptsas . Minimum qualifications: A Bachelor's or Master's degree in an appropriate field of evolutionary biology or molecular ecology/genetics and the demonstrated ability to perform the molecular laboratory techniques listed above.

To apply, pleases send a pdf containing a coverletter, a CV, and names and contact information for two recommendation letter writers to Dr. Daniel Bolnick (danblonick@austin.utexas.edu). Previous experience in the laboratory should be highlighted in both the cover letter and letters of recommendation wherever possible. Questions may be directed to the same email address.

Applications will be reviewed starting July 1, 2013, though additional applications may be considered after this deadline until the position is filled.

This is a full-time position, initially appointed for a period of 12 months at a starting salary of approximately $2,500 per month (depending on qualifications), plus benefits. The research technician will be an employee of the Howard Hughes Medical Institute. The position duration could be extended, depending on performance and availability of research funds. The chosen applicant will ideally start work in late August or early September. Applications will be accepted until the position has been filled.

Dr. Daniel I. Bolnick

Early Career Scientist Howard Hughes Medical Institute

Associate Professor Section of Integrative Biology One University Station C0990 University of Texas at Austin Austin, TX 78712

512-471-2824 fax 512-471-3878 danbolnick@austin.utexas.edu https://webspace.utexas.edu/dib73/TheBolnickLab/Home.html danbolnick@austin.utexas.edu

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UTexas Austin LabTech SticklebackEvolution

University of Texas/Austin: laboratory technician position

The laboratory of Dr. Daniel Bolnick, in the Section of Integrative Biology at the University of Texas at Austin, seeks an organized and experienced individual to fill a laboratory technician position. The technician will be expected to work with lab members to carry out morphological measurements, stable isotope analysis, and genotyping of three-spine stickleback (Gasterosteus aculeatus), as part of an NSF-funded project studying the evolution of assortative mating. Applicants should have lab experience with molecular genetics, including DNA extraction, quantitation, PCR, and sequencing. Strong organizational skills and a good work ethic are necessary, as is an ability to work with others.

The Bolnick lab's research focuses on evolutionary ecology of trait variation within populations, including variation in diet, courtship traits, and immune function. More information on research in the lab can be found at https://webspace.utexas.edu/dib73/Bolnicklab/Bolnicklab.htm?uniq=3D5ptsas . Minimum qualifications: A Bachelor's or Master's degree in an appropriate field of evolutionary biology or molecular ecology/genetics and the demonstrated ability to perform the molecular laboratory techniques listed above.

To apply, pleases send a pdf containing a coverletter, a CV, and names and contact information for two recommendation letter writers to Dr. Daniel Bolnick (danblonick@austin.utexas.edu). Previous experience in the laboratory should be highlighted in both the cover letter and letters of recommendation wherever possible. Questions may be directed to the same email address.

Applications will be reviewed starting July 1, 2013, though additional applications may be considered after this deadline until the position is filled.

This is a full-time position, initially appointed for a period of 6 months at a starting salary of approximately $2,500 per month (depending on qualifications), plus benefits. The position duration could be extended, depending on performance and availability of research funds. The chosen applicant will ideally start work in late August or early September. Applications will be accepted until the position has been filled.

Dr. Daniel I. Bolnick

Early Career Scientist Howard Hughes Medical Institute

Associate Professor Section of Integrative Biology One University Station C0990 University of Texas at Austin Austin, TX 78712

512-471-2824 fax 512-471-3878 danbolnick@austin.utexas.edu https://webspace.utexas.edu/dib73/TheBolnickLab/Home.html danbolnick@austin.utexas.edu

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UVienna ProfSystematicEvolutionaryBotany

The Faculty of Life Sciences of the University of Vienna announces the position of a

Full Professor of Systematic and Evolutionary Botany

(full time, permanent position under private law). The University of Vienna intends to increase the number of women on its faculty, particularly in high-level positions, and therefore specifically invites applications by women. Among equally qualified applicants women will receive preferential consideration.

Applicants should have a strong record in studying processes and mechanisms of plant or fungal evolution with emphasis on phylogenetics, systematics or on genetic, genomic, biogeographic or ecological aspects of speciation.

Candidates should be interested in interdisciplinary research together with major branches of organismic biology within the Faculty of Life Sciences.

The professorship will be part of the Faculty Center of Biodiversity. The center offers excellent research and teaching conditions including a well equipped set of molecular, cytogenetic, phytochemical, and morphological laboratories; IT facilities; an extensive botanical library; a herbarium (1.4 million sheets); a Botanical Garden (Core Facility of the Faculty; 8ha, with more than 11,000 species); and access to a tropical research station (La Gamba, Costa Rica).

The candidate is expected to teach systematic and evolutionary botany at all academic levels. Excellent teaching and mentoring skills are necessary and should be documented in the application. Successful candidates will have the following qualifications: - PhD and post-doctoral experience at a university or other research institution. (Austrian or equivalent international academic degree in the relevant field) - Outstanding research and publication record, with an excellent reputation as an active member in the international academic community (Habilitation (venia docendi) or equivalent international qualification in the relevant field is desirable) - Experience in designing, procuring and directing major research projects, and willingness and ability to assume the responsibility of team leadership - Experience in university teaching, and willingness and ability to teach at all curricular levels, to supervise theses, and to further the work of junior academic colleagues The University of Vienna expects the successful candidate to acquire, within three years, proficiency in German sufficient for teaching in Bachelor programmes and participation in committees

The University of Vienna offers - Attractive terms and conditions of employment with a negotiable and performance-related salary, associated with a retirement fund - a “start-up package” for the initiation of research projects - an attractive and dynamic research location in a city with a high quality of life and in a country with excellent research funding provision - Support for relocation to Vienna, where appropriate

Candidates should send an application containing at least the following documents: - Academic curriculum vitae - Brief description of current research interests and research plans for the immediate future - List of publications together with a) specification of five key publications judged by the applicant to be particularly relevant to the advertised professorship together with an explanation of their relevance b) PDF versions of these five publications provided either as email attachments or through URLs of downloadable copies (PDF versions of monographs need only be provided if easily available.) - List of talks given, including detailed information about invited plenaries at international conferences - List of projects supported by third-party funds - Short survey of previous academic teaching and list of supervised PhD theses

University professors will be classified according to the Collective Bargaining Agreement for University Staff into the salary group A1. The salary will be individually negotiated under consideration of the previous career development and in case of an appointment from abroad of the different tax situation.

Applications, written in English and in electronic form (preferably as one PDF file), should be sent to the Dean of the Faculty of Life Sciences of the University of Vienna, O. Univ.-Prof. Dr. Horst Seidler, (dorothea.prenner@univie.ac.at), no later than September 25th, 2013 with reference 20/6-2013.

gerald.schneeweiss@univie.ac.at

UppsalaU EvolutionaryEcol

Senior Lecturer in Biology with specialization in Animal Ecology

2013-06-28

at the Department of Ecology and Genetics Application no later than 2013-08-29. UFV-PA 2013/1812

The Department of Ecology and Genetics is included in the Evolutionary Biology Centre, one of the world’s major centers for evolutionary biology research and education. The program in Animal Ecology has about 60 employees and a focus on empirical studies of natural model systems in the field and in the laboratory environment (http://www.ebc.uu.se/forskning/-IEG/zooeko/), but have recently also started purely theoretical research. The Department of Ecology and Genetics have programs in Plant Ecology and Evolution, Limnology and Evolutionary Biology, enabling interdisciplinary collaborations.

Description of the subject area: The subject comprises mainly empirically and theoretically oriented animal ecology and evolutionary ecology, for example studies of speciation, conservation biology, life history evolution, sexual selection and sexual conflict in animals, but the position is not limited to these areas. Teaching involves teaching at the undergraduate and graduate level in biology, evolution and ecology.

Duties: The position includes teaching, research and administration. Teaching duties include course responsibility, course administration and supervision of second- and third-cycle students. The holder shall also keep abreast of developments within the subject area and the developments in wider community that are significant for the work at the university.

Qualifications Required: According to the Swedish Higher Education Ordinance those qualified for appointment as senior lecturer are persons who have demonstrated teaching expertise and been awarded a PhD or has the corresponding research competence or some other professional expertise that is of value in view of the subject matter of the post and the duties that it will involve. According to the appointment regulations of Uppsala University to be eligible for appointment as senior lecturer applicants also must have completed teacher training of relevance to operations at the University, comprising ten weeks, or have acquired the equivalent knowledge. If special circumstances apply, this training for teachers in higher education may be completed during the first year of employment. A general eligibility requirement is that the applicant must possess the personal capabilities necessary to carry out fully the duties of the appointment.

Documented ability to teach in Swedish and/or English is a requirement unless special reasons prevail.

An applicant who is offered an employment as senior lecturer can be promoted to professor if he/she has applied for this, is qualified for such a post, and moreover has been deemed suitable on the basis of the specific criteria established by the faculty board.

Assessment Criteria/Ranking Research Expertise and Teaching Expertise: The ranking of eligible applicants will be based primarily on research and teaching expertise, which will be given equal importance.

Research expertise comprises research merits including research merits obtained outside the academy, which includes for example technology development and innovation ability. In assessing research expertise special weight will be attached to research merits in animal ecology and evolutionary ecology.

In assessing research expertise research quality must be the prime consideration. The scope of research, primarily in regard to depth and breadth, must also be afforded consideration. Furthermore, consideration must be given to the capacity to plan, initiate, lead, and develop research and education in the third cycle, the ability to acquire funding for research in competition, as well as the demonstrated capacity to interact with others both within academia and in the wider community.

As much attention shall be given to the assessment of teaching expertise as to the assessment of research expertise. Teaching expertise comprises educational and teaching qualifications. This expertise can have been achieved outside the academy through supervision, internal training, mentoring programs, etc.

In assessing teaching expertise teaching quality must be the prime consideration. The scope of teaching experience, in terms of both breadth and depth, must also be afforded consideration. Furthermore, consideration must be given to the capacity to plan, initiate, lead, and develop teaching and instruction, as well as the ability to connect research to teaching in respect to research in the subject at hand, subject didactics, as well as teaching and learning in higher education. The ability to interact concerning issues of teaching and learning in higher education with actors inside and outside the University is also included in teaching expertise.

All merits must be documented in a manner that makes it possible to assess

— / —

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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VolFieldAssist Panama

Subject Header: Job:VolFieldAssist.Panama.

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 (http://www.zsl.org/science/ioz-staff-students/bell,2041,AR.html) and the University of Bristol (http://www.bristol.ac.uk/biology/people/seirian-r-sumner/index.html). 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 2013 field site is based near the Smithsonian Tropical Research Station at Galatea, Colon, Republic of Panama and the field season will run from the end of June until the beginning of August.

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. Experience gained on the project will be especially useful for those about to commence a field-based MSc or PhD project. 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 £500 towards travel costs (e.g. air ticket). More details are available from Dr Seirian Sumner (seirian.sumner@bristol.ac.uk) and/or Emily Bell (emily.bell@ioz.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 Emily Bell by Thursday 20th June 2013. Shortlisted applicants will be notified by email, and will be invited for interview either in person or over skype/phone soon afterwards. Applicants must be available to travel to Panama immediately after the confirmation of their appointment from their skype/phone interview.

The Zoological Society of London is incorporated by Royal Charter Principal Office England. Company Number RC000749 Registered address: Regent's Park, London, England NW1 4RY Registered Charity in England and Wales no. 208728

Emily.Bell@ioz.ac.uk

Other

Australia VolunteerFieldAssist

Volunteer field assistant for Behavioural Ecology in Australia. August-September 2013.

We are seeking a field assistant for six weeks (August 11-September 21) to help with a research on brood parasitism in yellow rumped thornbills. These birds are hosts of cuckoos and my PhD focuses on how they defend from parasitism. I perform field experiments in their nests and do behavioral observations so it would be great for people with interests in ethology. Fieldwork will be in Canberra (Campbell park), biking distance from the center of the city. The main duties are finding nests and monitoring them. Banding will be performed occasionally. We will provide AUD 2000 for accommodation and food, but assistants must cover their trip to Canberra. The work is not physically demanding, but enthusiasm, patience and work ethic are a must.

If you are interested please send me an email (medina.iliana@gmail.com) with relevant field experience and a CV.

Best, Iliana Medina PhD candidate Australian National University email: medina.iliana@gmail.com http://-www.wix.com/medinailiana/ilianamedina#! Iliana Medina <medina.iliana@gmail.com>

BioNames database

I've released BioNames http://bionames.org , a database of taxonomic names for animals (and other organisms covered by the ICZN code). This database was an entry in the Encyclopedia of Life's Computational Data Challenge http://eol.org/info/323 BioNames' key features include:

1. Names from the Index of Organism Names (ION) database are linked (wherever possible) to the primary literature, much of which is freely viewable in BioNames

2. Names are linked to the GBIF and NCBI (GenBank) classifications for ease of navigation

3. Where available, images of the corresponding taxa from EOL are displayed

4. For taxa in the NCBI classification the database displays available phylogenies from the PhyLoTA database

In addition to exploring BioNames itself (http://-bionames.org) you can get background on the project on the iPhylo blog http://iphylo.blogspot.co.uk/-search?q=3Dbionames Feedback is welcome.

Regards

Rod

Roderic Page Professor of Taxonomy Institute of Biodiversity, Animal Health and Comparative Medicine College of Medical, Veterinary and Life Sciences Graham Kerr Building University of Glasgow Glasgow G12 8QQ, UK

Email: r.page@bio.gla.ac.uk Tel: +44 141 330 4778 Fax: +44 141 330 2792 Skype: rdmpage Facebook: http://www.facebook.com/rdmpage Twitter: http://twitter.com/rdmpage Blog: http://iphylo.blogspot.com Home page: http://-taxonomy.zoology.gla.ac.uk/rod/rod.html Wikipedia: http://en.wikipedia.org/wiki/Roderic_D._M._Page Citations: http://scholar.google.co.uk/citations?hl=-3Den&user=3D4Z5WABAAAAAJ ORCID id: http:/-/orcid.org/0000-0002-7101-9767 r.page@bio.gla.ac.uk

Biodiversity Heritage Library

The Biodiversity Heritage Library < http://-www.biodiversitylibrary.org/ >

Do you need access to taxonomic and biodiversity literature for your research? Do you need to review a natural history rare book but dont have access to a library collection that owns it? Do you need to retrieve a species bibliography listing citations of species names occurrences throughout the published literature record? Do you want to be able to download copies of these books to your personal computer? Do you want all of this for free?

Check out the Biodiversity Heritage Library < http:/-/www.biodiversitylibrary.org/ >, an open access digital library for biodiversity literature. BHL provides free, full-text access to over 114,000 natural history books (amounting to over 40 million pages) digitized from the collections of its 15 members libraries < http://biodivlib.wikispaces.com/-BHL+Consortium+Membership > and six global partner projects < http://biodivlib.wikispaces.com/About >. BHL collections are truly comprehensive, spanning the 15th-21st centuries, and including some of the rarest titles in the natural history canon.

You can download the full PDF < https://-docs.google.com/document/d/1XXFm4MsAEX-3iZq7UlZDGvxkZHvFztf0gcINEfDU27s/-pub#h.xh7tgdhetmkx > of any book in BHL, as well as create custom PDFs < https://-

docs.google.com/document/d/1XXFm4MsAEX-3iZq7UlZDGvxkZHvFztf0gcINEfDU27s/-pub#h.xn37bnfgusb5 > from select pages. Using BHLs taxonomic intelligence service (Advanced Search\Scientific Names < http://-www.biodiversitylibrary.org/advsearch >), you can search for a specific scientific name and have a list of all mentions of that name throughout the BHL corpus returned to you as a species bibliography. Want something that BHL doesnt have? You can submit a request < http://www.biodiversitylibrary.org/-contact#/request > for the item to be scanned, free of charge to you!* Need access to scientific illustrations? BHLs Flickr account < http://www.flickr.com/-photos/biodivlibrary/sets > provides access to over 70,000 illustrations gleaned from the BHL collection, all made freely available under Creative Commons licenses.

Check out our collections today < http://-www.biodiversitylibrary.org/ >! Stay in touch with project updates via our Newsletter < http:/-/biodivlib.wikispaces.com/Newsletters >, Quarterly Reports < http://biodivlib.wikispaces.com/Reports >, Blog < http://blog.biodiversitylibrary.org/ >, Facebook < https://www.facebook.com/BioDivLibrary >, and Twitter < https://twitter.com/BioDivLibrary >. Have questions, comments, or suggestions? Contact us today < http://www.biodiversitylibrary.org/contact/ > !

* Copyright and content availability restrictions apply. Learn more < http://biodivlib.wikispaces.com/-Guidelines+for+Submitting+Scanning+Requests >.

PS: I will be at SMBE meeting in Chicago in July and please ask me in person if you are interested in learning more about this useful tool for teaching and publications. BHL collections are copyright free and free access!

Tomoko Steen

*Tomoko Y. Steen, Ph.D. * *The Georgetown University, School of Medicine Department of Microbiology and Immunology *Associate Editor**, Journal of Heredity (Oxford University Press)* http://www.theaga.org/editors.php Tomoko Steen <tomoko.y.steen@gmail.com>

CanadianInstEcolEvol CallForWorkinGroupProposals

CIEE Thematic Programs

The Canadian Institute of Ecology and Evolution seeks proposals for Thematic Programs (Working Groups) to be staged over the following 12 months. Thematic Program proposals should outline a plan to address significant questions in ecology and evolution through synthesis and integration of existing data (e.g., quantitative research synthesis, compilation and meta-analysis of existing data sets, etc.)

For further details, please see: http://ciee-icee.com/ Thanks,

Andrew Simons & Mark Forbes Carleton University Ottawa, Ontario

Andrew.Simons@carleton.ca

EurSocEvolBiol Outreach fund

ESEB Outreach Fund

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

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

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

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

European Society for Evolutionary Biology www.eseb.org office@eseb.org

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Gene network comparison

Dear EvolDir,

I have generated several gene networks and want to test if they are statistically different from each other, of from a random network. Does anyone know of a paper or software that describes such a test?

This problem is reminiscent of comparing two phylogenetic topologies - for example, via a Shimodaira-Hasegawa test. In my case, the topologies are gene co-citation networks inferred using GENOMATIX PATHWAY SYSTEM software. Unlike phylogenetic topologies, these networks are not bifurcating, but they do have nodes and edges. I did locate one paper on this topic (http://www.biomedcentral.com/1471-2105/14/-94) but it is not obvious how to implement the test.

Thanks for any suggestions.

Graham

Graham Thompson Assistant Professor Western University, Biology 1151 Richmond Street North London, Ontario N6A 5B7 CANADA

519 661 2111 (ext 86570) 519 615 6066 (iPhone) graham.thompson@uwo.ca http://www.uwo.ca/biology/-Faculty/thompson graham.thompson@uwo.ca

HoneyBee LinkageDisequilibrium

I am studying the population genetics of honey bees using 6 microsatellite markers chosen from different chromosomes and screened across 21 populations sampled across regions of India, as part of the analysis i have calculated Linkage Disequilibrium. For marker pairs i have got chi-square values as infinite and p-values as highly significant. initially i taught it to be some calculation error but i am surprised to find out same out put across the three species. can any one explain why i am getting this infinite value. is this value expected or is there anything wrong in my data. kindly help me to resolve this issue.

Thank you and regards

omkar

K.Omkar Babu Senior Research Fellow Institute of Biotechnology UAS Dharwad INDIA

Omkar Babu <omkarzf@gmail.com>

Imaging system need

Dear List,

Currently, I am in the process of developing a prototype of an affordable (US$15,000-20,000) fully automated 3D imaging system that can accurately obtain 3D surface renderings including color of small 3D objects such as the head of a fruit fly, the proboscis of a butterfly, and other micrometer size objects. This system will automatically image the object from all sides, extract the surface data and stores it as a single object. In order to obtain a grant for the development of this system, I need to access whether there would be a market for such a system. To help me with that, could you, if you, your lab or institution would be a potential customer, please let me know (kim@kimvdlinde.com).

