EvolDir

May 1, 2014

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

Belgium EMPSEB 20 Sep1-6 DeadlineExtended

EMPSEB 20- DEADLINE FOR ABSTRACT SUBMISSION EXTENDED TO 1st OF MAY 2014.

Dear Colleagues,

The registration deadline for EMPSEB 20 (European meeting of PhD students in evolutionary Biology) has been extended to the 1st of May, giving PhD students at all stages of their research another month to apply! Themeeting will this year be held in La Roche-en-Ardenne in Belgium, from the 1st-6th of September, 2014.

Plenary speakers have been confirmed and their talks will cover an array of diverse topics, e.g. sexual and asexual evolution, phenotypic plasticity, non-genetic heredity and epigenetics, complex systems and the evolution of viruses, venoms and stress resistance, involving methods like genomics, proteomics, quantitative genetics or modelling.

Details about the confirmed plenaries and how to register can be found on the EMPSEB website:

http://empseb20.com/ Registration fee:

350 euro (price includes transport from the airport to La Roche-en-Ardenne, accommodation, and meals during the conference)

EMPSEB in a nutshell:

EMPSEB provides a platform for PhD students studying evolutionary biology to present their work and meet their peers from all over Europe. It takes place in a different European city each year, and is organised by the PhD students of the host country. The meeting is now an annual tradition that started 19 years ago with the first meeting being held in Zurich, Switzerland in 1995.

EMPSEB 20 will last for 5 days and will involve a variety of activities... plus an optional excursion on the last day!

A number of senior evolutionary scientists have been selected to give plenary talks and to provide constructive feedback on the participants' research. All PhD students are required to give a presentation of 15 minutes.

Besides the website, you can also follow EMPSEB 20 on Facebook (https://www.facebook.com/EMPSEB20) and Twitter (https://twitter.com/EMPSEB20)

Any enquiries can be directed tosecretary@empseb20.com

We would be very grateful if you could forward this message to anyone you think might be interested. We additionally included an EMPSEB 20 flyer in attachment to easily advertise and spread information about this interesting meeting for PhD students.

Best regards,

Gwennaël Bataille, EMPSEB20 President

Gwennaël BATAILLE, PhD student - Teaching assistant

Earth and Life Institute Université Catholique de Louvain SST/ELI/ELIB Bâtiment Carnoy, c.145 Croix du sud 4-5, bte L7.07.04 1348 Louvain-la-Neuve BELGIUM

gwennael.bataille@uclouvain.be

Brazil EVOLUTION2015 SymposiumProposals

Call for Symposia for 2015 Annual Meeting

The 2015 annual meeting of the Society for the Study of Evolution is planned for June 26-30, 2015 in Guaruja, Brazil. The SSE Council invites proposals for the two Society-sponsored symposia to be held in conjunction with the meeting. Symposium proposals should include: (1) a synopsis of the symposium theme (about one page); (2) a tentative list of speakers, including institutional affiliations, and topics; (3) a rationale for the symposium explaining why this topic and this group of speakers are particularly appropriate for a Society-sponsored symposium; and (4) a statement that all potential speakers have been contacted and agree to participate in the symposium.

In evaluating proposals, SSE Council seriously considers the diversity of participants as a major qualification. Symposium organizers are expected to take into account gender, seniority, nationality, and other aspects traditionally underrepresented in Society symposia when preparing proposals. In addition, Council will favor those proposals whose topics concern newly emerging fields, fields ripe for syntheses, and fields different from those that have been included in recent Society symposia.

The Council will select two proposals for half-day symposia at the annual meeting in June 2014. All applicants will be notified of the Council's decision in August. The Society provides travel support for organizers and participants in sponsored symposia. Details are available on request. To be assured of full consideration, proposals must be received by midnight Eastern Standard Time on June 6, 2014:

Proposals should be sent by email (bbrodie@virginia.edu) as a single attachment in PDF format (under subject heading: SSE Symposia Proposal). Please expect and request confirmation of receipt of the proposal.

Butch Brodie

Executive Vice President, SSE

bbrodie@virginia.edu

CzechRepublic CladoceraEvolution Sept28-Oct3

Dear colleagues,

we are happy to announce that after several delays caused by technical issues, the registration for the 10th Symposium on Cladocera, to be held in the Czech Republic, is finally open.