Feel free to forward this to other lists where people could be interested.

Thanks,

Kim

Kim van der Linde <kim@kimvdlinde.com>

KyotoPrize 2013 for MasatoshiNei

I would like to share with you the news that Masatoshi Nei at Penn State has been honored as the recipient of the 2013 Kyoto Prize in the field of Biological Sciences (Evolution, Behavior, Ecology, Environment) from the Inamori Foundation.

According to the Foundation, “Dr. Masatoshi Nei made it possible to discuss evolutionary divergence, genetic diversity, and the mode of selection on genes in a quantitative manner by devising diverse statistical methods such as Nei^{1}s genetic distance, and applying them to molecular data. Using these methods, Dr. Nei^{1}s research has yielded important contributions to molecular evolutionary biology, as well as many other academic disciplines including ecology and conservation biology.”

Some of his achievements can be seen from the website “Masatoshi Nei ’ Google Scholar Citations < http://scholar.google.com/citations?user=-

VxOmZDgAAAAJ&hl=en >." The total number of citations for him is about 176,000. His papers are labeled as Evolution, Evolutionary biology, Molecular evolution, Population genetics, and Phylogenetics, and in all of these categories, he is at the top.

Shozo Yokoyama Emory University

"Yokoyama, Shozo" <syokoya@emory.edu>

LGBTQ

Folks,

I'm collaborating on a survey of the experiences of LGBTQ individuals working in science, tech, engineering, and math, and I'm hoping that the EvolDir community will help us share it with as many people as possible. We're using a "snowball sample" distribution model, in which we as respondents to help distribute links to the survey to their own professional and personal networks, so we can hear from as many people as possible.

There's more information below my signature, or you can go directly to the survey website, www.queerstem.org, to learn more, take the survey, and find out how to help spread the word.

thanks! Jeremy Yoder

—- Jeremy B. Yoder Postdoctoral Associate University of Minnesota Department of Plant Biology

www.jeremybyoder.com jbyoder@umn.edu

Sent with Sparrow (http://www.sparrowmailapp.com/?sig)

In the fields of science, technology, engineering and mathematics (STEM), the social experiences of lesbian, gay, bisexual, transgendered, or queer (LGBTQ) professionals are often overlooked. Those of us who work in STEM research or teaching know that LGBTQ colleagues are out there, if we know where to look, but we know very little about the LGBTQ folks who work in STEM, as a group. Basic, general information regrading the following questions is hard to come by:

What do we study? What kinds of institutions do we work at? What kinds of communities do we live in? What degree of acceptance and support have we found in our chosen career fields?

We are conducting a new, nationwide survey to begin to answer some of these questions, by eliciting feedback from as large a sample of LGBTQ folks working in STEM fields as possible. By participating, you will contribute to efforts to document the contributions of LGBTQ individuals to STEM fields and inform advocacy efforts to improve occupational experiences.

Although we welcome as much feedback as possible, please note that this survey is primarily targeted toward individuals who have completed an initial Bachelor's or Technical degree and are working in a STEM field within or outside of academia. Undergraduate experiences are unique and several quality studies exist regarding LGBTQ identity across fields of study at the postsecondary level–with this survey we aim to fill a different gap in the field.

The survey should take about 15-20 minutes to complete, and will ask about your research, your career path, your gender identity and sexual orientation, and your experience at the institution where you work and the community in which you live.

Thank you in advance for your valuable feedback!

Take the survey here: http://www.queerstem.org/p/take-survey.html jbyoder@gmail.com jbyoder@gmail.com

MacOSX Java update may break BEAST Tracer FigTree

Dear All,

Please ignore if you are not using Mac OS X.

It appears Apple have corrected their revision to fix this issue. If you update now then FigTree, Tracer, BEAST will work. If you have updated Java earlier today or yesterday then you will need to download the new updater and install it.

To check if you have the newer or older (broken) update, open Terminal.app and type:

```
java -version
```

If you see this number:

```
build 1.6.0_51-b11-457-11M4509
```

You have the new and working version. If you see '4508' at the end of this number then you have the older version and you need to re-update the update.

Download the update from here (but only if you see 4508 in the version number):

http://support.apple.com/kb/DL1572 Andrew

On 21 Jun 2013, at 14:17, Andrew Rambaut <a.rambaut@ed.ac.uk> wrote:

> Dear all, > > This is a warning that the latest update to Java for Mac OS X released > yesterday ('Java for OS X 2013-004') will stop the current version of > most of the GUI versions of programs in the BEAST/FigTree family from > working. This includes BEAUti, BEAST, FigTree, Tracer etc. > > The fix is relatively straight forward but it will take a few days > to test everything and package it all up. In the meantime, you may > want to consider holding off from installing this update. The > update fixes some security issues with using the Java Applet plugin > for web browsers which is something that is probably not a good > idea to use anyway. > > The issue is derived from the programs using a technically incorrect > way of initialising the user interface that up until this point has > worked fine. It is possible therefore that this issue could occur on > other platforms in future so all versions will be updated. > > Thanks, > Andrew > >

Andrew Rambaut Institute of Evolutionary Biology University of Edinburgh Ashworth Laboratories Edinburgh EH9 3JT EMAIL - a.rambaut@ed.ac.uk TEL - +44 131 6508624

Andrew Rambaut <a.rambaut@ed.ac.uk> Andrew Rambaut <a.rambaut@ed.ac.uk>

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Malaysia VolFieldAssist

Subject Header: VolFieldAssist.Malaysia.Job

VOLUNTEER FIELD ASSISTANT needed for 6 weeks starting mid Aug, for study of hover wasp behavioural ecology in peninsular Malaysia (note: these are small wasps that rarely sting, with average colony sizes <5 individuals). The work will involve helping a PhD student to census and observe colonies, and collect wasps for genetic analysis.

The successful applicant must be prepared to work hard and have an interest in behavioural/evolutionary biology and enthusiasm for fieldwork. A driving license is advantageous and, because the work involves recording colour marks on individual animals, the job would not be suitable for someone who is colourblind! For further details of the research that we do, see: http://www.sussex.ac.uk/lifesci/fieldlab/ Accommodation will be provided, and air fare (from the UK) will be reimbursed on successful completion of the field trip, with the applicant needing to pay for only their own food/personal expenses, which are relatively cheap in Malaysia. Accommodation will be a room in a small flat- relatively good for tropical research (shower, cooking facilities, TV etc.), with the apartment shared with the female PhD student. The field site is in a small village which is a centre for bird-watchers.

APPLICATIONS PROCEDURE

Applicants should send a covering letter and a CV, including contact details (including e-mail addresses/telephone nos.) for the applicant and 2-3 referees who would be available to provide references as soon as possible. Applicants must be available for interview in the UK during June or July. Review of applications will begin immediately and continue until the position is filled.

Applications should be sent to:

Professor Jeremy Field,

School of Life Sciences,

John Maynard Smith Building

University of Sussex

Brighton BN1 9QG, UK.

Or e-mail your application as a single Word document to: j.field@sussex.ac.uk AND l.holt@sussex.ac.uk

Lauren Holt <L.Holt@sussex.ac.uk>

PHYLIP clustering

Dear EvolDir,

I have reached a problem I think is driven by the missing data structure in my data. I am attempting to use clustering (PHYLIP) to demonstrate that single genome genotypes we have obtained from parasites within infections are more related to one-another than genotypes from the pathogen population in other patients from the same region (i.e. are parasites within infections are more related to one-another than parasites between infections). There is understandably large scale random dropout of alleles in the single cell data (about half the SNPs called per cell, though quite randomly distributed), and near complete data from the between infection data (not single cell genotypes). Using fairly standard tree generation methods (dnadist (Jukes-Cantor) and UPGMA tree from neighbor in PHYLIP) the resulting trees show a great degree of fragmentation at the tips of branches which contain single genome genotyping giving the suggestion that there is quite a degree of variation in these infections. When I inspect the data manually there are no differences between these genotypes, aside from the patterns of missing data between them. What is the most appropriate way of dealing with such data? Given the random nature of allelic dropout removing SNPs which show large amounts of missing data would substantially impact the size of my dataset.

Many Thanks for any assistance

Ian Cheeseman

ianc@txbiomedgenetics.org

PuertoRico FieldVolunteers AnoleEvolution

Field Volunteer Needed for Anole Research in Puerto Rico

I am looking for two field assistants to survey populations of Anolis cristatellus in Puerto Rico from July 21 - August 15, 2013. This project is part of my dissertation research at the University of Massachusetts Boston. Our activities will involve habitat surveys and morphological data collection. Daily activities include searching for and capturing lizards in both forest and human dominated habitats (i.e. suburban neighborhoods). We will work long hours on most days (beginning 7-8am), with about half of the day in the field and half indoors collecting data. Assistants will also have the opportunity to attend the Caribbean and Latin American Boid Meeting, which will be held in Puerto Rico while we are there. Applicants should be physically fit and be prepared for very hot and humid work conditions. Applicant must be able to work independently and be comfortable handling lizards, should be enthusiastic about reptiles, and have a good work ethic. Ideal applicants will have research or field experience with herpetofauna and be conversational to fluent in Spanish. This opportunity is unpaid, but all expenses (airfare from the US, food, lodging, and incidentals) will be covered. For more information about the Revell lab, see: http://faculty.umb.edu/liam.revell/ If interested, please contact Kristin Winchell: Kristin.Winchell001@umb.edu with a brief letter describing why you are interested in this position and any relevant research experience along with your CV and 2 professional references that I may contact by email. I will review applications as they arrive until the positions are filled.

kmwinchell@gmail.com

Reference selection AlleleFreq

Hi all!

I'm afraid my memory isn't helping me, and my google-fu isn't up to the ask of replacing it. I remember reading a paper from the 1960's about measuring allele frequencies, and showing that if they are measured before selection is complete then inferences about selection are biased. Does anyone happen to remember it better than me?

Thanks in advance.

Bob

– Bob O'Hara

Biodiversity and Climate Research Centre Senckenberganlage 25 D-60325 Frankfurt am Main, Germany

Tel: +49 69 798 40226 Mobile: +49 1515 888 5440 WWW: http://www.bik-f.de/-root/index.php?page_id=219 Blog: http://-blogs.nature.com/boboh Journal of Negative Results - EEB: www.jnr-eeb.org Bob O'Hara <bohara@senckenberg.de>

Software DAMBE update

Dear Colleagues,

A number of bug reports have recently come from MAC users of DAMBE. I have fixed them now. Please download and use the new version at:

http://dambe.bio.uottawa.ca/-dambe_installation_mac.asp 2. Some of the DAMBE functions that do not run well on MAC is simply due to the msvcirt.dll file that comes with WINE. I have added a link in the Mac installation page to a functional msvcirt.dll file so that you can download and save to the system32 folder (e.g., '/users/xxia/Wine Files/drive_c/windows/system32'):

http://dambe.bio.uottawa.ca/download/msvcirt.dll The DAMBE installation page for Mac has been revised accordingly.

3. Please cite DAMBE with the new citation: Xia, X. 2013. DAMBE5: A comprehensive software package for data analysis in molecular biology and evolution. Molecular Biology and Evolution doi: 10.1093/molbev/mst064

Best Xuhua

Xuhua Xia Professor Biology Department University of Ottawa Rm 278 Gendron 30 Marie Curie, Ottawa, Ontario Canada K1N 6N5 Tel: (613) 562-5800 ext 6886 http://dambe.bio.uottawa.ca http://www.biology.uottawa.ca/details.php?lang=-3Deng&id=3D31 Xuhua.Xia@uottawa.ca

Software PartitionFinder update

Dear all,

We're pleased to announce the release of PartitionFinder v1.1.1. This version contains a number of major improvements over previous versions, including the ability to rapidly analyse genomic datasets.

PartitionFinder is a program that allows for the combined selection of partitioning schemes and models of molecular evolution for DNA and amino acid datasets. It works on Windows, Mac, and Linux.

It is available here:

www.robertlanfear.com/partitionfinder Version 1.1.1 includes a number of improvements:

* Support for very large datasets (1000s of genes, 1000s of taxa) * Faster algorithms * Support for partitioning scheme searches using RAxML * Improved memory efficiency * Output of the best partitioning scheme in RAxML format * A number of bug fixes and other minor improvements

A full description of all the methods can be found in the manual, along with some hints on the best method to use for datasets of different sizes. The methods are more fully described and compared in an in prep paper.

Please get in touch if you have questions, suggestions, or comments.

Yours,

Rob Lanfear & Brett Calcott

– Rob Lanfear Research Fellow, Ecology, Evolution, and Genetics, Research School of Biology, Australian National University

www.robertlanfear.com rob.lanfear@gmail.com

mtDNA div high Nuclear low

Dear colleagues, In one of my datasets I found a striking pattern of high mtDNA diversity (nice, reticulated haplotype network; not star-like) but low microsatellite diversity. In all other cases I'm aware of, the pattern is reversed because mtDNA drifts faster than nucDNA, or is selectively swept every now and then. In the quest to understanding this I'd be curious to read about examples with a similarly biased diversity pattern (high mtDNA div but low microsatellite div). I tried literature data bases but could not find anything useful. Adaptive/Selectionist hypotheses are an option, too, but as my nucDNA is microsatellite this is only sort of the second route I would follow. Is anyone here aware of a paper they could send me? (high mtDNA div vs. low nucDNa div)

Cheers, Robert

rkraus@senckenberg.de

nextRAD

SNPsaurus announces launch of nextRAD genotyping

Enables genotyping by sequencing on low input samples

May 15, 2013. SNPsaurus, a genomic services company based in Eugene, Oregon, today announced the launch of their nextRAD genotyping platform. The nextRAD (Nextera-tagmented reductively-amplified DNA) marker platform is designed for genotyping large populations and for samples with limited availability of genomic DNA.

"The distinguishing feature of nextRAD compared to other genotyping-by-sequencing methods is that it does not use restriction enzymes to reduce the complexity of the genome." said SNPsaurus founder Eric Johnson. "This allows us to make high quality sequencing libraries that sample thousands to hundreds of thousands of loci across a genome from less than 10 ng total genomic DNA."

Director of Research Paul Etter said, "We tried to design nextRAD for the rapidly increasing capabilities of next-generation sequencers. It has the throughput for genotyping thousands of samples because of the streamlined protocol and the ability to multiplex hundreds of samples in a lane of a sequencer."

SNPsaurus also unveiled their nextRAD Project Explorer, at http://snpsaurus.com/project/, an online tool for exploring the parameters of a genotyping project, from low-coverage mapping of recombinant inbred lines to high-coverage genotyping for creating genetic maps, and getting a project price estimate.

SNPsaurus has licensed nextRAD technology from the University of Oregon.

About SNPsaurus

SNPsaurus is a privately owned genomic services company founded in 2013. Based in Eugene, Oregon, SNPsaurus works with researchers to rapidly provide high-quality genotyping data.

contact:

Eric Johnson, founder

<eric@snpsaurus.com>

PostDocs

ArizonaStateU MutationBioinformatics

As a follow up to the previous announcement:

I will be at both Evolution 2013 and SMBE 2013 in the coming weeks if anyone wants to discuss this opening in person with me.

A copy of the announcement can be found at the following link:

http://www.biodesign.asu.edu/jobs/postdoctoral-research-associate-2013-06-13-13-51 Reed A. Cartwright, PhD Assistant Professor of Genomics, Evolution, and Bioinformatics School of Life Sciences Center for Evolutionary Medicine and Informatics The Biodesign Institute Arizona State University - Address: The Biodesign Institute, PO Box 875301, Tempe, AZ 85287-5301 USA Packages: The Biodesign Institute, 1001 S. McAllister Ave, Tempe, AZ 85287-5301 USA Office: Biodesign A-224A, 1-480-965-9949

POSTDOCTORAL RESEARCH ASSOCIATE OPENING

http://www.biodesign.asu.edu/jobs/postdoctoral-research-associate-2013-06-13-13-51 The Cartwright Lab at Arizona State University in Tempe, AZ is seeking a Postdoctoral Research Associate in the area of Computational/Statistical Genomics to study evolutionary questions using mutation accumulation lines of the ciliate, Tetrahymena thermophila. These lines are being generated as part of an NIH funded collaboration with the Zufall and Azevedo labs at the University of Houston.

The Cartwright Lab is part of the Center for Evolutionary Medicine and Informatics (CEMI), one of 10 research centers in the Arizona State University's Biodesign Institute. Research in the Cartwright Lab covers many different questions in population genetics and molecular evolution, at the interface of biology, statistics, and computer science. A majority of our research involves developing, implementing, and applying novel methodologies to study genomic datasets.

As part of this project, the Postdoctoral Research Associate is expected to be able to: 1. Assemble the genomes of the dozens of Tetrahymena thermophila lines from short-read sequences 2. Develop novel, high-throughput methodologies to identify de novo mutations by comparing multiple lines 3. Work closely with collaborators at the University of Houston to develop statistical methods to estimate the phenotypic effects of mutations 4. Present the results of research at meetings, in publications, etc.

Required Qualifications: Ph.D. in genomics, bioinformatics, or related field

Desired Qualifications: 1. Experience working with microbial genomes 2. Knowledge of programming languages including Python and C++ 3. Knowledge of statistical methodologies 4. Experience with short-read sequencing

Application must contain one document which includes 1. Resume/CV 2. Cover Letter 3. Names, addresses, and phone numbers of three professional references

Deadline for applications is July 21, 2013. Applications will continue to be accepted and considered until the job is filled/closed.

For more information see http://cartwrig.ht/-lab/, http://bchs.uh.edu/ ˜ rzufall, and http://wwworm.biology.uh.edu.

To apply, forward one document that includes a cover letter, detailed CV, and names of 3 references to cartwright@asu.edu. Please put the job title in the subject line of the letter.

Arizona State University is an Equal Opportunity/Affirmative Action employer. A background check is required for employment.

Reed A. Cartwright, PhD Assistant Professor of Genomics, Evolution, and Bioinformatics School of Life Sciences Center for Evolutionary Medicine and Informatics The Biodesign Institute Arizona State University

Address: The Biodesign Institute, PO Box 875301, Tempe, AZ 85287-5301 USA Packages: The Biodesign Institute, 1001 S. McAllister Ave, Tempe, AZ 85287-5301 USA Office: Biodesign A-224A, 1-480-965-9949

rcartwri@asu.edu

Barcelona ComparativeGenomics

Postdoc position in Comparative Genomics in Spain

I am looking for a highly motivated candidate that can apply for a postdoctoral fellowship within the programme alliance4universities at Universitat Autònoma de Barcelona (Spain) (http:/-/www.alliance4universities.eu/a4u/en/content/-postdoctoral-mobility-0).

The aim of the project is to study the genomic structure of evolutionary genomic regions in different mammalian species. Interest in evolutionary biology, molecular biology and cell biology is required. Applicants should have a PhD in a relevant area (evolutionary biology, genomics, genetics and cell biology). I am seeking for someone with a vivid interest in evolution research and a strong background in population genetics/ statistical genetics.

Requirements:

-PhD degree obtained between 01/01/2010 and 15/10/2013.

- Competitve publication record.

- Skills in bioinformatics and/or programming.

Our group works in the fields of comparative genomics, evolution and chromosomal instability and, in particular, we are interested in the mechanisms that are driving karyotype evolution and genomic architecture in mammals. For further information please see our webpage (http://grupsderecerca.uab.cat/evolgenom/).

The Universitat Autònoma de Barcelona (UAB) is located close to the city of Barcelona and is one of the major public universities in Spain. The UAB is internationally acknowledged for its quality and innovation in research. It coordinates a potent scientific and technological centre, which comprises all the departments, science and technology services, research centres, institutes and university hospitals affiliated with the UAB.

Complete application packages, including a CV, a brief (1-page) statement of research interests, and the names and e-mail addresses of two referees should be sent to:

Dr. Aurora Ruiz-Herrera

Email:aurora.ruizherrera@uab.cat

Application deadline: 15 June 2013.

– Aurora Ruiz-Herrera, Ph.D.

Cytology and Histology Unit Dept. Cell Biology, Physiology and Immunology Universitat Autònoma de Barcelona Efidici C E-08193 Bellaterra, Spain Phone +34935812051 Fax +34935813357 aurora.ruizherrera@uab.cat http:/-/grupsderecerca.uab.cat/evolgenom/en http://-scholar.google.es/citations?sortby=pubdate&hl=-ca&user=i5EWfDsAAAAJ&view_op=list_works Cytogenetics Group Institut de Biotecnologia i de Biomedicina Universitat Autònoma de Barcelona E-08193 Bellaterra, Spain Phone +34935811379 aurora.ruizherrera@uab.cat

"Ruiz-Herrera, A" <aurora.ruizherrera@uab.cat>

BowdoinCollege PopulationBiology

Postdoctoral Position in Marine Biology

Bowdoin College invites applications for a one-year Doherty Marine Biology Postdoctoral Scholar beginning September 1, 2013, renewable for a second year. The Bowdoin Marine Laboratory seeks to build strength in climate change research of near-shore and coastal systems. Applicants with physiological, population, or community approaches to changing environments are particularly encouraged. Familiarity with bioinformatics and "omic" tools is a plus. The Scholar will maintain an active research program, participate for one week in the teaching of an appropriate biology course in the fall semester, teach either a non-majors course or an advanced seminar during the spring semester, and supervise undergraduate research at the marine lab during the summer and academic year. Bowdoin's Marine Lab is located at the Coastal Studies Center on Orr's Island, 20 minutes from campus, and offers access to a boat and excellent wet laboratory facilities with a high-capacity, flowing-seawater system. The Center includes 118 acres of forests and fields with 2.5 miles of marine shoreline. Other research instrumentation available for use on campus. The annual stipend for this benefits-eligible position is $50,000. Applicants must have received, or anticipate receiving, a Ph.D. between September 1, 2007 and September 1, 2013.

Bowdoin College accepts only electronic submissions. Please visit https://careers.bowdoin.edu to submit letter of application, curriculum vitae, statement of research and teaching interests, and the names and contact information for three references who have agreed to provide a recommendation.

Review of applications begins immediately and will continue until the position is filled.

A highly selective liberal arts college on the Maine coast with a diverse student body made up of 30% students of color, 4% International students and approximately 15% first generation college students, Bowdoin College is committed to equality and is an equal opportunity employer. We encourage inquiries from candidates who will enrich and contribute to the cultural and ethnic diversity of our college. Bowdoin College does not discriminate on the basis of age, race, creed, color, religion, marital status, gender identity and/or expression, sexual orientation, veteran status, national origin, or disability status in employment, or in our education programs.

Bowdoin College http://www.bowdoin.edu/ Bowdoin Marine Laboratory at the Coast Studies Center http://www.bowdoin.edu/coastal-studies-center/-facilities/marine-laboratory.shtml Additional questions can be directed to : Dave Carlon. I start as Director of the Bowdoin Marine Laboratory on Aug. 5

David B. Carlon

Associate Professor

Mailing address: Biology Department University of Hawaii at Manoa 2450 Campus Road, Dean Hall, Room 2 Honolulu, Hawaii 96822 U.S.A.

Lab/office address: Biomedical Sciences A-204

e-mail: carlon@hawaii.edu http://carlonlab.com Office: 808-956-9523 Lab: 808-956-5999 Fax: 808-956-4745

carlon@hawaii.edu

Chile WineBiodiversity

Call for a Postdoctoral Position to join the Wine, Biodiversity & Climate Change Program

The Wine, Biodiversity & Climate Change Program is a scientific initiative of the Institute of Ecology and Biodiversity, developing strategies for biodiversity conservation along with Chilean wine industry. The project's objective is to develop and promote conservation planning in human dominated ecosystems

Application Deadline: August 1st, 2013.

This program was initiated in 2008 to engage winegrowers in the protection of the Chilean Mediterranean ecoregion, which lacks adequate protection in the Chilean Protected Area Network, is highly impacted by human activities and contains more than 50% of Chilean vascular plants and vertebrates. Our primary interest has been to study how this ecosystem can continue providing ecosystems services to the industry and the local community today and under future climate change scenarios. We aim to generate research led conservation plans promoting stewardship of these ecosystems by knowledge transfer to wine growers and local communities.

We are looking for a postdoctoral fellow with expertise in community & landscape ecology, ecosystem ecology and/or environmental change and conservation. The candidate should possess good statistical skills and GIS modelling experience. Opportunities to participate in soil microbiology and metagenomics aspects of the project are possible.

The post will be based at the Instituto de Ciencias Ambientales y Evolutivas, Universidad Austral de Chile, in

Valdivia, Chile. The candidate will need to be expected to travel to winegrowing regions of Chile and Santiago for meetings. The post requires a valid driving license and a minimum level of Spanish. Additional Spanish language training will be available.

The position will be initially for one year starting in September 2013 (negotiable), and renewable depending on performance (measured in publications), for up to 3 years.

Applicants should submit: ï CV ï Certificate of Doctoral Degree ï Cover Letter describing motivation ï Two letters of recommendation by researchers with extensive knowledge of the applicant

Recommendation letters and all the other documentation should be sent directly to Dr. Olga Barbosa (olga.barbosa@uach.cl) More info: www.vccb.cl / www.ieb-chile.cl / olga.barbosa@uach.cl

Dra. Olga Barbosa Laboratorio de Sustentabilidad Urbana y Cambio Global Instituto de Ciencias Ambientales y Evolutivas Avenida Rector Eduardo Morales Miranda, Edificio Pugín, 3r piso, oficina nÂ307 Universidad Austral de Chile, Valdivia *56-63-221217* www.uach.cl Instituto de Ecología y Biodiversidad (IEB) www.ieb-chile.cl www.vccb.cl Olga Barbosa <olgabarbosa@gmail.com>

CzechRep FishEvolutionaryEcolPhysiology

A new postdoctoral position in our lab is available for work with automated respirometry system.

POSTDOCTORAL RESEARCH POSITION FOR 12 MONTHS, FURTHER EXTENSION NEGOTIABLE

TOPIC: Evolutionary ecology of fish: physiological mechanisms and constraints in the life history evolution

REICHARD LAB, INSTITUTE OF VERTEBRATE BIOLOGY ACADEMY OF SCIENCES OF THE CZECH REPUBLIC

One full-time postdoctoral position is available in the lab of Martin Reichard at the Institute of Vertebrate Biology, Czech Academy of Sciences, located in Brno, Czech Republic (http://www.reichardlab.eu). Position may start as soon as filled; all application submitted until 14 July 2013 will be fully considered. One year contract initially, further extension possible. Project will use automated respirometry system (including respirometry in a swim tunnel) (Loligo Systems) to compare individual and population differences in annual killifish metabolic rates and associate them with other life history traits measured during a large-scale common garden experiment. Collaboration on studies testing the effect of parasites on fish condition (bitterling fish, annual fish) and their metabolic rate will be encouraged. Work will be done within the framework of European Center for Ichthyoparasitology, funded by Czech Science Foundation.

QUALIFICATIONS - PhD in Biology and experience with aquatic respirometry is required. SALARY - 44 000 CZK, c. 1800 EUR per month

APPLICATION PROCEDURE V For formal applications, please submit a CV and explain your previous work and motivation to apply for this position in your Cover Letter. For informal enquires and more details, feel free to email reichard@ivb.cz

Martin Reichard Institute of Vertebrate Biology Academy of Sciences of the Czech Republic Kvetna 8, 603 65 Brno Czech Republic www.reichardlab.eu reichard@ivb.cz

DukeU EvolutionaryBiology

Postdoctoral Position in Evolutionary Biology at Duke University

Applications are invited for a postdoctoral (Postdoctoral Associate) position to study mechanisms of female dominance and reproductive skew in meerkats.

Occupational Summary:

A full-time research position, funded by the National Science Foundation, is immediately available to assist with an integrative project that combines behavioral, endocrine, and chemical approaches to study female development, with the aim of better understanding the evolution of female dominance and reproductive skew. The work is to be conducted partly at Duke University (http://evolutionaryanthropology.duke.edu/) in North Carolina and partly at the Kalahari Meerkat Project (http://www.kalahari-meerkats.com/) in South Africa. Applicants should be ready to spend up to six-month stretches in the field; field experience in behavioral endocrinology is preferred. Experience in analytical chemistry and other laboratory techniques is desired, but on-the-job training is available. The opportunity to develop independent research is also available. The initial appointment is for one year, with subsequent funding conditional on satisfactory performance. Salary will be partly based on previous experience and includes benefits.

Qualifications:

The successful candidate will have earned a PhD in a relevant discipline.

Applicants should have a strong background in one or more of the following areas: animal behavior/behavioral ecology, endocrinology, chemical ecology, evolutionary or field biology, population dynamics/genetics.

Experience working with wild animals and in a laboratory is required

The applicant should work well independently and as part of a team, and should be enthusiastic and highly motivated.

Responsibilities:

Animal handling and administration of hormonal preparations

Behavioral data collection on free-ranging meerkats, using hand- held computers

Collection of biological material (blood, fecal, glandular) from animals

Oversight of field assistants on all aspects of data collection

Transportation or shipment of biological samples to the US

Performance of various assays (e.g. RIA, EIA, GCMS, LCMS, HPLC)

(Assistance in DNA extraction and various genetic analyses, as necessary)

Data maintenance and analysis

Coordination with field and laboratory managers

Assistance in the training and review of new personnel or procedural developments

Performance of other related duties incidental to the work described herein

Please email an application, consisting of a cover letter summarizing your qualifications and interests, curriculum vitae, representative reprints or preprints, and the names and contact information for two references, to Christine Drea (cdrea@duke.edu). Evaluation of applicants will begin immediately and will continue until the position is filled.

Duke University is an Equal Opportunity/Affirmative Action/ADA Employer.

Christine Drea <cdrea@duke.edu>

FloridaStateU EvolBiolBehavEcol

POSTDOCTORAL RESEARCHER IN EVOLUTIONARY BIOLOGY AND BEHAVIORAL ECOLOGY: FLORIDA STATE UNIVERSITY Dr. Emily Moriarty Lemmon Department of Biological Science Florida State University

Position Description: A postdoctoral position (up to two years) is available in the laboratory of Dr. Emily Moriarty Lemmon to collaborate on an NSF-funded project to study the effect of community interactions on evolution of male reproductive signals and female preferences in chorus frogs (Pseudacris) and the genetic consequences for speciation.

The postdoctoral scientist will lead a team of graduate students and field technicians to conduct fieldwork across the southeastern United States and perform behavioral experiments in a portable lab during the spring field seasons (approximately two months per year). Outside of the field season, the postdoctoral scholar will analyze behavioral data, genotype samples, and collect high-throughput sequencing data via anchored phylogenomics.

The postdoctoral researcher will have the opportunity to gain training in high-throughput data collection for phylogenomics and population genetics, analysis of phylogenetic data, bioinformatics, and behavioral ecology.

The ideal candidate will have field experience with frogs, experience conducting behavioral experiments, training in molecular biology, and computational experience. However, applicants with some combination of the above qualifications will also be considered. The start-date for this position will be Fall 2013 (exact date flexible), and salary will be competitive.

Interviews: Dr. Lemmon will be attending the Evolution 2013 meetings June 21-26. Qualified applicants should specify whether they will be available for an interview during these meetings. Other applicants will be contacted as needed.

Minimum Qualifications: A Ph.D. in biology, molecular biology, or a related field with a focus on evolution Previous research experience and a strong publication record Extensive field experience, preferably with amphibians Ability to communicate clearly, work efficiently and independently, interact collaboratively, and lead a field team Additional Preferred Qualifications: Molecular biology and genetics training (e.g., phylogenetics, population genetics, phylogeography) Computational experience Experience in high-throughput sequencing Experience conducting behavioral studies

Application Deadline: 15 July 2013 (or until filled).

Start date: Fall 2013 (exact date flexible up to December).

To Apply: Application materials consisting of (1) a CV, (2) a statement of research interests and experience including how previous experience relates to the position description (2 page max), and (3) contact information for three references must be submitted to chorusfrog@bio.fsu.edu. Review of applications will begin June 21, 2013 and will continue until the position is filled. Informal inquiries are welcome. General information about the lab can be found at http://www.bio.fsu.edu/chorusfrog/index.html . About Florida State University: The successful applicant will be affiliated with the Department of Biological Science (http://www.bio.fsu.edu/) and will also interact with the Department of Scientific Computing (http://www.sc.fsu.edu/), and the College of Medicine (http://med.fsu.edu/). These groups collaborate extensively on evolutionary, behavioral, statistical, mathematical, genomic, and computational projects. The postdoctoral researcher will join this community of highly interactive research laboratories. Florida State University is located in capital city Tallahassee on the Florida Panhandle immediately adjacent to the Apalachicola National Forest, which is the largest national forest in Florida (nearly 900 sq. mi.). The forest borders the Apalachicola National Estuarine Research Reserve, which is one of the most productive estuarine systems in the Northern Hemisphere. The Apalachicola River basin contains the highest herpetofaunal diversity in the U.S. and Canada.

The researcher chosen will become part of the integrative laboratory groups of Emily Moriarty Lemmon and Alan Lemmon at Florida State University. The Lemmons collaborate extensively on projects involving collection of high-throughput phylogenomic data and on the development of new approaches to analysis of these data. More information is available at these websites: http://www.bio.fsu.edu/chorusfrog/index.html http://www.bio.fsu.edu/faculty-moriarty-lemmon.php http://www.evotutor.org/LemmonLab/ Emily Moriarty Lemmon, Assistant Professor Department of Biological Science

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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

GeorgeWashingtonU HumanEvolutionaryBiol

The George Washington University Department of Anthropology announces a Research Associate position in Human Evolutionary Biology. This is a one-year, full-time position in the Center for the Advanced Study of Hominid Paleobiology (CASHP) that may be extended at the discretion of the department contingent on the availability of funding. The successful candidate will work closely with the Principle Investigator and will contribute to a systematics-related research agenda in the area of human evolutionary biology. The Research Associate will also be expected to contribute to undergraduate and/or graduate training in the conduct of research. Applicants should include a cover letter with a brief proposal describing the research they intend to perform while funded by CASHP.

Salary is commensurate with experience. Preference will be given to applicants who have demonstrated their ability to conduct and publish their research, have research experience in the area of human evolutionary biology, and who have completed their PhD.

Full details of the position are at the George Washington University Employment Portal: https://www.gwu.jobs/postings/15979. Please send all applicant materials directly to Dr. Bernard Wood at bernardawood@gmail.com, as well through the GWU Employment Portal. For more information, contact Charlotte Krohn, chark629@gwu.edu, 202-994-0351. Find more information about CASHP at cashp.gwu.edu.

Thanks so much,

Charlotte Krohn

"Krohn, Charlotte" <chark629@email.gwu.edu>

GhentU PhD Postdoc GeneDuplications

The following positions are now open in the Van de Peer Lab at VIB/Ghent University, Belgium (http://bioinformatics.psb.ugent.be/), in relation to the ERC Advanced Grant Double-Up, on the importance of gene and genome duplications for natural and artificial organism populations.

2 PhD positions 1 Postdoc position

The long-term establishment of ancient organisms that have undergone whole genome duplications has been exceedingly rare. On the other hand, tens of thousands of now-living species, both plants and animals, are polyploid, and contain multiple copies of their genome. The apparent paucity of ancient genome duplications and the existence of many species that are currently polyploid provide an interesting and fascinating enigma. A question that remains to be answered is whether these older genome duplications have survived by coincidence or whether they could survive only because they did occur, or were selected for, at very specific times, for instance during major ecological upheavals and periods of extinction. We hope to address these questions at different levels through 1) the analysis of whole plant genome sequence data and 2) the in silico modeling and evolution of artificial gene regulatory networks to mimic the genomic consequences of genome doubling and how this may affect network structure, redundancy, rewiring, and dosage balance. Furthermore, we aim at using simulated robotic models running on artificial gene regulatory networks in complex and challenging environments to evaluate how both natural and artificial organism populations can potentially benefit from gene and genome duplications for adaptation, survival, and evolution in general.

DOUBLE-UP is a truly interdisciplinary proposal that will open up new horizons and perspectives for different fields of research, from bioinformatics and systems biology over comparative and evolutionary biology, to network modeling and evolutionary robotics.

We are looking for 2 highly motivated PhD students and 1 highly motivated Postdoc to help us achieve these ambitious goals. A strong (bio)informatics background, good programming skills, and previous modeling/simulation experience are all required. A background in evolutionary biology and population biology is strongly preferred. Some interest in evolutionary robotics and artificial life is an advantage. Applicants should be proficient in English, both speaking and writing. The positions are available starting October 1st, 2013, with funding secured for at least four years.

Contact Yves Van de Peer at yves.vandepeer@psb.ugent.be for more information and/or to apply. To apply, please send a detailed CV and motivation letter before August 15th. –

Check out http://www.plantgenomeevolution.com/

Yves Van de Peer, PhD.

Professor in Bioinformatics and Genome Biology Group Leader Bioinformatics and Systems Biology, VIB Department of Plant Systems Biology Ghent University Technologiepark 927 B-9052 Ghent Belgium

Phone: +32 (0)9 331 3807 Cell Phone: +32 (0)476 560 091 Fax: +32 (0)9 331 3809 email: yves.vandepeer@psb.vib-ugent.be

http://bioinformatics.psb.ugent.be/ Yves Van de Peer <yves.vandepeer@psb.vib-ugent.be>

HarvardU Bioinformatics Comput Biol

Postdoctoral Position in Bioinformatics and Computational Biology

The Lemos laboratory at Harvard University is searching for a postdoctoral fellow in bioinformatics / computational biology interested in pursuing research in epigenomics, population genomics, genotype-environment interaction, and the architecture of complex diseases. The fellow should be interested in working with computational data analysis, and be motivated by research that combines careful genetics and extensive computational and statistical analyses of genome-wide data from a variety of experimental sources.

The laboratory is housed at the Harvard School of Public Health located within a vibrant research community that includes the Harvard Medical School, and several affiliated hospitals. The school has significant strengths in computational biology, biostatistics, genomics, and engineering that will be all within close reach of the fellow. Applicants must be extremely curious and motivated by science, be genuinely enthusiastic, and have the ability to work independently within a collegial and collaborative team. Applicants should expect a fun and creative research environment in which I can provide plenty of individual mentoring and support to develop your own interests and ideas.

Applicants must have a PhD at the time of the appointment and have a strong analytical background with proficiency in one or more programming languages.

Applications should be sent to blemos@hsph.harvard.edu. Please send a cover letter (max 2 pages) describing your research interests and experience, a C.V. and contact information for three references. Review of applications will start on July 15th, and will continue until the position is filled.

Informal enquires of interested candidates with other backgrounds are also welcome.

Bernardo Lemos Assistant Professor Harvard School of Public Health http://www.hsph.harvard.edu/faculty/bernardo-lemos/ blemos@hsph.harvard.edu

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INRA Sophia DNABarcoding

Post-Doctoral Position in DNA Barcoding, Taxonomy and Phylogenetics of biological control agents and their target crop pests.