The Symposium on Cladocera, a traditional triannual meeting of researchers studying cladoceran crustaceans, will be held this autumn in the Czech Republic. To celebrate the anniversary 10th meeting, it is fitting to find a spectacular place, and invite special guests. Thus, we will hear talks and admire posters on ecology, evolutionary biology, diversity, systematics, genomics... and many other aspects of these increasingly important model organisms in the recently restored baroque riding hall of the Lednice chateau, one of the landmarks of the UNESCO World Heritage area Lednice-Valtice Cultural Landscape.

The keynote talks will be presented by Luc De Meester (Katholieke University Leuven, Belgium) and Michael Lynch (Indiana University, Bloomington, USA). As it became tradition, a special issue of Hydrobiologia will be published as conference proceedings.

Apart from an exciting scientific programme, the conference participants and their accompanying persons will get opportunities to admire the historical, natural and oenological treasures of this unique region of Central Europe. To learn more, visit the conference website www.cladocera2014.org . The registration form allows online payments by credit/debit cards, and you may use it also to book accommodation in one of the hotels in the immediate vicinity of the conference venue. The deadline for early bird discount is on June 15. However, the first 30 registered participants will get a very special surprise gift upon arrival, so we recommend not to wait too long! Those who register early can also expect the best rooms in the conference hotels. Note that you do not need to submit your presentation abstract together with the registration. The abstracts (to be provided by e-mail) can be sent up to July 15.

With regards

Adam Petrusek & the organization team

Pokud je tento e-mail souèástíobchodního jednání, Pøírodovìdecká fakulta Univerzity Karlovy v Praze: a) si vyhrazuje právo jednáníkdykoliv ukonèit a to i bez uvedenídùvodu, b) stanovuje, $\frac{3}{4}$e smlouva musímít písemnou formu, c) vyluèuje pøijetínabídky s dodatkem èi odchylkou, d) stanovuje, $\frac{3}{4}$e smlouva je uzavøena teprve výslovným dosa$\frac{3}{4}$ením shody na v^{1}ech nále$\frac{3}{4}$itostech smlouvy.

petrusek@natur.cuni.cz

Ecuador Biodiversity

Symposio: Biodiversidad del género Solanum: Caracterización, conservación y aprovechamiento; 7 y 8 de Mayo del 2014, Loja, Ecuador

(Symposium: Biodiversity in Solanum: Characterization, Conservation and Utilization; 7-8 May 2014, Loja, Ecuador)

Los invitamos al 2014 simposio intrenacional: “Biodiversidad del género Solanum: Caracterización, conservación y aprovechamiento”. A realizarse los días 7 y 8 de Mayo del 2014 en la Universidad Técnica Particular de Loja, Ecuador

El sur del Ecuador es una de las regiones de mayor diversidad en el mundo, debido a la presencia de la depresión de Huancabamba (Andes), donde la ruptura de la cordillera de los Andes ha dado lugar a la fragmentación del hábitat. La radiación adaptativa de especies de plantas y animales en esta región la convierten en un laboratorio natural para el estudio de la especiación. Este simposio será un escaparate de la biodiversidad de Solanum, un género complejo, con muchas especies silvestres y de cultivos comerciales importantes, como la papa, el tomate, el pimiento y la berenjena, asícomo otros cultivos regionales como naranjilla, tomate de árbol, y pepino dulce, que tienen el potencial para una mayor distribución. Además, la reunión de dos días incluirá paneles y discusiones informales de la protección del germoplasma silvestre, y el desarrollo de la investigación en colaboración internacional para identificar, conservar y utilizar la biodiversidad en este rico y diverso grupo de organismos.

La lista de ponentes incluye: - Pablo Acosta, Universidad Técnica Particular de Loja, Ecuador - Patricia Bedinger, Colorado State University, USA - Merideth Bonierbale, Centro Internacional de la Papa, Lima, Peru - Joaquın Canizares, Instituto de Conservación y Mejora de la Agrodiversidad Valenciana. Valencia, España -Patricio Castro, Universidad Nacional de Loja, Ecuador - Roger Chetelat, Director, Tomato Genetics Resource Center, University of California, Davis, USA - Robert Last, Michigan State University, USA - Bruce McClure, University of Missouri, USA - Leonie Moyle, Indiana University, Bloomington - Jaime Prohens, Instituto de Conservación y Mejora de la Agrodiversidad Valenciana. Valencia, España - Flor Rodriguez, Centro Internacional de la Papa, Lima, Peru

La inscripción para el Simposio de 2 días es de $ US30.