INRA Sophia Antipolis (France) is searching for a postdoctoral fellow to lead research and training activities in DNA-barcoding, taxonomy and phylogenetics on several groups of arthropods of agronomic interest.

The successful candidate will work within the consortium involved in the European Commission project FP7-IAPP Colbics± (industry/academia collaboration on biological control using macro-organisms): Institut National de la Recherche Agronomique (France), Universidad Politcnica de Valencia (Spain), Universidad Catolica de Chile (Chile), Biobest (Belgium), In-Vivo Agrosolution (France), ANASAC (Chile). The fellow will: - Coordinate of the DNA-Barcoding activities to be performed at INRA Sophia Antipolis with other Colbics± participants. - Train students and researchers to the basic methods of phylogeny reconstruction and associated DNA sequence analysis techniques. - Investigate the phylogenetic relationships within complexes of cryptic taxa of agronomic relevance. This activity will benefit from abundant DNA multi-locus data produced for 4 years by the teams (e.g. on Hemiptera:Pseudococcidae, Hymenoptera:Eupelmidae, and Hymenoptera:Trichogrammatidae).

Main scientific contacts: Thibaut Malausa (tmalausa@sophia.inra.fr), Nicolas Ris (ris@sophia.inra.fr).

The ideal candidate will have: - Experience of large DNA dataset handling and analysis - Excellent understanding of phylogeny reconstruction methods. - Experience of phylogenetic studies based on multilocus data. - Basics in the taxonomy of insects, especially Hymenoptera. - Published works (in peer-reviewed international journals) including comprehensive phylogenetic analyses; - Skills in bioinformatics - Basic knowledge of Next-Generation DNA sequencing techniques and data.

Candidate Eligibility Criteria (EU FP7-IAPP rules): (1) PhD Degree. (2) Full-Time Research experience between 4 and 10 years since the Master Degree (or equivalent degree that enables to embark a PhD). (3) Less than 12 months spent in France since July 2010.

Contractual conditions: - Full-time contract. - Employer: Institut National de la Recherche Agronomique. - Duration: 24 months. - Contract starting date: From August 2013. - Gross salary: 4,500 EUR (net salary around 3,600 EUR). - Work place: INRA Sophia Antipolis, 400 route des Chappes. BP 167. 06903 Sophia Antipolis, France (near Antibes and Nice, Southern France).

Instructions to applicants: (1) Eligibility Check (deadline 30th of June): Applicants are asked to fill the online form at https://enquetes.inra.fr/index.php?sid=73914&lang=en; (2) Preliminary Selection: Eligible candidates will be asked to provide recommendation letters, a detailed C.V. and a cover letter; (3) Final selection: up to 4 candidates will be interviewed.

– Thibaut Malausa Charg de Recherches INRA UMR 1355 ISA 400 route des Chappes. BP 167 06903 Sophia Antipolis cedex. FRANCE Tel: +33 (0)4 92 38 65 06 Tel: +33 (0)9 77 21 71 66 E-mail : tmalausa@sophia.inra.fr Web : http://www.paca.inra.fr/institut-sophia-agrobiotech/Equipes-de-recherche/BPI Thibaut Malausa <tmalausa@sophia.inra.fr>

KielU MicrobialGenomeEvolution

A post-doctoral position is currently available for three years with Tal Dagan at the Institute of Microbiology, Christian-Albrechts-University Kiel, Germany (http:/-

/www.mikrobio.uni-kiel.de/de/ag-dagan). The position is within the framework of the Future Ocean Cluster (www.futureocean.org) that includes scientists from Kiel University and GeoMar. For candidates in pursuit of a habilitation thesis, the term of the position may be extended to five years. The successful applicant will be expected to participate in teaching of molecular evolution, genomics, or biostatistics.

The Dagan group research interests are focused on microbial genome evolution. Our current research projects include the study of DNA acquisition dynamics in natural environments, the evolution of protein interaction with molecular chaperones and the evolution of phenotypic diversity in cyanobacteria. In our research we use both computational and experimental approaches.

Candidates must have a Ph.D. in Evolutionary Biology, Molecular Biology, Microbiology or related fields. Proved expertise in molecular evolution or bioinformatics are required. To apply, please submit applications by e-mail to Tal Dagan (tdagan@ifam.uni-kiel.de), as a single PDF including (1) a CV, (2) a brief statement of past accomplishments and PDFs of most relevant publications, (3) research interests and (4) names and contact information of three referees. Interested applicants attending the SMBE 2013 conference in Chicago are invited to approach Tal Dagan for an informal chat.

tdagan@ifam.uni-kiel.de

MaxPlanckInst Leipzig Bioinformatics

Max-Planck Institute for Evolutionary Anthropology Bioinformatics and Genome Analysis

Post-doctoral positions are available in the Bioinformatics and Genome Analysis groups at the Max Planck Institute for Evolutionary Anthropology in Leipzig, Germany.

The goal of the research groups is to develop and apply computational methods for the analysis of genome and transcriptome sequence data from primates, archaic humans and model organisms. A major focus is understanding the evolution of modern humans through the comparison of human genomes with the genomes of other primates and archaic humans.

The candidates will work on the analysis of next generation sequence data of archaic and modern human genomes. S/he will have the opportunity to interact with colleagues in population genetics and statistics and will collaborate closely with experimental groups generating genome sequence and expression data.

The successful applicants will hold a doctoral degree in computer sciences, statistics, or biological sciences with demonstrated experience in computational and statistical approaches and a solid publication record. Previous experience in the analysis and integration of data, particularly next generation sequence data, as well as the statistical interpretation of datasets is required. The applicant should have demonstrated experience in the implementation of scientific algorithms in software.

Proficiency with at least one high level programming language (eg: C++) and appropriate scripting languages and statistical data analysis tools (Python/Perl, R/MATLAB) is expected. The applicant should have a demonstrated ability to work independently, and to devise and implement his/her own ideas and bring projects to publication. S/he should have excellent written and spoken communication skills. The ability to work in an inter-disciplinary setting and to communicate with both computational and wet-lab colleagues is essential.

WHERE Max-Planck Institute for Evolutionary Anthropology. Leipzig, Germany http://-www.eva.mpg.de/ HOW TO APPLY: Interested applicants should send a cover letter and CV including at least 2 references by email to: kelso@eva.mpg.de or pruefer@eva.mpg.de

Kay Pruefer <pruefer@eva.mpg.de>

NewYorkU EvolutionarySystemsBiology

Postdoctoral Researcher, Siegal Lab, New York University

A postdoc position is available in Mark Siegal's lab at NYU's Center for Genomics and Systems Biology. The Siegal lab uses a variety of experimental and computational approaches to understand phenotypic robustness and variability. The successful candidate will work on an NIH-funded project to understand the effects of mutations on variation in yeast-cell growth, using high-throughput microscopy and automated image analysis. The postdoc will also have the opportunity to pursue independent research related to this work.

The Center for Genomics and Systems Biology is a dynamic and interactive research environment, with a unique concentration of labs investigating questions at the intersection of systems biology and evolution. NYU is located in the wonderful Greenwich Village neighborhood of New York City.

Applicants should be motivated, creative and collegial. Prior experience with relevant experimental methods (yeast molecular genetics, microscopy, image analysis) is advantageous. Review of applications will begin immediately and continue until the position is filled. To apply please email Mark Siegal <mark.siegal@nyu.edu> with CV, a list of references and a brief statement of research experience and interests. New York University is an equal opportunity employer.

Mark L. Siegal Associate Professor and Director of Undergraduate Studies Center for Genomics and Systems Biology Department of Biology New York University 12 Waverly Place, 8th Floor New York, NY 10003

mark.siegal@nyu.edu http://www.nyu.edu/projects/-siegal mark.siegal@nyu.edu

NorthCarolina BehavioralEvolution

POSTDOCTORAL RESEARCH ASSOCIATE

COCKROACH BEHAVIORAL AND NUTRITIONAL ECOLOGY

North Carolina State University

A postdoctoral research position is available in the lab of Jules Silverman to study cockroach behavioral and nutritional ecology. This is a collaborative project with Coby Schal with the specific aim to understand how glucose-averse *Blattella germanica* compete with non-averse conspecifics in nutrient constrained environments. The project could involve a mix of experimental, observational, nutritional geometry, genetic, biochemical and other tools, depending on the interests of the successful applicant. The successful candidate will have the opportunity to interact with a broad group of students, postdocs and faculty in the departments of Entomology and Biology at North Carolina State University working on insect-host plant interactions, behavior, physiology, genetics and chemical ecology. This is a two-year appointment with a possible one-year extension, depending on the availability of funds.

Project Background: In response to strong selection with toxic baits, populations of the German cockroach *Blattella germanica* have developed behavioral deterrence to d-glucose, a universal phagostimulant. This trait is heritable, the behavior is elicited by glucose alone, glucose-containing disaccharides remain palatable, and the trait confers great fitness advantage under selection pressure of glucose-containing baits (Silverman and Bieman 1993, *J. Insect Physiol.* 39:925-933). Recently, we determined that this behavior is mediated by a gain of function chemosensory mutation whereby glucose elicits strong responses from both sugar and bitter gustatory receptor neurons (Wada-Katsumata et al. 2013, *Science* 340: 972-975). Since glucose is ubiquitous within the natural environment of the German cockroach we are particularly interested in uncovering behavioral and physiological adaptations linked to glucose-aversion, which allow this trait to persist in the absence of selection with glucose-containing baits.

Qualifications: Ph.D. in a biological science, e.g. Entomology, Zoology, Ecology and Evolutionary Biology, Behavioral Biology. Research experience with insect foraging behavior and nutrient regulation preferred.

To apply, send curriculum vitae, statement of interest and qualifications, names and contact info for three references, and up to three relevant publications to:

Dr. Jules Silverman

jules_silverman@ncsu.edu.

Department of Entomology North Carolina State University Raleigh, NC, USA 27695

Application review will start June 24, 2013 and continue until the position is filled. Salary (plus benefits) will be commensurate with experience and qualifications. See http://www.cals.ncsu.edu/entomology/-silverman and http://www.cals.ncsu.edu/entomology/-schal for information about our labs.

jsilver@ncsu.edu

Omaha MadagascarBiodiversity

Postdoctoralâ© Fellow - Madagascar Biodiversityâ© Genomics

Job Description: Omaha's Henry Doorly Zoo and Aquarium Conservation Genetics Department (OHDZA-CG) based in Omaha, Nebraska is seeking a post-doctoral researcher with interest/expertise in the generation and analysis of next-generation sequencing data of lemurs, tortoises, and other taxa from Madagascar.

Duties: The successful applicant will construct genomic library for high throughput sequencing as well as assemble and analyze sequence data and manage nextâgeneration sequence workflows. This individual will be responsible for development, implementation, and support of software applications related to variant detection and interpretation from high-throughput experiments involving multiple species of lemurs, tortoises, and taxa from Madagascar. Interested candidates should be highly motivated, organized, independent, and have extensive experience with molecular genomics and bioinformatics. Travel to Madagascar to support the field programs of OHDZA-CG is required for a minimum of five week intervals twice a year.

Basic Qualifications: Applicants should hold a PhD in bioinformatics, computer science, molecular genomics or related field and have more than one year of experience in highâthroughput genome sequence analysis. Applicants should be experienced at software related to next generation sequencing data and be able to manipulate genomic data for phylogenetics and phylogeography. Our group's focus is large-scale sequencing for phylogenetics, phylogeography and evolutionary studies of lemurs, tortoises and other taxa from Madagascar. Thus, previous experience in genome assemblies, annotation and analysis of next generation sequencing (NGS) are preferable. The ideal candidate will be independent, highly motivated, productive, and able to work effectively in a team with members from a variety of diverse backgrounds with outstanding written and verbal communication skills. The successful applicant must be interested in interdisciplinary science and field research and have a solid publication record that illustrates ability to conduct novel, independent research.

Must be legally entitled to work in the USA. Visa sponsorship is not available at present.

Preferred Qualifications: Candidates should have 3+ years of experience in molecular biology, genetics, or bioinformatics. The position requires proficiency in programming (Perl, C++) and Linus operating systems. Applicants are also expected to be familiar with bioinformatics tools and genomics databases and have extensive and creditable laboratory experience with constructing genomic libraries.

Appointment: The selected candidate will be based primarily at OHDZA-CG, but the individual will be required to travel and conduct field work with the projects under the management of the Madagascar Biodiversity Partnership, ONG (www.madagascarpartnership.org). Salary/benefits are based on OHDZA-CG's salary/benefits structure, and are commensurate with experience. The initial appointment is for duration of twoâyears, but is renewable for an additional two years based on performance.

Application: Applicants should send curriculum vitae, a statement of research interests and career goals, and the names and addresses of three academic references to:

Dr. Edward E. Louis, Director of Genetics department, Center for Conservation and Research, Omaha's Henry Doorly Zoo and Aquarium, 3701 South 10th Street, Omaha, NE 68107; Email: edlo@omahazoo.com; genetics@omahazoo.com

Review of applications will begin on July 15, 2013 and the position selected by August 1, 2013. The position will begin on September 1, 2013.

Contact Information: Dr. Edward E. Louis Director of Conservation Genetics Department Center for Conservation and Research Omaha's Henry Doorly Zoo and Aquarium 3701 South 10th Street, Omaha, NE 68107 Email: edlo@omahazoo.com; genetics@omahazoo.com

genetics@omahazoo.com

PennStateU Paleontology

Postdoctoral position in paleontology, Penn State University

We invite applications for a postdoctoral researcher to participate in a collaborative research project (A. Krug and M. Patzkowsky) investigating the Late Ordovician mass extinction and recovery using phylogenetic methods that quantify evolutionary history. The NASA funded research involves the development of brachiopod phylogenies for use in analyzing changes in evolutionary patterns, fluctuations in phylogenetic diversity, and changes in community composition across the Ordovician-Silurian boundary. Experience with quantitative methods in paleobiology is required. Knowledge of phylogenetic methods and analyses is preferable. The position is located within the Department of Geosciences at Penn State University. Starting date negotiable but prefer September 2013, potentially extending for 3 years. Requires either PhD in hand or dissertation submitted and approved for degree. Please send an application letter, CV, and email addresses of two references via email to Dr. Andrew Z. Krug

<azk102@psu.edu<akrug@psu.edu>> at Penn State University.

Dr. Andrew Z. Krug Research Associate Department of Geosciences The Pennsylvania State University

Andrew Krug <azk102@psu.edu>

Perth Australia AdaptiveGenomics

Perth Australia: Adaptive genomics

A postdoctoral position is available in the Department of Environment and Agriculture, Curtin University (Perth, Western Australia) to participate in an Australian Research Council Discovery Project. The joint project, with investigators from Curin University (Tianhua He), Murdoch University (Prof Neal Enright) and University of Oklahoma (Prof Yiqi Luo), integrates field/glasshouse experiments with genomic analysis to investigate whether the adaptation andevolution of plants is rapid enough to keep pace with climate change. The postdoc will be expected to lead population genomics analyses, and participate in field/glasshouse work with technical assistance. The ideal candidate will have: 1. experience in next generation sequencing technologies, particularly transcriptome sequencing and analysis, EST-SSR screening and genotyping - essential; 2. written and published articles in scientific journalsV essential; 3. good knowledge in plant ecology and/or evolution, and/or phylogeneticsV highly desirable; 4. skills in bioinformatics V highly desirable; 5. knowledge of Australias plant families such as the Proteaceae and Myrtaceae V desirable.

The appointment will be made for one and half years commencing from late 2013 (overseas applicants note that the process of getting a working visa in Australia could take 4-5 months), with the possibility of renewal for a second year. Commencing salary (before tax) will be in accordance with qualifications and experience and within the range AU$58091- $78831 per annum (Academic Level A, minimum salary for a PhD degree holder is AU$73439). Other benefits include 9% employer superannuation contribution, and 4 weeks annual leave with pay. Successful candidate is expected and will be assisted to develop new projects and secure funding as independent investigator.

To apply for the position, go to http://-futurestaff.curtin.edu.au/job-vacancies/. Tianhua He is available for enquiries.

please send a CV and a cover letter describing your background andresearch interests, and name and contact information of three referees to Tianhua He (also available for enquiries).

The research in our group utilizes population genetics/genomics, phylogenetic analysis, reconstruction of ancient ecological and functional traits, and field experiments on nature populations/species to address questions related to adaptation and diversification in southwest Australias biodiversity hotspot.

Tianhua He Depart. Environ. & Agric., Curtin University; PO Box U1987, Perth, WA 6845, Australia E: Tianhua.He@curtin.edu.au T: +61 8 9266 7964; +61 437 788 235

Tianhua He <Tianhua.He@curtin.edu.au>

RutgersU PopulationGenomics

Postdoc -Population Genomics

Postdoctoral positions in Population Genomics at Rutgers University

Seeking qualified applicants for a post-doctoral position with Andrew Kern in the Department of Genetics and the Human Genetics Institute of New Jersey at Rutgers University. One postdoc position in unassociated with a particular project, however recent work in the lab spans the intersection of machine learning, population genetics, comparative genomics, and evolutionary biology. The other postdoc position is NIH funded to work on methods development for parameter inference in Isolation with Migration (IM) models. This work will be done in collaboration with the lab of Jody Hey.

More information about the Kern lab can be found here: http://kernlab.rutgers.edu . Information about our collaborator Jody Hey can be found here: http://genfaculty.rutgers.edu/hey . More information about the department can be found here: http://-genetics.rutgers.edu/. The Kern lab is located on the Busch campus of Rutgers University, in central New Jersey, and is in easy commuting range to New York City.

The ideal candidate would hold a Ph.D. and have a record of research achievement in population genetics, computational biology, computer science, statistics, or a related field. A background in comparative/population/evolutionary genomics is of course highly desirable. In addition the candidate should have experience programming in C, a scripting language (Ruby, Python, or Perl is fine), and would ideally be comfortable with cluster computing environments.

Review of applications will begin immediately and continue until the positions are filled. The position could begin as early as August, 2013. Interested candidates should submit an electronic version of their CV along with a cover letter describing their qualifications and relevant experience to Andrew Kern (kern@biology.rutgers.edu)

Andrew Kern Assistant Professor of Genetics Rutgers University kern@biology.rutgers.edu

Kern@dls.rutgers.edu

StanfordU PopGenetics

Postdoc in population genetics, Stanford University

Postdoctoral positions are available in Jonathan Pritchard's lab, which will be moving to Stanford University in August 2013.

Current work in the group uses computational and statistical methods to study a variety of problems in population genetics and molecular evolution. One focus is on the evolution of gene regulation, in collaboration with Yoav Gilad's lab. We are also interested in a variety of other problems including the genetics of complex traits; models of genetic architecture and genetic load; natural selection; and methods for studying population structure and demographic history. At Stanford we will be joining an outstanding community in population genetics, evolutionary biology and genomics. Much of our current work is in humans, but we are potentially interested in a broad range of organisms. Successful applicants will have considerable latitude and resources to design their own projects.

Applicants for the position must have a background in population genetics or come from a quantitative field (such as statistics or computer science) and have a demonstrated interest in genetics and evolution. Strong programming and bioinformatics skills are essential. Applicants must be highly motivated and able to work independently when needed.

Informal inquiries as well as applications (including a CV and description of research interests) should be emailed to Jonathan Pritchard (pritch@uchicago.edu). Applications will be considered as they are received; positions will be available any time starting in August.

Jonathan Pritchard Howard Hughes Medical Institute Departments of Genetics and Biology Stanford University

pritch@uchicago.edu

Switzerland Evolutionarydynamics

A collaborative research team led by Blake Matthews, Ole Seehausen, and Bernhard Wehrli are seeking a postdoctoral researcher with a background and interest in evolutionary biology, community ecology, and/or ecosystem science.

The aim of the project is to understand the interaction between eco-evolutionary dynamics and the functioning of aquatic ecosystems. Specifically, we are interested in how organism-mediated changes to the temporal and spatial heterogeneity of ecosystems can alter environmental sources of selection, so as to either promote or constrain further adaptive evolution. The project involves large-scale eco-evolutionary experiments that address fundamental links between the ecology and evolution of food webs and the physical environment and biogeochemistry of aquatic ecosystems. An ideal candidate would have some experience with next generation sequencing methodologies and strong analytical abilities for the analysis of ecological communities.

Eawag's Center for Ecology, Evolution & Biogeochemistry (CEEB) is located on the shore of Lake Lucerne in Switzerland, and is a strong nucleus of Eawag research groups aimed at integrating evolutionary biology, community ecology, and ecosystem science http://www.eawag.ch/forschung/cc/ceeb/index_EN. The postdoc will interact with a diverse range of researchers studying community ecology, evolutionary biology, ecological genetics, ecosystem science, and applied environmental science.

The starting date for the postdoc is flexible, but a starting date in 2013 is preferred. Applications should include a cover letter, a curriculum vita, and the names of three references. Copies of 3-5 prior publications will also be considered if made available via PDF.

Please submit your application by 1 July 2013. Applications must be submitted online via this link: http://internet1.refline.ch/673277/0201/++publications++/1/index.html For further information: please contact

Blake Matthews by email (blake.matthews@eawag.ch), or visit our webpages below.

Blake Matthews: http://homepages.eawag.ch/~matthebl/Welcome.html Ole Seehausen: http://www.eawag.ch/about/personen/homepages/seehauso/index_EN Bernhard Wehrli: http://www.eawag.ch/about/personen/homepages/wehrli/index Blake.Matthews@eawag.ch

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TexasTechU EvlutionaryGenomics

Postdoctoral Position in Bioinformatics and Genome Analysis

The laboratory of David Ray (www.crocoduck.bch.msstate.edu) is seeking a postdoctoral associate in the areas of genome analysis and bioinformatics.

The successful candidate will perform a variety of routine and specialized duties in the laboratory. Duties will require knowledge of the principles of bioinformatics and genome analysis including the generation and analysis of next generation sequence data (454 and Illumina). Current projects focus on transposable elements, small RNAs, and whole genome comparisons. Applicants must exhibit curiosity and an interest in basic evolutionary questions. They should also be enthusiastic and have the able to work independently within a dynamic an collaborative working environment.

Training will be provided but preference will be given to those with experience working with next-generation sequence data, whole genome analyses, and/or transposable element sequences. Duties will include the creation of custom scripts to analyze large sequence databases from a variety of taxa including reptiles, mammals, and insects. He/She will also interact with undergraduate and graduate students. The successful candidate will be expected to produce first-authored papers as well as collaborate on others. Note that this position is for three years but renewal each year is contingent on performance.

Position Location: Department of Biological Sciences, Texas Tech University, Lubbock TX.

Department Profile The Department of Biological Sciences is a comprehensive department with an academic, research and service mission. The Department offers B.S., M.S., and Ph.D. degrees from within the College of Arts and Sciences, and currently advises 880 undergraduate, 120 graduate students and 10 postdoctoral associates, many of whom are involved in evolution and/or genomics.

Minimum Qualifications: Ph.D. degree with major course work in curriculum appropriate for the field of assignment bioinformatics, molecular biology, etc.

Preferred Qualifications: Experience with genome annotation techniques, custom scripting, and intergenomic analysis.

Instructions for Applying: Screening will begin June 15, 2013 and will continue until the position is filled. Please submit a letter of application indicating experience and research interests, curriculum vitae, and contact information for three references to:

Dr. David A. Ray david.4.ray@gmail.com 662-325-7740

Texas Tech University is an affirmative action/equal opportunity employer.

– David A. Ray Associate Professor Department of Biochemistry, Molecular Biology, Entomology and Plant Pathology Mississippi State University Mississippi State, MS 39762

Websites: http://www.crocoduck.bch.msstate.edu http://www.crocgenomes.org/ E-mail: dray@bch.msstate.edu Office: 662-325-7740 Lab phone: 662-325-7746 Fax: 662-325-8955

Even the best of us have bad days. “I am very poorly today and very stupid and hate everyone and everything.” - Charles Darwin - Oct. 1, 1861

dray@bch.msstate.edu

UBourgogne Fragmentation LandscapeGenetics

A postdoctoral research assistant is required for a project entitled *’Consequences of forest fragmentation on population biology of tropical birds*’. The post is available for 1 year (with possible renewal for 1 year depending on funding) and will be based in the Laboratory BioGéoSciences (CNRS & Université de Bourgogne, Dijon, France).

Project summary

This project aims to assess effects of fragmentation on several attributes of individuals/populations in a set of bird species with contrasted levels of forest specialization: (i) genetic diversity, due to demographic changes (smaller and more isolated populations), (ii) phenotypic (morphological, ornamental, immunological) quality of individuals, and (iii) host-parasite interactions. This project will be conducted on four territories: French Guiana, Guadeloupe, Martinique, and Montserrat. If these territories host a high endemic biodiversity, they are faced with real problems of forest loss and fragmentation mainly due to human activities and demographic growth. In addition to contribute to a better knowledge of ecological and evolutionary consequences of habitat fragmentation, the integrated approach of this project will produce valuable results for decision rules in nature and wildlife management frameworks. The collaboration of scientific partners and partners concretely involved in local conservation plans ensures the integration of research and management.

Postdoc tasks

The main research aim for the grant is to determine how the landscape structure influences genetic diversity in several bird species. However, we also expect the postdoc to contribute to the study of phenotypic variation and host-parasite interactions in the context of habitat fragmentation. Original intellectual contributions will of course be welcome too.

Part of samples is already available, but there will be opportunities to contribute to fieldwork (if desired). The postdoc will mainly contribute to and co-supervise production and analyses of genotypic data, as well as manuscript writing.

Qualifications of the most competitive candidate

-Strong background in evolutionary biology, ecology, and conservation

-Strong experience with lab work in molecular biology, especially microsatellite genotyping (and possibly AFLP) and DNA sequencing

-Good experience with relevant analytical methods in population genetics and landscape genetics (and secondary in phylogeography)

-Good skills in general statistics (experience with GIS data analyses or meta-analyses would be a plus)

Further information can be asked to:

Stéphane Garnier (stephane.garnier@u-bourgogne.fr)

Bruno Faivre (bruno.faivre@u-bourgogne.fr)

Applications (including a cover letter, a CV, and contact information for two academic referees) should be sent to:

Stéphane Garnier (stephane.garnier@u-bourgogne.fr)

Review of applications will begin at the end of July and continue until filled)

Start dates for the position will be from 1st of October 2013 to *1^st of December 2013*

– Clfiughdf

Stéphane Garnier

UMR CNRS 6282 Biogéosciences Université de Bourgogne 6 Bd Gabriel 21000 Dijon - France

stephane.garnier@u-bourgogne.fr Tel: +33 (0) 3 80 39 90 58 Fax: +33 (0) 3 80 39 62 31

stephane.garnier@u-bourgogne.fr

UCalifornia Berkeley NeanderthalGenomics

Postdoctoral position in Neanderthal genomics

We are searching for someone to fill a postdoctoral position jointly sponsored by the Max Planck Institute for Evolutionary Anthropology in Leipzig, Germany, and the Department of Integrative Biology at the University of California, Berkeley, USA. The successful candidate will be based in Montgomery Slatkins lab in Berkeley but will make regular trips to Leipzig. We are looking for someone with training in statistics, population genetics and genomics who is interested in helping with the analysis of genomic data from archaic hominims, including early modern humans, Neanderthals and Denisovans. The duties include helping develop new methods of data analysis for the purpose of characterizing past relationships among populations and detecting evidence of natural selection and inbreeding. The initial appointment will be for two years with the possibility of renewal for up to two more years. The position is restricted to people who received a Ph. D. or equivalent no more than three years ago. The planned starting date is September 1, 2013 but that date can be adjusted if necessary. The initial salary will be US $42,000 per year with health insurance. The University of California is an equal opportunity employer. Applications from underrepresented minority groups are especially encouraged. To apply, please send a curriculum vitae. a list of publications and the names and email addresses of three references to Montgomery Slatkin, slatkin@berkeley.edu. Review of applications will begin July 1, 2013. The search will continue until the position is filled.

Montgomery SLATKIN <slatkin@berkeley.edu>

UCollege London Bioinformatics

Dear all,

UCL's Research Department of Genetics, Evolution and Environment invites expressions of interest from potential applicants to NERC's Independent Research Fellowships in Bioinformatics.

NERC has recently launched a research programme in "Mathematics and Informatics for Environmental 'Omic Data Synthesis" and funds 5-year fellowships for early-career scientists wishing to establish independent research groups. More information on the scheme and the background of the programme can be found on the NERC website (http://www.nerc.ac.uk/research/programmes/-omics/events/ao-bioinformaticsfellowships.asp).

If you have the appropriate expertise and would like to apply for a fellowship hosted in our department, please get in touch with Max Reuter (m.reuter@ucl.ac.uk). We will support selected candidates through all stages of their application.

Our department fosters young talent and provides a stimulating and multi-discilinary research environment. It has strengths in evolutionary and statistical genetics, genomics, evo-devo and environmental and biodiversity research. For more information about our research, please visit the department's website (http://-www.ucl.ac.uk/gee/) as well as those of departmental sub-nuits including the UCL Genetics Institute (http:/-/www.ucl.ac.uk/ugi/) and the Centre for Biodiversity and Environment Research (http://www.ucl.ac.uk/-cber/).

Best regards, Max

Max Reuter

Research Department of Genetics, Evolution and Environment Faculty of Life Sciences University College London Darwin Building Gower Street London WC1E 6BT, UK

Phone: +44-20-76792201 (internal 32201)

Lab: http://www.homepages.ucl.ac.uk/ ~ ucbtmre/-Labsite/ Department: http://www.ucl.ac.uk/-gee Centre for Ecology and Evolution: http://-www.ceevol.org.uk m.reuter@ucl.ac.uk

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UCollege London EvoDevo

UCL Research Department of Genetics, Evolution and Environment

Research Associate: Comparative morphology and developmental biology

The appointment will be full time on UCL Grade 7. The salary range will be £32,375 - £34,165 per annum, inclusive of London Allowance.

The Telford Lab in the Research Department of Genetics, Evolution and Environment is seeking to appoint a postdoctoral Research Associate to join a team funded by an ERC advanced grant. The project aims to study the morphology, embryology and genetics of the Xenacoelomorpha (Xenoturbellida and Acoelomorpha) - a newly identified phylum of worms that have been linked to the deuterostomes.

The Research Associate will contribute to a study of the morphology, ultrastructure and developmental biology of several species of Xenacoelomorpha.

The post is available immediately and is funded until 31st May 2018 in the first instance.

The successful applicant will have a PhD (awarded or about to be awarded) in a relevant area. The ideal candidate will have a knowledge of standard molecular biological techniques with a special focus on comparative developmental biology and a strong interest in animal evolution. They will have a proven track record of high quality research in molecular biology/ developmental biology/ evolutionary biology. Experience in in situ hybridisation, antibody staining, sectioning and microscopy will be desirable.

For further details about the vacancy and how to apply online please go to http://www.ucl.ac.uk/hr/jobs/ and search on Reference Number 1339496.

Please attach a CV and a brief personal statement, explaining how your qualifications and experience make you a suitable candidate for the post.

For informal queries about the posts, please contact Professor Max Telford, email: m.telford@ucl.ac.uk . If you have any queries regarding the application process, please contact Jeremy Guyer, email: jeremy.guyer@ucl.ac.uk .

Closing Date: 10th July 2013.

Latest time for the submission of applications: 5 pm.

UCL Taking Action for Equality

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

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

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

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

Xenoturbella You Tube video < http://uk.youtube.com/watch?v=3DyJXNcoxL2Xs >

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

m.telford@ucl.ac.uk

UCollege London GenomicsOfXenoturbella

http://www.nature.com/naturejobs/science/jobs/328474-Research-Associate-Comparative-genomics
UCL Research Department of Genetics, Evolution and Environment

Research Associate: Comparative genomics

The appointment will be full time on UCL Grade 7. The salary range will be £32,375 - £34,165 per annum, inclusive of London Allowance.

The Telford Lab in the Research Department of Genetics, Evolution and Environment is seeking to appoint a postdoctoral Research Associate to join a team funded by an ERC advanced grant. The project aims to study the morphology, embryology and genetics of the Xenacoelomorpha (Xenoturbellida and Acoelomorpha) - a newly identified phylum of worms that have been linked to the deuterostomes.

The Research Associate will contribute to a comprehensive comparative study of the genomes and transcriptomes of the Xenacoelomorpha and their relatives.

The post is available immediately and is funded until 31st May 2018 in the first instance.

The successful applicant will have a PhD (awarded or about to be awarded) in a relevant area. The ideal candidates will have a good knowledge of bioinformatics and especially comparative genomics and a strong interest in animal evolution. They will be responsible for the assembly and annotation of genomes and transcriptomes of members of the Xenacoelomorpha and for developing and implementing methods to enable the large scale analysis of these genomes and performing comparisons with genomes from other metazoans in an evolutionary framework.

For further details about the vacancy and how to apply online please go to http://www.ucl.ac.uk/hr/jobs/ and search on Reference Number 1341661.

Please attach a CV and a brief personal statement, explaining how your qualifications and experience make you a suitable candidate for the post.

For informal queries about the post, please contact Professor Max Telford, email: m.telford@ucl.ac.uk . If you have any queries regarding the application process, please contact Jeremy Guyer, email: jeremy.guyer@ucl.ac.uk .

Closing Date: 10th July 2013.

Latest time for the submission of applications: 5 pm.

UCL Taking Action for Equality

Max Telford Professor of Zoology Department of Genetics, Evolution and Environment, University College London, Darwin Building, Gower Street, London WC1E 6BT, UK. Tel: +44 (0)20 7679 2554 (Internal: 32554) Fax: +44 (0)20 7679 7096

a new open access journal EvoDevo: http://www.evodevojournal.com/ Telford & Littlewood: Animal Evolution. OUP < http://ukcatalogue.oup.com/product/9780199570300.do >

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

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

Downloads.html >

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

Xenoturbella You Tube video < http://uk.youtube.com/watch?v=3DyJXNcoxL2Xs >

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

m.telford@ucl.ac.uk

UEdinburgh EvolBiol

Postdoctoral Researcher, University of Edinburgh

Applications are invited for a 5-month appointment as Post-doctoral Researcher based in the Institute of Evolutionary Biology, University of Edinburgh. The position is funded by a Wellcome Trust project grant.

Applicants should have, or shortly obtain, a PhD in evolutionary genetics or bioinformatics and have experience in computer programming and population genetics or molecular evolution. The project aims to increase the understanding of the nature and strength of natural selection operating in various kinds of functional elements of the mammalian genome. In particular, the post holder could work on the evolutionary genetics of adaptation in the murid genome by analysis of next-generation sequence data of multiple individuals sampled from natural populations.

Informal enquiries can be made to peter.keightley.ed.ac.uk

Peter Keightley Professor of Evolutionary Genetics Institute of Evolutionary Biology University of Edinburgh West Mains Rd Edinburgh EH9 3JT UK http://homepages.ed.ac.uk/eang33/ Full applications by 24th June 2013 can be made under reference 014484 at https://www.vacancies.ed.ac.uk/ peter.keightley@ed.ac.uk

UHouston CiliateMutation

POSTDOCTORAL RESEARCH ASSOCIATE OPENING

The Zufall Lab at the University of Houston is seeking a Postdoctoral Research Associate in the area of Evolutionary Genetics to create and study mutation accumulation lines in the ciliate Tetrahymena thermophila. These lines will form the basis of an NIH funded collaboration with the Azevedo (University of Houston) and Cartwright labs (Arizona State University), which will take advantage of the unusual nuclear architecture of ciliates to study the rate, types, and fitness effects of spontaneous mutation.

As part of this project, the postdoc is expected to be able to: develop and culture T. thermophila mutation accumulation lines, conduct genetic analyses and fitness assays on these lines, and interpret data using computational and statistical analyses in collaboration with the Azevedo and Cartwright labs. Candidates should possess a Ph.D. in Evolution or Genetics. Experience with microbial eukaryotes is desirable and skill in computational and statistical analysis is preferred.

Information about the labs involved can be found here: bchs.uh.edu/˜rzufall, wwworm.biology.uh.edu, and cartwrig.ht/lab

Applications can be made at jobs.uh.edu (Posting Number: S001408) and must include a cover letter, detailed CV, and names of 3 references. The initial closing date is July 15, 2013, but applications will continue to be accepted and considered until the job is filled/closed.

The University of Houston is an Equal Opportunity/Affirmative Action employer. Minorities, women, veterans, and persons with disabilities are encouraged to apply.

Contact Becky Zufall at rzufall@uh.edu for more information.

rzufall@uh.edu

UHouston ExperimentalEvolution

Post-doctoral position in experimental evolution:

Applications are invited for a postdoctoral position in Tim Cooper's lab in the Department of Biology and Biochemistry at the University of Houston.

The successful applicant will examine the basis of evolvability - differences in the capacity to adapt to novel environments - in bacterial populations. This project will extend existing approaches to evaluating evolvability, examine its influence on evolutionary outcomes, and test candidate mechanisms that might explain differences in evolvability. Work will initially focus on lab-evolved populations of Escherichia coli and then extend to natural isolates. Research will involve a combination of molecular genetic and genomic techniques. (Funded by the National Science Foundation.)

The University of Houston is a member of the Texas Medical Center - a large, diverse and vibrant research community that includes many laboratories working at the intersection of experimental, theoretical and systems biology.

Applicants must have a Ph.D. in Biology or a related discipline and should have experience in molecular and/or evolutionary genetics. Microbiology experience would be an advantage. The initial term of the position will be for a period of one year with the likelihood of a one year extension. Applications should be emailed to Tim Cooper (tfcooper@uh.edu). Review will begin immediately and continue until the position is filled. Applications should include a cover letter, CV and the names and contact details of three referees.

Houston is a diverse, growing, and very livable city. It has many good bars and restaurants, and has one of the largest amounts of green space of any US city.

Tim Cooper Department of Biology and Biochemistry University of Houston http://cooperlab.org tim.f.cooper@gmail.com

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ULausanne AntEvolution 2pdf 1PhD

1 PhD position and 2 postdoctoral positions: Ant behaviour/ genomics/ bioinformatics University of Lausanne, Department of Ecology and Evolution We are looking for one PhD student and two postdoctoral researchers to work on three lines of research in Laurent Keller's group:

1. Ant behaviour. The idea is to study the dynamics of division of labour with a new system based on fiducial identification labels and video tracking. This system which automatically follows all the individuals in a colony will allow the first quantitative studies of behaviour.

2. Artificial evolution with robots. We want to study how the level of cooperation within colonies, the reliability of communication systems and division of labour have been shaped by within-colony relatedness and other social factors.

3. Ant genomics. We are currently sequencing the fire ant genome and are looking for bioinformaticians and molecular biologists interested in making use of this genome to address questions related to social behaviour. Other topics of research on social behaviour are also possible if they fit the research interests of our group:

http://www.unil.ch/dee/page7717.html These positions will be funded by an ERC-funded grant and/or the Swiss FNS, and will be filled as soon as suitable candidates are found.

The Department of Ecology and Evolution is a well-funded and vibrant research institution, with superb facilities:

http://www.unil.ch/dee/page5090_en.html Application can be sent to nathalie.stroeymeyt@unil.ch. Applications should comprise a CV, a list of publications, 1 page describing why you are interested in joining our group and two letters of reference. Only complete applications will be considered.