Detalles (en Español y Inglés), incluyendo la información de registro y los viajes, se pueden encontrar en la página web del Simposio: www.utpl.edu.ec/diversidadsolanum/ ******

Symposium: Biodiversity in Solanum: Characterization, Conservation and Utilization Universidad Técnica Particular de Loja, Loja, Ecuador, 7-8 May 2014

We are pleased to announce the Symposium ’Biodiversity in Solanum: Characterization, Conservation and Utilization’ to be held at Universidad Técnica Particular de Loja, Loja, Ecuador, May 7-8.

Southern Ecuador is one of the megadiverse regions of the world due to the presence of the Huancabamba (Andes) depression, where the breakup of the Andes cordillera has led to habitat fragmentation. Adaptive radiation of both plant and animal species in this region make it a natural laboratory for the study of speciation. This symposium will showcase the biodiversity of Solanum, a complex genus with many wild species and important crop species including potato, tomato, pepper and eggplant, as well as other regional crops such as naranjilla, tamarillo, and pepino, which have the potential for wider distribution. In addition, the two day meeting will involve panel and informal discussions of the protection of wild germplasm, and the development of international collaborative research to identify, conserve, and utilize biodiversity in this richly diverse group of organisms.

Confirmed symposium speakers include: - Pablo Acosta, Universidad Técnica Particular de Loja, Ecuador - Patricia Bedinger, Colorado State University, USA - Merideth Bonierbale, International Potato Institute, Lima, Peru - Joaquın Canizares, Institute for the Conservation and Improvement of Agricultural Biodiversity, Valencia, Spain -Patricio Castro, Universidad Nacional de Loja, Ecuador - Roger Chetelat, Director, Tomato Genetics Resource Center, University of California, Davis, USA - Robert Last, Michigan State University, USA - Bruce McClure, University of Missouri, USA - Leonie Moyle, Indiana University, Bloomington - Jaime Prohens, Institute for the Conservation and Improvement of Agricultural Biodiversity, Valencia, Spain - Flor Rodriguez, International Potato Institute, Lima, Peru

Registration for the 2-day symposium is $US30.

Details (in English and Spanish), including information for registration and travel, can be found at the Symposium website: www.utpl.edu.ec/diversidadsolanum/ lmoyle@indiana.edu

Greifswald Germany Phylogenetics Jul14-16 Deadline

Attention! The deadline is approaching for the 1st Greifswald Phylogenetics Meeting, which will be held in July 2014!!!!

I herewith want to announce the 1st Greifswald Phylogenetics Meeting, which will be held in Greifswald (north eastern Germany) from the 14th till the 16th of July 2014.

Registration is now open and the deadline (both for registration as well as for abstract submission) is the 30th of April. There are still a few free slots, so please register asap!

Our conference poster can be found here: http://stubber.math-inf.uni-greifswald.de/ ˜ spillner/gpm-2014/poster-gpm-2014.pdf Feel free to print it and forward it to anybody who might be interested! For more details, please visit the conference website: http://stubber.math-inf.uni-greifswald.de/ ˜ spillner/gpm-2014/gpm-2014.html This meeting will have a particular focus on mathematical (e.g. graph theoretical, combinatorial, probabilistic and algebraic) aspects of evolutionary tree or network reconstruction, but it will also bring together scientists from different disciplines in order to provide the opportunity of close collaboration.

Scope:

Phylogenetics is an interdisciplinary research area that aims at reconstructing the evolutionary history of biological systems such as, for example, collections of species, populations or groups of bio-molecules. To achieve this, biologists work closely together with mathematicians and computer scientists. The conference will provide researchers from all three involved disciplines an opportunity to present their recent work and exchange ideas.

Location: Greifswald is a beautiful little town located directly at the Baltic Sea in close proximity to the famous islands Rügen and Usedom. Greifswald university was founded in 1496 and has therefore a long tradition and history. Being a former Hanse town, Greifswald is famous for its historic market square, its cathedral and the museum harbor. Other famous towns like Stralsund with the Oceaneum or the world cultural heritage city of Wismar are nearby, as well as the city of Rostock with its newly established Darwineum. The region is a holiday region but not too crowded by tourists. In July the weather is most likely to be great and we hope that if you can come to our meeting, you will find the time to stay longer and enjoy this unique area. There is a direct and regular train connection to and from Berlin, and the nearest international airports are Hamburg and Berlin.