Nathalie Stroeymeyt <Nathalie.Stroeymeyt@unil.ch>

ULausanne OwlPolymorphisms

One-year PostDoc position at the University of Lausanne, Prof. Alexandre Roulin (Alexandre.Roulin@unil.ch)

Polymorphisms of pro-opiomelanocortin (POMC) polymorphisms as well as alteration of POMC maturation by the proprotein convertase (PC)-1/3 are crucial determinants for physiology and behavior in humans and animals, including feeding behavior, skin pigmentation, stress response, the immune system, and sexual functions. Barn and tawny owls are a powerful system to study the role of POMC in this context. Our extensive studies over the past years acquired a unique and comprehensive set of phenotypic and genetic data for over 4000 individual birds. These studies revealed striking correlations between genetic polymorphisms in POMC precursors and specific alterations in PC1/3. Undetectable PC1/3 expression and mutant PC1/3, in barn owl growing feathers and brain respectively, coincides with a unique POMC polymorphism characterized by poly-serine insertions. In the present project, we will undertake an in-depth molecular characterization of the system to establish a link between the observed POMC polymorphisms and PC1/3 variants. Using state-of-the-art biochemical and cell biology techniques, we will characterize the physiological importance of POMC polymorphism found in barn owls and link these mechanistic data to the available physiological and behavioral observations. This interdisciplinary project directed by Prof. Alexandre Roulin (Department of Ecology and Evolution, UNIL) will for the first time illuminate the molecular basis underlying the role of POMC in complex behavioral patterns of a highly relevant species. For this exciting project, we are looking for a post-doctoral candidate with a strong background in biochemistry and molecular biology. Financial support is guaranteed for one year according to the salary levels of Swiss national Science Foundation with the option of prolongation.

alexandre.roulin@unil.ch

UMichigan PlantGenomics

A postdoctoral position is available in the Baucom lab, which is relocating to the EEB dept at the University of Michigan in Ann Arbor this July. Members of the lab work on projects that range from plant evolutionary ecology to plant population genetics and comparative genomics: see (http://baucomlab.org/Baucom_Home.html) for more information about our ongoing projects.

For this postdoctoral position, we seek an enthusiastic and independent researcher interested in the role of the plant metagenome (microbial and eukaryotic root associates) on the evolution of weediness and invasiveness. The work thus requires basic molecular lab and field ecology experience, along with previous experience analyzing large genomic datasets and basic command line capabilities.

Funding for this position is available for 2 years (contingent upon satisfactory progress). To apply, please send a single pdf with a cover letter, a CV, 1-2 representative publications, and names and contact information for 3 references to gina.baucom@gmail.com by July 10. Start date is flexible.

If interested in this position, I will be at the SSE meetings in Snowbird and very happy to discuss the opportunities in the lab personally – please contact me via email prior to the meeting.

The University of Michigan is an equal opportunity/affirmative action employer.

Regina S. Baucom baucomlab.org < http://baucomlab.org/Baucom_Home.html > gina.baucom@gmail.com

gina.baucom@gmail.com

UMontpellier CancerEvolution

Postdoctoral research opportunity - "Evolutionary models of cancer progression and therapies" V University of Montpellier, France

* *

We are looking for a motivated Postdoctoral researcher to employ mathematical and/or computer models to better understand the evolutionary dynamics of cancer progression and chemotherapeutic treatments. We are especially interested in applications of ecology, evolution, and population genetics towards more general descriptions and ultimately predictive theories.

The Postdoc is for two years, with a starting date on or before January 1st, 2014. The contract is funded by INSERM Cancer and is in collaboration with two cell biology research laboratories (Pr. Urszula Hibner and Pr. Daniel Fisher, IGMM).

Selection criteria: (1) PhD; (2) Considerable experience in mathematical or computer modeling in the context of cell biology, population ecology and/or evolutionary biology; (3) Command of written scientific English; (4) Demonstrated track record of refereed publications in leading journals; (5) Demonstrated capacity to work under limited supervision.

Interested candidates should send (1) a letter of motivation, (2) a CV, and (3) the names, institutional addresses, and emails of 3 persons who can be contacted for references, on or before July 30th, 2013 to Michael Hochberg (mhochber@univ-montp2.fr). Information about our interdisciplinary research group can be found at http://www.eec.univ-montp2.fr/people/mike-hochberg/ Michael Hochberg <mhochber@univ-montp2.fr>

UMontpellier HIV Bioinformatics

POSTDOC POSITION "BIOINFORMATICS OF HIV"

Computational Biology Institute (IBC) http://www.ibc-montpellier.fr/ LIRMM, CNRS - Université Montpellier 2, France http://www.lirmm.fr/xml/fr/lirmm.html A postdoctoral position is available at IBC to work on the Bioinformatics of HIV. IBC aims at the development of innovative methods and software to analyze, integrate and contextualize large-scale biological data in the fields of health, agronomy and environment. IBC is a new multidisciplinary project center with broad spectrum, ranging from algorithmics and mathematical modeling, to genomics, cancer and epidemiology. IBC should become a privileged meeting place for computational biology and bioinformatics researchers, bringing together a large community on regional, national and international levels(e.g. http://www.lirmm.fr/mceb2013/).

The postdoc is focused on the evolutionary studies of HIV. We authored a number of phylogenetic programs (e.g. PhyML) and recently started applying these approaches to viruses (e.g. phylotype.org/). Our aim is to develop new fast methods able to handle the bunch of HIV sequence data that are available today and perform various analyses: dating, phylogeography, phyloanatomy, search for clusters of resistance..., which currently require huge computations with standard Bayesian methods. Fast algorithms will be designed, based on simplified approaches (distance, parsimony, simple probabilistic models), to be typically applied to day-to day surveillance tasks, personalized medicine and large scale epidemiological studies. We are collaborating with several groups and researchers (Martine Peteers (FR), Tulio de Oliveira (ZA), Stephane Hue (UK), Tanja Stadler (SW)). Various subjects are envisaged to be discussed with applicants (e.g. searching for therapy resistance clusters in the UK population (˜50.000 strains); fast inference of relaxed clock trees for dating purpose).

We are seeking highly qualified and motivated applicants in modeling and/or algorithmics, with extensive programming experience and a strong interest for viruses and evolutionary studies.

To apply send a detailed CV, a motivation letter and three references to Olivier Gascuel (gascuel@lirmm.fr), before June 20. Questions welcome!

.... Olivier Gascuel

Directeur de Recherche Institut de Biologie Computationnelle LIRMM, UMR 5506 CNRS - Université Montpellier 2 Case courrier 06011, 95 rue de la Galéra 34095 Montpellier cédex 5 - FRANCE Tel. 33 (0)4 67 41 85 47 http://www.lirmm.fr/gascuel gascuel@lirmm.fr

Olivier Gascuel <gascuel@lirmm.fr>

UPennsylvania EvolBiol

Postdoctoral Fellowships for Academic Diversity

The Postdoctoral Fellowship for Academic Diversity Program is a competitive program whose goal is to increase the diversity of the community of scholars devoted to academic research. We seek to attract promising researchers and educators from different backgrounds, races, ethnic groups, and other diverse populations whose life experience, research experience and employment background will contribute significantly to the academic mission. Fellowships are available for postdoctoral training in all areas of study at Penn. Successful candidates will receive mentored scholarly and research training as well as courses and workshops to enhance their research success skills and prepare them for a faculty position in a major university.

Eligibility

* Graduate students from PENN and other institutions who have completed, or will complete their requirements for Ph.D. by the Fellowship start date. * Postdoctoral scholars from other institutions who have completed their dissertation within the last three years. * Professional applicants (M.D., D.M.D., V.M.D., J.D., etc) within a year of completing their post-degree professional training. * Candidates must be US citizens or permanent residents. * Postdocs, residents and fellows who currently have a position at Penn are ineligible for this program.

Awards: Fellows receive a stipend of $43,000 in year 1 with $2,000 increments in years 2 and 3, as well as annual allowances for travel ($2,000) and research ($5,000), and a one-time relocation expense of $5,000. The University also provides a medical, vision, dental and life insurance benefits package. Successful candidates will receive highly mentored scholarly and research training as well as courses and workshops to enhance their research success skills and prepare them for a faculty position in a major university.

Start date will be arranged in consultation with the faculty mentor but can be as early as January 2, 2014.

More Information at: http://www.upenn.edu/research/postdocs_students/postdoctoral_fellowships_for_academic_diversity/

Sarah Tishkoff, Ph.D. David and Lyn Silfen University Professor Departments of Genetics and Biology University of Pennsylvania Tel: 215-746-2670 tishkoff@mail.med.upenn.edu < http://www.med.upenn.edu/tishkoff/ > http://www.med.upenn.edu/tishkoff/

tishkoff@mail.med.upenn.edu

UPennsylvania EvolutionaryTheory

POSTDOCTORAL FELLOWSHIP IN EVOLUTIONARY THEORY

A postdoctoral fellowship (2-3 years) is available in the mathematical biology group of Dr. Joshua B. Plotkin at the University of Pennsylvania (http://mathbio.sas.upenn.edu/).

The specific research project is flexible and can be tailored to the interests of the individual, but it will fall under the broad purview of evolutionary and ecological theory. Areas of interest in the Plotkin lab include theoretical population genetics, the evolution of robustness and adaptability, the inference of fitness landscapes, the role of epistasis in evolution, and the evolution of language and social norms.

Requirements for the position include: a proven record of self- motivated research; expertise in mathematics, statistics, physics, biology or related area; excellent communication skills. The ideal candidate should also be familiar with scientific programming.

The postdoctoral fellowship provides a competitive annual stipend (minimum $40,000) plus benefits and health insurance. Start date and terms are negotiable. Applications are welcome from candidates of any nationality. Women and under-represented minorities are especially encouraged to apply.

Applicants should email a statement of research interests, CV, and contact details for three references to jplotkin (at) sas.upenn.edu. Informal inquiries are also welcomed.

Joshua B. Plotkin Department of Biology University of Pennsylvania http://mathbio.sas.upenn.edu/ jplotkin@sas.upenn.edu

UPorto LivestockPopulationGenomics

TWO POST DOCTORAL RESEARCH ASSOCIATES IN BIOINFORMATICS AND POPULATION GENETICS

The Population Genomics and Traits Group at CIBIO-University of Porto (http://cibio.up.pt) is seeking candidates for two Posdoctoral fellowships. The successful candidates will be expected to engage in a vigorous basic and applied research program focused on NGS (next generation sequencing) and SNPchip 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 biology field 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.The projects, which include SNPChip, and Pool-Seq data require exper ience in working with large SNP data sets and sequence data. Good programming skills and familiarity with the available analysis tools are essential. 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 (at least 1 year of posdoc and not less than 5 published papers), and 3 publications (.pdfs) from peer-reviewed journals (one at least as first author), their CV, and the names and contact information of 2 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 2014. Fellowship wage will be 1495 euros /month (tax-free), with social security and national health system assess included.

Application review will start at June 15, 2013 and continue until the position is filled.

albanobp@fc.up.pt

UPorto Phylogenetics

ONE POST DOCTORAL RESEARCH ASSOCIATE IN MOLECULAR BIOLOGY AND PHYLOGENETICS

The Animal Diversity and Evolution Group at CIIMAR-University of Porto (http://www.ciimar.up.pt < http://cibio.up.pt/ >) is seeking candidates for one Postdoctoral fellowship under the annual application scheme (http://www.fct.pt/apoios/bolsas/regulamento.phtml#BPD). The successful candidate will apply to the Portuguese National Science Agency (FCT) and depending on the outcome is expected to start working in the first months of 2014. The research program focuses on the evolution of lipid metabolism in metazoans. The initial appointment to this position is for three years with a possible extension to six years. It requires a PhD in Molecular Biology and Phylogenetics and the goal of the research is to test hypotheses related with the evolution of lipid metabolic cascades in the context of genome duplications as well as adaption to novel habitats and food sources (e.g. colonization of land). This work will include a large amount of data analysis from available genomes and bioinformatics, as well as functional genomics approaches.

Instructions to Applicants: applicants should submit a cover letter describing their interests, skills, prior scientific experience (no less than 6 published papers, two at least as first author), and 3 publications (.pdfs) from peer-reviewed journals, their CV, and the names and contact information of 2 referees. Applications as well as requests for further information should be sent to Filipe Castro to the following email address: filipe.castro@ciimar.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 2014. Fellowship wage will be 1495 euros /month (tax-free), with social security and national health system assess included. Application review will start at the June 15, 2013 and continue until the position is filled.

– Filipe Castro, PhD Biomedical Sciences Researcher CIIMAR, Portugal email: lfilipecastro@gmail.com filipe.castro@ciimar.up.pt

Filipe Castro <lfilipecastro@gmail.com>

URhodeIsland MicroalgaeBioinformatics

*Postdoctoral Research Associate Position in Bioinformatics: *

Transcriptome analyses of large next-generation sequencing datasets

**

The Menden-Deuer and Rynearson labs at the University of Rhode Island invite applications for a Postdoctoral Research Associate in bioinformatics and computational biology.

*Project Overview:*This project aims to examine, quantify and understand gene expression in marine plankton. Plankton are single-celled eukaryotes that form the base of marine food webs and are therefore critical to the health and well-being of the world's oceans. This project represents an opportunity for a talented and creative postdoctoral researcher to work with sequencing data from ecologically important organisms.There will be opportunities to develop new or utilize the most recent algorithms for transcriptome assembly and mapping, particularly because most plankton genomes have not yet been sequenced. Datasets include Illumina sequencing of plankton transcriptomes from multiple species and experiments under different conditions.The successful candidate will lead the project on the de novo analysis of transcriptomic data, which includes setting up and/or using available computational pipelines for transcriptomic data processing, identifying novel 'high-responder' genes and statistical comparison of multiple single-cell transcriptomes.The first dataset is ready for analysis.

Responsibilities and Duties: The postdoctoral associate will be primarily responsible for analysis of the high-throughput sequencing component of the project (transcriptome sequence data). Responsibilities also include dissemination of results in publications and presentations and a willingness to assist with proposal preparation. The individual will be required to contribute to the functioning of the lab, assist with graduate and undergraduate student mentoring and help to develop future research projects.

Qualifications: Candidates are required to have a Ph.D. degree by August of 2013 in Computer Sciences, Statistics, Biology or a related field. Excellent command of the English language (written and verbal) and quantitative analytical skills are essential. Candidates should possess demonstrable experience with the analysis of high throughput sequencing data including strong programming skills. We prefer candidates who have an excellent background in statistics and data mining.

Appointment: The position is for 12-months initially, commencing August or September 2013 and renewable depending on performance. The successful candidate will receive training in research collaboration, presentation and publication of results, and outreach and mentoring. There will be opportunities for development of additional research projects and proposals.

To Apply: Applications must include (1) a maximum 3-page statement of experience,*__*career goals, research vision and interests; (2) curriculum vitae, (3) reprints of relevant publications and (4) names and addresses of three referees willing to write confidential letters of recommendation. All materials should be emailed as a single pdf document to: rynearson@mail.uri.edu with 'PostDoc Application' in the subject line. Candidates will be selected based on overall excellence, including academic qualifications, letters of recommendation, and prior skills, experience, and research goals that are compatible with the goals of the funded research. The position is compensated through a competitive salary and excellent benefits package. Please email rynearson@mail.uri.edu <mailto:rynearson@mail.uri.edu>with additional questions about the position.

Research will take place on the shores of Narragansett Bay, RI at the URI Graduate School of Oceanography.The labs are conveniently located along the eastern seaboard with easy access to Amtrak and major airports.The candidate will benefit from existing collaborations with researchers in computational biology both nationally and internationally.

Closing date: For full consideration, applications should be received by July 1, 2013.Further information: Rynearson lab: http://www.gso.uri.edu/-users/rynearson Menden-Deuer lab: http://-www.gso.uri.edu/smdlab__ URI Graduate School of Oceanography: http://www.gso.uri.edu/ –

Tatiana Rynearson Associate Professor Graduate School of Oceanography University of Rhode Island, Bay Campus South Ferry Road Narragansett, RI 02882-1197 Phone (401)874-6022 http://www.gso.uri.edu/users/rynearson rynearson@mail.uri.edu

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USouthFlorida EvolutionAvianDiseases

Post-doctoral opportunity in avian disease biology at USF

Drs. Lynn B. Martin and Thomas R. Unnasch are searching for a post-doc to collaborate on a recently NSF-funded project on the ecophysiology of superspreading. The post-doc will help execute projects directed at understanding the role of the stress hormones on interactions among birds, mosquitoes and West Nile virus.

Applicants should have a PhD (awarded before the project start date) in ecology, evolutionary biology, or the like. The most competitive individuals will have a background in endocrinology, immunology, and/or disease ecology and strong lab, experimental design and data analysis skills. Experience with songbird and mosquito husbandry/handling and ABSL-3 facility work are also pluses. A strong publication and grantsmanship record as well as evidence of independent thinking are also highly desirable. There are specific research aims for the grant, but our hope is for strong intellectual contributions by the postdoc, including postdoc-led side projects, manuscript first authorships, and additional grant proposals.

The position can be supported for up to 3 years, but renewal each year is contingent on performance and funding. Only US citizens and permanent residents are eligible for this position, as the research requires and FBI clearance to work with select agents. The position is based at the University of South Florida, Departments of Integrative Biology and Global Health (Tampa campus). The start date is somewhat flexible but can be on or after November 15, 2013. Note: Dr. Martin advertised recently for another postdoc (with Dr. Toru Shimizu, USF Psychology); the current position is distinct from that one.

Martin lab: http://lbmartin.myweb.usf.edu/-Martin_lab_at_USF/Welcome.html Unnasch lab: http://health.usf.edu/publichealth/gh/-Thomas+Unnasch.htm Applications should be submitted by email as a single PDF document to Dr. Lynn B. Martin (lbmartin@usf.edu) with the subject heading 'NSF postdoc application'. Complete application packets will include a cover letter, a CV, one relevant reprint, and the names and addresses of three referees preferably from former PhD/postdoc mentors. In your (2 pg maximum) cover letter, make sure to address your feelings about your: passion for scientific investigation, motivation to succeed, drive, work ethic, willingness to take risks, ability to overcome hardship, leadership capabilities, collaborative skills, and career aspirations. Written confirmation of the PhD will be required prior to hiring.

We will consider applications through 31 July 2013. Applications from women and minorities are especially encouraged. The University of South Florida is an Equal Opportunity/Affirmative Action Employer.

Thanks for your attention, and please email me with any questions, Marty

Lynn B. Martin Associate Professor Department of Integrative Biology University of South Florida 813-974-0157 lbmartin@usf.edu Lab website: http://lbmartin.myweb.usf.edu/Martin_lab_at_USF/-Welcome.html Google scholar page: http://scholar.google.com/citations?user=W7gGhjYAAAAJ
"Martin, Lynn" <lbmartin@usf.edu>

WorkshopsCourses

Anagni Italy ScientificData Sep1-7

Dear all,

we would like to inform you that the workshop entitled 'Scientific Data Sharing: An Interdisciplinary Workshop', will take place in Anagni, Italy, during the first week of September 2013.

Look at the preliminary programme < https://sites.google.com/site/openingsciencetosociety/news/-anagni-programme >

There will be three sessions:

- *The foundations of Open Science* will be concerned with the epistemological foundations of Open Science, with a focus on the Open Data principles and the impact of new technologies on the spread of scientific knowledge.

- *Data sharing in the scientific practice: experiences from different research fields*, in which empirical studies of data sharing practices in different research fields (e.g. archaeology, biodiversity, biomedicine, genomics, psychology) will be presented.

- *Facing the complexity of data sharing* will be dedicated to the discussion of the barriers to data sharing and what can be done to increase its rate.