Please note that the meeting starts early on the 14th with one of our highlight talks and ends in the evening of the 16th with another highlight talk - so if possible, please plan your stay from the 13th till the 17th of July.

The registration fee is 150 Euros (100 Euros for students).

Organizers: Mareike Fischer, Andreas Spillner, Martin Haase

Invited speakers: Olaf Bininda-Emonds, Mike Steel, Olivier Gascuel, Vince Moulton, Allen Rodrigo

For more details, visit our website http://-

stubber.math-inf.uni-greifswald.de/ ˜ spillner/gpm-2014/gpm-2014.html or contact Mareike Fischer: email@mareikefischer.de

Mareike Fischer <email@mareikefischer.de>

Guelph OE3C2014 May8-10 LastCall

Dear Colleagues,

Registration for the Ontario Ecology, Ethology, and Evolution Colloquium closes this Monday, April 7. OE3C 2014 is hosted by the University of Guelph and will be held on May 8-10.

We are still accepting abstract submissions for oral or poster presentations, especially from undergraduate or graduate students and post-docs. Abstract guidelines, conference logistics, and instructions about registration can be found on our website: http://www.uoguelph.ca/oe3c2014/ Please contact us at oe3c2014@gmail.com with any questions.

We hope to see you in May!

Kate Eisen http://www.uoguelph.ca/oe3c2014/ oe3c2014@gmail.com

OE3C 2014 <oe3c2014@gmail.com>

Innsbruck Austria Wolbachia Jun6-11

The end of extended early registration for the 8th International Wolbachia Conference is approaching fast: submission of poster and oral presentations will be possible exclusively until 4 April 2014; no exceptions will be made. Furthermore, 15% late registration charge will be added to the conference fees afterwards. Late registration (without possibility to submit presentations) will close on 23 May 2014. The conference will be held from 6 to 11 June 2014 in Innsbruck, Austria.

Please register now to get hold of the remaining presentation slots.

Conference 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.

Visit the conference website at http://wolbachia2014.org or proceed directly to the registration page at http://wolbachia2014.org/05-reg.php . Please also consider subscribing to our newsletter to be constantly informed about important news on the meeting: http://wolbachia2014.org/nl.php Kind regards from Innsbruck, Wolfgang Arthofer on behalf of the WOLBACHIA 2014 Organizing Committee

*8^th International Wolbachia Conference * *Wolfgang Arthofer Organising Committe*

Molecular Ecology Group, University of Innsbruck Technikerstr. 25, 6020 Innsbruck, Austria Phone +43 (0) 512 507 51751 Fax +43 (0) 512 507 51799 office@wolbachia2014.org http://wolbachia2014.org WOLBACHIA 2014 logo

office@wolbachia2014.org

JohnsHopkinsU Galaxy Jun30-Jul2 AbstractsDueApr4

Hello all,

This is a reminder that talk abstract submissions for the 2014 Galaxy Community Conference are due this Friday, April 4. See http://bit.ly/gcc2014abs for details. This is a great opportunity to share your work in high-throughput biology.

Accepted abstracts will be considered for the GigaScience “Galaxy: Data Intensive and Reproducible Research” series (announced for GCC2013). BGI is also continuing to cover the article processing charges until the end of the year

Poster abstracts are being accepted until April 25. Early registration (save a bundle, really) is also open.

Thanks, and I do hope you’ll join us in Baltimore,

Dave C, on behalf of the GCC2014 Organizing Committee

2014 Galaxy Community Conference (GCC2014) http://galaxyproject.org/GCC2014 June 30 - July 2, 2014 Homewood Campus Johns Hopkins University Baltimore, Maryland, United States

On Sat, Feb 22, 2014 at 3:29 PM, Dave Clements

<clements@galaxyproject.org> wrote: > > The 2014 Galaxy Community Conference (GCC2014, http://galaxyproject.org/GCC2014) features two full days of presentations, discussions, poster sessions, lightning talks and birds-of-a-feather, all about data-intensive biology and the tools that support it. GCC2014 also includes a Training Day with five concurrent tracks and in-depth coverage of thirteen different topics. > > GCC2014 will be held at the Homewood Campus of Johns Hopkins University, in Baltimore, Maryland, United States, from June 30 through July 2, 2014. > > Galaxy is an easily extensible data integration and analysis platform for life sciences research that supports hundreds of bioinformatics analysis tools. Galaxy is open-source and can be locally installed or run on the cloud. There are hundreds of local installs, and over 50 publicly accessible servers around the world. > > Early registration is now open. Early combined registration (Training Day + main meeting) starts at $140 for postdocs and students. Registration is capped this year at 250 participants, and we expect to hit that limit. Registering early assures you a place at the conference and also a spot in the Training Day workshops you want to attend. > > You can also book affordable conference housing at the same time you register. See the conference Logistics page for details on this and other housing options. > > Abstract submission for both oral presentations and posters is also open. Abstract submission for oral presentations closes April 4, and poster submission closes April 25. The GigaScience "Galaxy: Data Intensive and Reproducible Research" series (announced for GCC2013) is continuing to take submissions for this year's meeting and beyond. BGI is also continuing to cover the article processing charges until the end of the year, and for more information see their latest update. > > Thanks, and hope to see you in Baltimore! > > The GCC2014 Organizing Committee

– http://galaxyproject.org/GCC2014 http://galaxyproject.org/ http://getgalaxy.org/ http://usegalaxy.org/ https://wiki.galaxyproject.org/ clementsgalaxy@gmail.com

Kolympari Greece Lepidoptera Aug17-23

Announcing The Ninth International Workshop on MOLECULAR BIOLOGY AND GENETICS OF THE LEPIDOPTERA which will be held on August 17-23, 2014, at the Orthodox Academy of Crete in Kolympari, Crete, Greece.

Topics will include

* Genome Sequencing and Mapping * Comparative Genomics, Evolution and Phylogeny * Population and Evolutionary Genetics * Post-genomic and Functional Genomic Tools and Applications * Development and Differentiation * Endocrinology, Physiology and Biochemistry * Receptors and Ligands * Immunity * Neurobiology * Transgenesis and Paratransgenesis * Viruses, Other Pathogens and Pest Control * Chemical Ecology

Registration is now open at the conference website http://lepidoptera.ice.mpg.de The early registration deadline is 23 May 2014, final registration by 6 June 2014.

On behalf of the organizing committee, David G. Heckel lepidoptera (at) ice.mpg.de

lepidoptera@ice.mpg.de

Lausanne ESEB Aug10-15 CallForProposals GenderBias

Symposium proposals for ESEB 2015: potential gender bias

Further to our recent call for symposium proposals for ESEB 2015 in Lausanne next year, we wish to encourage potential symposium organisers to take diversity (of gender, nationality and age) into account when proposing speakers for their symposium.

As ESEB members will be aware, research shows clearly that (gender) bias in academia is usually not the result of intentional acts of exclusion, but rather the effect of more subtle mechanisms like implicit bias. Substantial concern has been raised about gender bias among invited speakers for symposia at previous ESEB (and other) meetings. The organisers of ESEB 2015 acknowledge this concern and wish to ensure that symposia selected for ESEB in Lausanne draw participants (both invited and those selected for inclusion when abstracts are reviewed) as broadly as possible to reflect the full research strengths of the fields represented. We thus encourage prospective symposium organisers to account for potential implicit bias before inviting speakers or submitting their proposals.

Balance in terms of gender, nationality and age will be included as one criterion used by the scientific committee when selecting symposia.

Further information about the symposia can be found at: www3.unil.ch/wpmu/eseb2015/symposium-information

For symposium submission, please go to: http://www3.unil.ch/wpmu/eseb2015/wpgforms/symposium/ The organisers and the scientific committee of ESEB 2015.

John Pannell <John.Pannell@unil.ch>

London CladeDynamics Nov10-11

Radiation and Extinction - Investigating Clade Dynamics in Deep Time 10th-11th November 2014 - Linnean Society of London (UK)

A two-day symposium and workshop bringing together a diverse array of researchers developing and applying methods for reconstructing deep-time macroevolutionary patterns in biodiversity, with a particular focus on analytical approaches that take advantage of the wealth of data available in the fossil record.