Furthermore, the round table entitled '*Toward an integrated approach to address scientific, educational and public aspects of data sharing*' will provide an opportunity for invited speakers to answer specific questions regarding data sharing in a wide perspective.

The list of speakers include: Neela Enke (Germany), Bernardino Fantini, Ilaria Fava, Pietro Greco, Roberto Lattanzi, Daniela Luzi, Fabio Parenti, Deborah Mascalzoni (Italy), Jelte Wicherts (Netherlands), Catherine Heeney (Spain), Geoffrey Boulton, Jennifer Molloy (United Kingdom).

If you are interested in attending the meeting please go to https://docs.google.com/-forms/d/1fdW1sMgmV4z1qhiOEm04F7hjCdLlQ EfY4CQecCiSlpY/viewform

Attendance to the meeting is free, but we can accept a limited number of participants and *registration* (open up to August 1st) *is* *mandatory*.

The organizers Paolo Anagnostou, Marco Capocasa and Giovanni Destro Bisol

web site *Opening Science to Society * *https://-sites.google.com/site/openingsciencetosociety *

Giovanni Destrobisol <giovanni.destrobisol@uniroma1.it>

Barcelona DynamicsModelling Feb4-7

Dear Colleagues,

Registration is open for the course “MODELLING DINAMICS IN BIOLOGY”, February 4-7, 2014.

Instructors: Dr. Andreea Munteanu (CGR, Spain) and Dr. Carlos Rodrguez-Caso (Universidad Pompeu Fabra, Spain)

Place: Premises of Sabadell of the Institut Catal de Paleontologia Miquel Crusafont, C/ de lEscola Industrial, 23, 08201 Sabadell, Barcelona (Spain)

The current course will present an overview of systems biology with emphasis on the necessity, uses and pitfalls of dynamical modelling in biology. It introduces the required language and philosophy for a smooth and fruitful collaboration between life scientists and theoreticians (i.e. mathematicians, physicists, computer scientists). The main goal of the course is not a detailed description of the modelling tools in systems biology, but a thorough overview of the terminology and applicability range of these methodologies. The time dedication throughout the course will be one third for theoretical introduction, and two thirds for modelling applications for very diverse biological systems. The participants will acquire the necessary skills to understand and interpret models and modelling results from scientific articles, and will take the first steps into building their own mathematical models.

Organized by: Transmitting Science and the Institut Catal de Paleontologia

More info: http://www.transmittingscience.org/-courses/syst-bio/intro-system-bio/ or writing to courses@transmittingscience.org

With best regards

Soledad De Esteban Trivigno, PhD. Course Director

Soledad De Esteban Trivigno <soledad.esteban@transmittingscience.org>

Barcelona GenomicsBioinformatics Sep16-20

BARCELONA SUMMER SCHOOL IN GENOMICS AND BIOINFORMATICS

This September the Barcelona Summer School in Genomics and Bioinformatics offers two courses:

Bioinformatic Analysis for Next Generation Sequencing Data This course will cover the theory and practical aspects of NGS data analysis, covering different genomic, transcriptomic and epigenomic NGS analyses. The course is designed to be of interest to masters and PhD students with an interest in NGS data handling and analysis, and will focus on the computational and statistical challenges inherent in NGS data analysis. Participants should have a background in bioinformatics, computer science, statistics or other mathematical discipline. The course will include both theoretical and practical sessions. Coordinated by Simon Heath, Centre Nacional d?An?lisi Gen?mica.

Next Generation Sequencing for Medical Genomics In this course we aim to familiarize the students with the different NGS technologies and their applications to the study of human genetic variation and disease. The course will cover aspects from technology and informatics to experimental design and data analysis. This course is designed to be of interest for master and PhD students preferentially with a background on human genetics. The course will include theoretical and practical sessions. Coordinated by Ferran Casals, Universitat Pompeu Fabra ? Institute of Evolutionary Biology.

Programs available at http://www.ibe.upf-csic.es/ibe/_pdf/bcnSSGB_1.pdf >From September 16th to September 20th 2013, at Universitat Pompeu Fabra, Barcelona.

Pre-registration: Please register at http://biologiaevolutiva.org/BSSGB2013/. Accepted participants will receive the instructions for the payment.

Number of participants: 25

Tuition: The registration fee of 500 Euros covers course materials, coffee breaks and lunches. Lodging costs are not included in the registration fee. If needed we can help participants to find economic accommodation in Barcelona.

Please contact bcnSSGB@gmail.com for further information.

Ferran Casals IBE, Institut de Biologia Evolutiva (UPF-CSIC) CEXS-Universitat Pompeu Fabra Parc de Recerca Biom?dica Doctor Aiguader 88 08003 Barcelona, Catalonia, Spain Tel. +34 93 316 08 64

ferran.casals@upf.edu

Copenhagen SpeciesDistributionModels Aug26-30

Closing soon!

We are now accepting applications for the international PhD Course Modelling Species Distributions under Climate Change at the University of Copenhagen. Application deadline is June 15; please note that applications sent outside of the application period will not be accepted. Find out more about the course here: http://macroecology.ku.dk/teaching/int_phd_course/ Applicants should send a letter including an explanation about how the course will benefit their PhD project, a brief description of their PhD project and a short CV. Maximum 2 pages. Deadline for application is 15th June. Send the applications to David Nogués-Bravo: dnogues@bio.ku.dk

Katharine Marske, PhD Assistant Professor Center for Macroecology, Evolution and Climate University of Copenhagen Denmark

+45 51 33 10 15

http://macroecology.ku.dk/ KAMarske@bio.ku.dk

CostaRica AmphibianDecline Jul29-Aug12

Hello all,

Below is a brief description of the Organization for Tropical Studies' Microbial Ecology of Amphibian Decline, an upcoming graduate-level specialty course which will be taught in Costa Rica from July 29 - August 12, 2013. The course is worth 2 graduate academic credits transferable to all institutions within the Organization for Tropical Studies consortium, which includes over 50 universities in the USA, Latin America, South Africa and Australia. This course may be of interest to students in the fields of microbial ecology, amphibian ecology, vertebrate survey techniques, disease ecology and amphibian decline, emphasizing on modern approaches: genomics, proteomics and metabolomics.

http://ots.ac.cr/images/downloads/education/graduate/specialty-courses/amphi biandecline.pdf

or

http://bit.ly/10MDY4T

Your circulation of this material among graduate students in different departments and programs would be greatly appreciated.

Many thanks!

–

Microbial Ecology of amphibian decline

Microbes are essential components of the environment because they provide key services that support ecosystem functioning. Our ability to understand these microbes has advanced substantially due to the recent development of rapid, low-cost, high-throughput sequencing. Entire microbiomes can now be characterized to understand both the identity and function of microbes within these communities. As a result, we are now gaining insights into microbial communities that are associated with animals. These recent developments in technology poise the field of microbial ecology to make important discoveries and advances regarding their relationship to amphibian decline.

This course will present students with a variety of topics relevant to the microbial ecology of amphibian decline, emphasizing on modern OMICS approaches (genomics, proteomics and metabolomics). During the first part of the course at La Selva Biological Station, students will learn to identify and sample amphibians in the field, detect by culture dependent and molecular techniques of both symbiotic and pathogenic microbes including Batrachotrychium dendrobatidis (Bd) and ranavirus, as well as build phylogenetic trees and analyze complete genomes of these microbes. At the end of this period, students will be able to design their own hypotheses and test them the following week at the University of Costa Rica, employing a combination of genetic, proteomic and metabolomics approach.

Course Content

Through fieldwork, computer-based and laboratory analyses, this course will help students gain basic knowledge and hands-on experience in the following diverse fields: amphibian ecology, vertebrate survey techniques, disease ecology, isolation and laboratory culture of amphibian pathogens, microbial ecology and diversity, host-microbe symbioses, molecular biology, phylogenetics, next generation sequencing technologies, comparative genomics, proteomics and metabolomics.

Participants

The course will be held in Costa Rica and is limited to 20 students. We anticipate that half of the students will come from Latin American institutions and about half from U.S. institutions. All participants should be fluent in English. A working knowledge of Spanish would be useful.

The course is intended for graduate students with an interest in amphibian conservation, microbial ecology or global change biology.

Course Instructors:

Adrian Pinto Director, Microscopic Structures Research Center. Course Coordinator.

Ibrahim Zuñiga Microscopic Structures Research Center. Microbiology research.

Invited Faculty

Bruno Lomonte Instituto Clodomiro Picado, Proteomic research.

Godofredo Solano Centro de Investigaciones en Productos Naturales. Metabolomics research.

Gilbert Alvarado, DVM Microscopic Structures Research Center. Pathology research.

Gabriel Vargas, Microscopic Structures Research Center. Bioinformatics research.

Juan Abarca Microscopic Structures Research Center. Field research.

Course dates: July 29 - August 12, 2013 (arrive July 28, depart 13 August)

Application Deadline: June 14, 2013. For priority consideration, followed by open enrollment until filled.

Tuition: OTS consortium applicants $2300; non-member applicants $2900

Tuition includes: all lodging (hotel and biological research stations), all meals, all transportation within Costa Rica, all course materials (sample equipment and lab). Does not cover personal expenses or airfare.

Partial need-based scholarships are available; priority given to OTS consortium and Latin American applicants.

For more information please consult the OTS website www.ots.ac.cr

or write to Andrés Santana andres.santana@ots.ac.cr or Barbara Lewis barbara.lewis@ots.ac.cr for application information

andres.santana@ots.ac.cr

CostaRica ArachnidEvolution Jan3-17

Hello all,

Below is a brief description of the Organization for Tropical Studies' Ecology and Evolution of Arachnids, an upcoming graduate-level specialty course which will be taught in Costa Rica from January 3-17, 2014. The course is worth 2 graduate academic credits transferable to all institutions within the Organization for Tropical Studies consortium, which includes over 50 universities in the USA, Latin America, South Africa and Australia. This course is relevant for all graduate students interested in arthropods and upper level undergraduates interested in being exposed to tropical research.

For more information go to http://bit.ly/12kdMC3 Your circulation of this material among graduate students in different departments and programs would be greatly appreciated.

Many thanks!

–

Ecology and Evolution of Arachnids

Unbeknownst to most biologists, the (mostly) predatory group of arthropods known as arachnids encompasses eleven extant orders, many of which can be found in the tropical forests of Central America. Within this incredibly specious group we observe tremendous diversity with respect to sensory systems (many of them unique to particular groups); morphological adaptations/ specializations; foraging strategies; mating strategies; communication systems; and ecological interactions (among others).

Course Content

This course will incorporate field-based observations, inquiry-based learning programs, hands-on experience, and interactive lectures to inform students of the basic natural history, structure, and function of all arachnid groups. Building upon this foundation, and in conjunction with knowledge gained through primary literature discussions and synthesis, students will develop their own research projects. Through fieldwork and laboratory analyses, this course will help students gain basic knowledge and hand-on experience in the following diverse fields as they pertain to arachnids: anatomy, physiology, behavior, ecology, evolution, phylogenetics and systematics. Additionally, students will be exposed to pedagogical tools that will augment their academic toolbox.

Course Objectives:

Delve into current scientific research and discover the cutting edge questions and approaches implemented by leading arachnologists.

Obtain fundamental understanding of arachnid evolution, with a focus on evolutionary relationships among extant and extinct chelicerate groups.

Develop basic skills in arachnid collection, preservation, and identification

Participants

All participants should be fluent in English. A working knowledge of Spanish would be useful. This course is relevant for all graduate students interested in arthropods and upper level undergraduates interested in being exposed to tropical research.

Course Instructors:

Eileen Hebets, Ph. D. University of Nebraska.

Jason Bond, Ph. D. Auburn University.

Ingi Agnarsson, Ph.D. University of Vermont.

Greta Binford, Ph.D. Lewis and Clark College.

Jay Stafstrom, M. Sc. University of Nebraska. Teaching Assistant.

Invited Faculty: Gilbert Barrantes, Ph.D. and William Eberhard, Ph.D, from the University of Costa Rica.

Course dates: January 3-17 (arrive January 2, depart January 18)

Application Deadline: October 1, 2013. (For priority consideration, followed by open enrollment until filled).

Tuition: OTS consortium applicants $2000; nonmember applicants $2800

Tuition includes: all lodging (hotel and biological research stations), all meals, all transportation within Costa Rica, all course materials (sample equipment and lab). Does not cover personal expenses or airfare.

Partial need-based scholarships are available; priority given to OTS consortium and Latin American applicants.

For more information please consult the OTS website www.ots.ac.cr

or write to Andrés Santana andres.santana@ots.ac.cr or Barbara Lewis barbara.lewis@ots.ac.cr for application information

Andres Santana

Graduate Education Department

Organization for Tropical Studies

San Pedro, Costa Rica. 676-2050

(506) 2524-0607 ext. 1511

www.ots.ac.cr

Leiden EvolutionOfNongeneticEffects Dec9-13

Workshop 'towards an Evolutionary Theory of Nongenetic Effects' Lorentz Centre, Leiden, the Netherlands December 9 - 13, 2013 http://transgenerational.zoo.cam.ac.uk/-LorentzWorkshop2013 Plenary speakers: Troy Day (UQueens) Alex Badyaev (UArizona) Jason Wolf (UBath) John McNamara (UBristol)

Organizing Committee: Rufus Johnstone (UCambridge) Ido Pen (UGroningen) Bram Kuijper (UExeter)

Goals: An accumulating number of studies demonstrate the widespread presence of alternative, non-genetic inheritance mechanisms, such as epigenetics, parental effects and cultural or ecological inheritance. As yet, however, existing evolutionary theory poorly accounts for these novel insights. The current workshop aims to fill this gap by working on theoretical models that provide testable predictions about the evolution of nongenetic effects in various social and ecological contexts.

Workshop setup: The workshop will take 5 days, during which we aim to identify the most timely questions that arise when considering an extended evolutionary synthesis which incorporates nongenetic inheritance. Each day of the workshop consists mainly of hands-on work in a number of small groups on theoretical problems, and/or on synthesis papers dealing with the subject. In between, there are number of plenary lectures and discussion meetings.

How to apply? We have only a limited number of places available for this workshop. Postgraduate researchers (PhD, postdoc and beyond) who work on topics related to nongenetic inheritance and who have an interest in crossing the bridge between theory and data are particularly encouraged to apply. Apply by sending a CV (2 pages max) and a cover letter (750 words max) to Bram Kuijper, bk319@cam.ac.uk. The application deadline is July 15, 2013. Bringing your own laptop to the workshop will be required.

There is no registration fee for the workshop, but we currently have no funding available to cover for accommodation or travel expenses.

More information can be found on the workshop's website: http://transgenerational.zoo.cam.ac.uk/-LorentzWorkshop2013 Rufus Johnstone, raj1003@hermes.cam.ac.uk Ido Pen, i.r.pen@rug.nl Bram Kuijper, bk319@cam.ac.uk

"B. Kuijper" <bk319@cam.ac.uk>

Leiden MitochondrialEvolution Jul8-12

Dear all,

We still have some open spaces for the workshop 'Recent Insights in Mitochondrial Evolution Applied to Health and Ageing' from July 8-12 in Leiden (http://www.lorentzcenter.nl/lc/web/2013/-553/info.php3?wsid=553&venue=Oort). Please find a description below. Please note that there is no registration fee for this workshop. You can register at http://www.lorentzcenter.nl/lc/web/2013/553/-info.php3?wsid=553&venue=Oort . 'Recent Insights in Mitochondrial Evolution Applied to Health and Ageing'

Aim and description

The endosymbiosis theory envisions cytoplasmic organelles, such as mitochondria and chloroplasts, as enslaved entities whose presence is only beneficial for the cell. We now know that this view is incorrect and that conflicts, both among mitochondrial genes and between mitochondrial and nuclear genes, are prevalent. Eukaryotic cells contain multiple mitochondria, each with multiple mitochondrial genomes, and selection among these genomes can reduce cell fitness. As a consequence, during somatic growth, deleterious mitochondrial mutations can accumulate and may contribute to the development of diseases such as cancer, and aging.

Recently, novel insights in the structure and transmission of mitochondria have been gained. Originally, it was believed that mitochondria formed distinct units within the cell, with separate genomes. However, we now know that mitochondria are much more plastic, that they frequently fuse to form networks, and divide again, and that they consequently share a pool of mitochondrial genomes. This has important repercussions for the way natural selection can act among mitochondria and mitochondrial genomes within the cell. This new insight may change the way in which we can explain the accumulation of mitochondrial changes during senescence and cancerous growth.

This symposium will bring together researchers studying the molecular details of such intra-cellular processes, with medical researchers interested in mitochondria-related diseases and evolutionary biologists interested in genetic conflicts. The interaction of these three fields will be reciprocally illuminating, as so far these research fields have operated separately. Combining the different kinds of expertise will provide researchers with the necessary details to make more specific predictions about the consequences of mitochondrial evolution, both long term and during somatic growth, on diseases and aging. Evolutionary biologists will gain from a deeper understanding of the exact mechanisms underlying mitochondrial evolution, whereas molecular and medical researchers will be able to test specific predictions aimed at preventing or curing mitochondrial diseases.

Aims

This workshop will be considered a success if new collaborations are established between evolutionary biologists and medical researchers. We particularly hope to encourage collaboration among junior scientists such as PhD students, postdocs and early-career researchers. As part of the program, we will include a half-day workshop on possibilities to apply for funding to establish cross-disciplinary research programs (eg Human Frontiers Science Program grants and Cross-disciplinary Research Fellowships).

Duur Aanen, Madeleine Beekman, Marc Maas, Hans Spelbrink.

Duur Aanen Laboratory of Genetics Wageningen University and Research Center The Netherlands Tel. +31(0)317 483144 Mobile: +31 (0)6 10327948 Fax: +31 (0)317 483146 http://www.gen.wur.nl/UK/Staff/Scientific%20Staff/Duur+Aanen "Aanen, Duur" <duur.aanen@wur.nl>

Leiden TropicalBiodiversity Feb3-28

Field Course in Tropical Biodiversity (Malaysia)

Registration is open for an MSc-level field course in Tropical Biodiversity, to be held in Leiden, The Netherlands, and Sabah, Malaysian Borneo, in weeks 7, 8, 9, and 10 of 2014. The course is organised by Naturalis Biodiversity Center, and consists of two weeks of theory in Leiden, followed by two weeks of field projects in Malaysia. Registration fee is 1,050 euros (this does not include air travel). Successful completion of the course is awarded with 6 EC. For more information, see: http://science.naturalis.nl/students/veldcursus . Menno Schilthuizen Naturalis Biodiversity Center, Leiden, The Netherlands

Prof. Dr. Menno Schilthuizen, professor for Character Evolution & Biodiversity Naturalis Biodiversity Center and Leiden University Room A105, Van Steenis Lab, Einsteinweg 2, 2333 CC Leiden, The Netherlands

Tel.: (+31-0)71-5687769, Mobile: (+31-0)6-22030313

Email: Menno.Schilthuizen@naturalis.nl Homepage: science.naturalis.nl/schilthuizen < http://www.naturalis.nl/ >

Skype: mennoschilthuizen Twitter: @schilthuizen

Menno Schilthuizen <menno.schilthuizen@naturalis.nl>

MNHN Paris BEAST2 Jul4

Dear colleagues

As part of the academic exchange scheme involving the University of Auckland and the Musée de l'Homme funded by the EU FP7 program under the IRSES scheme

there will be a one day workshop on the BEAST 2 software package.

It will be given by Remco Bouckaert from the Dept of Computer Science, University of Auckland,

on Thursday July 4th

in the Museum National d'Histoire Naturelle (Paris, France)

The day will consist of a seminar in the morning, followed by an afternoon of hands-on use of the software using example files

based on the Divergence Dating and STAR BEAST tutorial. Both available from http://beast2.cs.auckland.ac.nz/ The seminar will act as an introduction to several new models available in BEAST2; these include:

* the birth-death-skyline model, which allows estimation of parameters for epidemics,

* SNAPP, a multi-species coalescent model for SNP data that allows estimation of species trees,

* substBMA, a substitution model for nucleotide data that estimates per site rate and model parameters, which tends to have a much better fit to the data than other models.

IMPORTANT

Due to a strict limitation on the numbers of participants, entrance to this one day course will be*by invitation only.*

People wishing to attend should register their interest by Thursday June 20th, by sending a*CV* together with a*letter of motivation*

to myself at*endicott@mnhn.fr*

Invitations will then be forwarded together will full details of the day's schedule and personal requirements

cordially

Phillip Endicott Co-ordinator of the NEFREX scheme

frederic.austerlitz@mnhn.fr

Montana ConGen Sep2-7

ConGen 2013 Population Genomic Data Analysis Course http://www.popgen.net/congen2013/ Recent Approaches for Estimation of Population Structure, Gene-flow, Landscape Genomics, Selection Detection, and the Analysis of Next-Gen Sequence Data.

2-7 September 2013 Flathead Lake Biological Station, Montana, USA http://www2.umt.edu/flbs/ Applications for 2013 edition are now open!

Objective: To provide training in conceptual and practical aspects of data analysis for the conservation genomics of natural and managed populations. Emphasis will be on next generation sequence data analysis (RADs, exon capture, and whole genome sequence analyses) and interpretation of output from recent novel statistical approaches and software programs. The course also will allow daily discussions among young researchers (students/participants) and leaders in conservation genomics to help develop the "next generation" of conservation geneticists. We will identify and discuss developments needed to improve data analysis approaches. This course will cover analysis methods including the coalescent, Bayesian, approximate Bayesian, and likelihood-based approaches.

Who should apply: Ph.D. students, post-docs, and population biologists with a background of at least one semester university-level course in population genetics and a course in population ecology. Applicants must have a basic background in population genetic data analysis, including testing for Hardy-Weinberg proportions and gametic disequilibrium. Participation will be limited to 25-30 people allowing efficient instruction with hands-on computer exercises during the course. Priority will be given to persons with their own data to analyze (for example graduate students at the end of their degree program).

Course/Workshop Format: For each subject, we typically provide 30-45 minutes of background, theory, discussion and introduction to concepts. Immediately following, we will conduct data analyses together for 30-60 minutes using relevant software programs and real data sets. Evening hands-on computer sessions and lodging together of the instructors and students in the same location (the beautiful Flathead Lake field station) will allow for extensive exchange and facilitate learning.

Cost (before July 1st): $US 1,300 - which includes all lodging, meals (& coffee breaks etc.), transportation (to/from airport and Glacier National Park), a field trip to Glacier Park, and power point slide shows of all lectures (as well as audio-visual recordings of each lecture, including "question & answering sessions"). USD $1,500 if payment after July 1st.

Deadline for application is 1 July, 2013

More information on http://www.popgen.net/-congen2013/ tiagoantao@gmail.com

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NESCent EvolHumanViruses Nov2013

Dear colleagues,

Sarah Cobey and I are leading a NESCent working group on the evolution of common human viruses (description below and here https://www.nescent.org/-science/awards_summary.php?id=3D404). A working group consists of 10-12 people and meets 3 times for 3-4 days to work on a collaborative project. We have decided to leave several spaces in the working group open to researchers whom we don't know, or whose interest we haven't suspected. We currently have an overrepresentation of USA-based researchers, so we especially encourage researchers outside the USA to apply. The group is open to all levels of seniority (graduate student - PI).

If you are interested in joining our working group, please read the description below carefully and visit the relevant NESCent site (http://www.nescent.org/-science/workinggroup.php). Please then send us a one-page pdf that includes a short description of your interests, background, and reasons for wanting to join the working group. We will decide whom to invite based on replies received by June 23, 2013.

Working group description: The first aim of our group is to perform a comparative review of how viruses in humans are evolving and why, focusing on antigenic phenotype. We will start by considering the relative (census) population sizes of different groups of viruses and select a dozen or so common candidates. We'll review what is known about each virus's antigenicity, population structure, genetic evolution, and other aspects of phenotypic evolution. One of our outcomes will be identification of the viral groups and aspects of viral evolution that are understudied. Next, we will turn to theory, asking why we see the genetic and antigenic patterns that we do. We'll consider the phylodynamic framework, examining it in light of various definitions of antigenic phenotype and correlating the trends we find in human viral evolution with viral life history and epidemiology. The expected outcome will be a perspective paper addressing these questions and related ideas deemed important by the group. Our last ma jor goal is to create a collaborative environment that immediately enriches members' research and that may lead to future projects. For this reason, we aim to include scientists with diverse methodological backgrounds and different model viruses, who remain interested in the overarching questions.

The working group will meet three times, each for 3-4 days. The first meeting will occur in November 4-7, 2013, and the remaining two in early 2014 (dates TBD). All meetings will take place in North Carolina. NESCent will cover all travel expenses. Group members are expected to attend all three meetings.

Kind regards, Sarah Cobey and Pleuni Pennings

Pleuni Pennings Website: http://-pleunipennings.wordpress.com/ Petrov lab website: http://petrov.stanford.edu/ pleuni@stanford.edu

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NESCent EvolutionaryQuantGenetics Aug5-10

Title: Evolutionary Quantitative Genetics Instructors: Stevan Arnold, Joe Felsenstein, Thomas Hansen, Trudy Mackay, Brian O'Meara, Patrick Phillips, Liam Revell, Josef Uyeda Dates: August 5-10, 2013 Application review begins: June 1, 2013 Website: academy.nescent.org Where: National Evolutionary Synthesis Center, Durham, NC, USA

As part of the NESCent Academy, we are pleased to open applications for Evolutionary Quantitative Genetics. In this workshop we will review the basics of theory in the field of evolutionary quantitative genetics and its connections to evolution that is observed at various time scales. Quantitative genetics deals with the inheritance of measurements of traits that are affected by many genes. Quantitative genetic theory for natural populations was developed considerably in the period 1970-90 and up to the present time. It has been applied to a wide range of phenomena including the evolution of differences between the sexes, sexual preferences, life history traits, plasticity of traits, as well as the evolution of body size and other morphological measurements. Textbooks have not kept pace with these developments, and currently few universities offer courses in this subject aimed at evolutionary biologists. There is a need for evolutionary biologists to understand this field because of the ability to collect large amounts of data by computer, the development of statistical methods for changes of traits on evolutionary trees and for changes in a single species through time, and the realization that quantitative characters will not soon be fully explained by genomics. This workshop aims to fill this need by reviewing basic aspects of theory and illustrating how that theory can be tested with data. Participants will learn to use R, an open-source statistical programming language, to build and test evolutionary models. The intended participants for this workshop are graduate students, postdocs, and junior faculty members in evolutionary biology.

The course is co-sponsored by the American Society of Naturalists, and reduced tuition will be offered to participants who are ASN members.

Questions? email academy@nescent.org

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karen.cranston@gmail.com

@kcranstn

Karen Cranston <karen.cranston@gmail.com>

Portugal 2 Bioinformatics Jun13-14 27-28

APPLICATIONS ARE *OPEN* FOR:

IPTB13 - Introduction to Phylogenetic Tree-Building

http://gtpb.igc.gulbenkian.pt/bicourses/IPTB13/ IMPORTANT DATES for this Course Deadline for applications: *June 7th 2013* Notification of acceptance within 72 hours of application. Course date: June 13th and June 14th 2013

Course fee: Euro 160.00

The course will cover, at a basic level, building phylogenetic trees based on molecular sequence data. This will include the general context and uses of tree-building, choosing models of DNA and protein evolution, tree-building methods including distance, parsimony, maximum likelihood and Bayesian MCMC, and confidence in results.

Thanks

Pedro

– – Pedro Fernandes Instituto Gulbenkian de Ciência Apartado 14 2781-901 OEIRAS PORTUGAL Tel +351 21 4407912 http://gtpb.igc.gulbenkian.pt ——

APPLICATIONS ARE *OPEN* FOR:

AWGSMD13 - Analysing Whole-Genome Shotgun Metagenomic Data

http://gtpb.igc.gulbenkian.pt/bicourses/-AWGSMD13/ Deadline for applications: June 21st 2013 Notification of acceptance within 72 hours of application. Course date: June 27th and June 28th 2013

Course fee: Euro 160.00

In this two-day *intermediate-level* course we will cover the basics of analysing whole-genome shotgun metagenomics data generated from high-throughput sequencing instruments. This would interest those interested in taxonomic and functional characterisation of complex microbial communities from clinical or environmental samples. Topics covered will include design of sequencing experiments, quality control of data, de novo assembly and co-assembly, mapping reads to reference assemblies, contig clustering, whole-genome and haplotype reconstruction methods, taxonomic assignment of contigs, and cross-sample comparisons of microbial communities.

Target Audience The course will suit those already familiar with bioinformatic analysis of microbial whole-genome sequences and/or 16S phylogenetic profiling who now wish to gain knowledge of new techniques for whole-genome metagenomic studies.

Course Pre-requisites The course will be performed on Linux workstations and will feature a large hands-on component with real datasets, therefore knowledge of the UNIX command-line is essential, as well as familiarity with microbial genomics and ecology and a basic grasp of statistics.

Thanks

Pedro

– Pedro Fernandes Instituto Gulbenkian de Ciência Apartado 14 2781-901 OEIRAS PORTUGAL Tel +351 21 4407912 http://gtpb.igc.gulbenkian.pt Pedro Fernandes <pfern@igc.gulbenkian.pt>

Sevilla Spain ClimateAdaptation Sep30-Oct11

The Estación Biológica de Doñana (CSIC) (Sevilla, Spain) invites applications for its fourth international course on climate change entitled 'Ecological Consequences of Climate Change: Integrating Research Approaches' taking place from 30 September to 11 October 2013 in the heart of Doñana National Park. The course is open to students at the early postdoc, PhD and Master/advanced Diploma levels who are involved in global-change research. Its aim is to provide a synthetic overview upon different research perspectives ranging from paleoecology to population genetics, ecophysiology and bioclimatic modeling. The course will include lectures and practical exercises provided by an international panel of high-profile researchers, as well as field trips within the National Park.

Invited teachers:

Isabelle Chuine, CEFE (CNRS), Montpellier, France. Solomon Dobrowski, University of Montana, USA. Mary Edwards, University of Southampton, UK. Arndt Hampe, UMR1202 BIOGECO (INRA), Cestas, France. Ingolf Kühn, Helmholtz Centre for Environmental Research-UFZ, Germany. Jorge Lobo, Museo Nacional de Ciencias Naturales (CSIC), Madrid, Spain Fernando Valladares, Museo Nacional de Ciencias Naturales (CSIC), Madrid, Spain

Organizers: Juan José Negro, director of Estación Biológica de Doñana, and Arndt Hampe.

The course language will be English. Support from the Gas Natural Chair 'Biodiversity Conservation under Climate Change' and 7FP project ECOGENES, enables us to limit registration fees to 100 Euros and to cover all costs for transportation between Sevilla and Doñana National Park, accommodation and meals during the 2-weeks course. Applicants should provide a brief CV (max. two pages) as well as a statement (max. 500 words) about their research interests/current projects and why they would like to attend to the course. Application deadline is 7 July. Please send applications in a single pdf file and any related questions to Begoña Arrizabalaga (bego@ebd.csic.es).

Begoña Arrizabalaga Coordinación Dirección Estación Biológica de Donana (CSIC). Americo Vespucio s/n. Isla de la Cartuja. E-41092 Sevilla. España. Tlno. +34 95 4466707/00 Fax +34 95 4621125 e-mail: bego@ebd.csic.es

Begoña Arrizabalaga <bego@ebd.csic.es>

UIllinois TeachingEvolution Jul17-19

Please forward to teachers in your area who might be interested. All teachers are welcome, but we suspect that this workshop will be of interest to biology teachers in the Midwest.

Workshop in Evolutionary Biology: Developing Tools to Teach Evolution and Dispel Common Misconceptions

A teacher workshop in evolutionary biology is being hosted at the University of Illinois at Champaign-Urbana by the laboratories of Dr. Alison Bell, Dr. Zac Cheviron, and Dr. Becky Fuller from Wednesday, July 17 to Friday, July 19, 2013.

Who should apply? This workshop is open to secondary science teachers and informal science educators interested in evolution.

How to apply: Contact Becky Fuller (fuller@life.uiuc.edu) if interested.

Description: This workshop is an opportunity for teachers to interact with nationally and internationally acclaimed evolutionary biologists involved in cutting-edge research. It incorporates scientific presentations, discussions, and original lesson plans all aimed at helping teachers incorporate evolution into their classrooms. We will review the evidence for evolution and common misconceptions held by students. There is an emphasis on current topics, ongoing research, and real data.

Participants will receive a $250 stipend, breakfast and lunch, continuing professional development credits, and a copy of the book 'Why Evolution is True'. Housing is provided for out-of-town participants.

Goals: (1) Provide an introduction to evolutionary concepts and common misconceptions of students; (2) Develop a framework for engaging students in critical thinking about evolution; (3) Provide dynamic tools and lesson plans for teachers; (4) Build bridges between educators, scientists, and students.

The deadline for application is June 15, 2013.

More details on the workshop can be found at - http://www.life.illinois.edu/evolutionworkshop/-Evolution_Workshop/Summer_Workshop.html Sponsored by the School of Integrative Biology, the Department of Animal Biology, and the National Science Foundation.

Becky Fuller Associate Professor University of Illinois Animal Biology

Becky Fuller <fuller@life.illinois.edu>

UMontreal CoalescentTheory Oct6-11

On behalf of the Centre for Mathematics Research, and as part of the Thematic Semester on Biodiversity and Evolution (2013), we are pleased to announce the genomics workshop, "Coalescent Theory: Developments and Applications, October 7-11, 2013.

Details of the meeting, including registration can be found at the following site: http:/-/www.crm.umontreal.ca/2013/Coalescent13/-index_e.php . Overview: Coalescent theory is one of the most elegant and powerful probabilistic approaches in mathematical population genetics. It formalizes the backward perspective on evolution in large finite populations, providing a link between evolutionary models and empirical data.

Researchers who are actively working on algorithms for the analysis of human genetic data and the mapping of disease genes benefit from new theoretical developments. There are now massive genomic programs associated with whole-genome sequencing of very deep pedigrees, 1000s of complete genomes sampled from populations, and in some cases, the sequencing of entire populations.

This workshop is an opportunity to bring together theoretical and empirical molecular evolutionists, mathematical population geneticists, statisticians and epidemiologists to study new theoretical developments in coalescent theory and to discuss current challenges raised by the availability of large amounts of genetic data.

This workshop will be preceeded by the mini-course: Theoretical and Applied Tools in Population and Medical Genomics, October 6, 2013. Registration information for the mini-course can be found at http://www.crm.umontreal.ca/2013/Population13/-index_e.php Confirmed Speakers: G. Abecassis (Michigan) A. Auton (Albert Einstein, Yeshiva) J. Berestycki (Pierre et Marie Curie) M. Birkner (JGU Mainz) J. Blath (TU Berlin) A. Clark (Cornell) G. Coop (UC Davis) J. Degnan (Canterbury) S. Evans (UC Berkeley) W. Ewens (Pennsylvania) S. Gravel (McGill) R. C. Griffiths (Oxford) O. Hossjer (Stockholm) J. Hussin (Montréal, Oxford) T. Mailund (AArhus) S. Mano (ISM Tokyo) P. Marjoram (USC) G. McVean (Oxford) S. Myers (Oxford) J. Novembre (Chicago) N. Rosenberg (Stanford) Y. Song (UC Berkeley) J. Wakeley (Harvard) Y. Wu (Connecticut) X. Zhou (Concordia).

Instructors for the mini-course are: J. Hussin (Montréal, Oxford) J. Novembre (Chicago) J. Wakeley (Harvard)

We hope to see you in October!

Organizing committee: Philip Awadalla (Montréal, McGill) Robert C. Griffiths (Oxford) Fabrice Larribe (UQÀM) Sabin Lessard (Montréal)

Philip Awadalla <awadallp@gmail.com>

UOulu EvoDevPopGenet Sep12-13

EARLY ANNOUNCEMENT: Welcome to Workshop on Evolutionary, Developmental and Population Genetics on September 12-13 2013 in the University of Oulu, Finland. The event is organized in cooperation by the Biocenter Oulu Doctoral Programme (BCO-DP) and the national Population Genetics Graduate School (PopGenSchool).

Fellow bioscientists, please keep these dates free to attend this workshop. There will be talks about e.g., epigenetics, experimental evolution and EvoDevo.

Confirmed speakers:

Brandon Gaut Miltos Tsiantis Hadi Valadi Ram Reshef Jukka Jernvall Racel Giles Moises Mallo Mark Hankins

A detailed programme will be posted later.

For further information, please contact: Tanja Pyhäjärvi (tanja.pyhajarvi@oulu.fi)

Tanja Pyhäjärvi, Senior Research Fellow University of Oulu, Department of Biology email: tanja.pyhajarvi@oulu.fi

Tanja Pyhäjärvi <tanja.pyhajarvi@oulu.fi>

UWashington SummerInstStatGenetics Jul8-26 NewModules

Some of the modules in the Summer Institute in Statistical Genetics are now full. Other modules are filling.

There have been changes to the forensic genetics offering: Module 21 has moved to July 22-24, and a new Module 23 has been added during July 24-26. The new module provides training in STRmix, a software package with a continuous treatment of DNA profile evidence.

Details at http://sisg.biostat.washington.edu -

Bruce Weir <bsweir@uw.edu>

Instructions

Instructions: To be added to the EvolDir mailing list please send an email message to Golding@McMaster.CA. At this time provide a binary six letter code that determines which messages will be mailed to you. These are listed in the same order as presented here — Conferences; Graduate Student Positions; Jobs; Other; Post-doctoral positions; WorkshopsCourses. For example to receive the listings that concern conferences and post-doctoral positions this would be 100010. Messages are categorized on the basis of their subject headings. If this subject heading is not successfully parsed, the message will be sent to me at Golding@McMaster.CA. In addition, if it originates from 'blackballed' addresses it will be sent to me at Golding@McMaster.CA. These messages will only be read and dealt with when I have time. The code 000000 has all channels turned off and hence gets only a once monthly notifcation of the availability of a monthly review pdf file.

To be removed from the EvolDir mailing list please send an email message to Golding@McMaster.CA. Note that 'on vacation', etc, style messages are automatically filtered and should not be transmitted to the list (I hope), but should you wish to avoid the e-mail's your code can be temporarily changed to 000000.

To send messages to the EvolDir direct them to the email evoldir@evol.biology.McMaster.CA. Do not include encoded attachments and do not send it as Word files, as HTML files, as LaTeX files, Excel files, etc. ...plain old ASCII will work great and can be read by everyone. Add a subject header that contains the correct category "Conference:, Graduate position:, Job:, Other:, Postdoc:, Workshop:" and then the message stands a better chance of being correctly parsed. Note that the colon is mandatory.

The message will be stored until the middle of the night (local time). At a predetermined time, the collected messages will be captured and then processed by programs and filters. If the message is caught by one of the filters (e.g. a subject header is not correctly formated) the message will be send to me at Golding@McMaster.CA and processed later. In either case, please do not expect an instant response.

Afterword

This program is an attempt to automatically process a broad variety of e-mail messages. Most preformating is collapsed to save space. At the current time, many features may be incorrectly handled and some email messages may be positively mauled. Although this is being produced by LaTeX do not try to embed LaTeX or TeX in your message (or other formats) since my program will strip these from the message.