Dan Rabosky (University of Michigan) will deliver the plenary talk, with additional confirmed presentations from Tracey Aze (University of Oxford), Natalie Cooper (Trinity College Dublin), Mario dos Reis (University College London), John Finarelli (University College Dublin), Matt Friedman (University of Oxford), Melanie Hopkins (American Museum of Natural History), Graeme Lloyd (University of Oxford), Emily Rayfield (University of Bristol), Marcello Ruta (University of Lincoln), Graham Slater (Smithsonian National Museum of Natural History), Jeroen Smaers (Stony Brook University), Tanja Stadler (ETH Zürich), Gavin Thomas (University of Sheffield), and Chris Venditti (University of Reading).

Further details and registration here:

http://www.linnean.org/Meetings-and-Events/Events/Radiation+and+Extinction+-+Investigating+Clade+Dynamics+in+Deep+Time Dr. Anjali Goswami Reader in Palaeobiology Department of Genetics, Evolution, and Environment and Department of Earth Sciences University College London Darwin Building 218A Gower Street London WC1E 6BT +44 (0)20 7679 2190 www.goswamilab.com "Goswami, Anjali" <a.goswami@ucl.ac.uk>

Montreal GenomeBiomes May25-29 RoommateNeeded

PhD student seeking a male roommate to share a double room at the upcoming joint CSZ/CSEE Genomes to Biomes Meeting in Montreal,Canada, 25-29 May 2014. Student plans to stay for the entire meeting, including the night of 29 May (departure 30 May). Anyone interested in sharing should contact Roohollah Abbasi: roohollahabbasi@gmail.com

Jeffrey Marcus <Jeffrey.Marcus@umanitoba.ca>

NewYork EvolutionaryGenomics Jun6

Dear Colleagues,

Please join us in New York for "Genomes Evolving: The 13th Annual Symposium of NYU's Center for Genomics and Systems Biology." The one- day meeting will be Friday, June 6th. Our keynote speakers are Deborah Charlesworth and Greg Gibson.

Register (free!) at http://biology.as.nyu.edu/object/2014.cgsb.symposium Talks: Adam Auton (Einstein University) Understanding patterns of variation in human meiotic recombination

Chip Aquadro (Cornell University) Sex, flies and conflict: the molecular evolution of germline stem cell genes in Drosophila

Leonie Moyle (Indiana University) Evolutionary genomics of plant reproductive behavior

Ulises Rosas (New York University) Genetic mechanisms regulating root allometry responses and variation in Arabidopsis natural populations

Greg Gibson (Georgia Institute of Technology) Keynote: Are humans getting fitter, sicker, neither or both?

Elodie Ghedin (New York University) Escape the virus: swarm transmission of flu

Itsik Pe'er (Columbia University) Sequencing the Ashkenazi genome

Kirsten Bomblies (Harvard University) Adaptation to whole genome duplication in Arabidopsis arenosa

Casey Dunn (Brown University) Phylogenetics will be the new genetics

Deborah Charlesworth (University of Edinburgh) Keynote: What can plants tell us about sex chromosome evolution?

mrockman@nyu.edu

NHM London CollectionsClimateChange Jun25

Colleagues,

Scientific Collections International (SciColl) and The Natural History Museum London (NHM) will host a breakout session at the Society for the Preservation of Natural History Collections (SPNHC) 2014 Annual Meeting, held during the afternoon sessions on 25 June 2014. The main theme is the integration of scientific collections into environmental change research. Natural history and other scientific collections, such as core, soil and genetic libraries, offer relatively under-utilized or under-integrated sources of critical evidence about the past, and hold the potential for refining our understanding of how natural systems respond to environmental change.

We would like to hear your experiences and have your input regarding the use of collections in environmental and climate change research, especially cases where research and collections have bridged multiple disciplines, including connections to anthropology and archaeology.

We ask that those interested in presenting either as a full speaker (15 minutes w/ questions) or lighting talk and panel member (5 minute lighting round) submit abstracts following the SPNHC 2014 system here: http://www.museumwales.ac.uk/-spnhc2014/submissions/. Additionally, please add "SciColl/NHM" in the subject line of your submission email. Submissions are due by 5 May 2014.

Not interested in presenting, but still have something to share about collections, environmental change, and interdisciplinary work? Join us for our panel and open discussions. We want to hear from you, the collections professionals, about how you think your collections could be better utilized and how communication and access across collections can be improved.

See our full session description here: http:/-/www.museumwales.ac.uk/media/31183/-SciCollNHM_SPNHC-18Mar14.pdf **Additional Event: Save the Date** We will also be hosting a 2-day conference at NHM London, 15-16 September 2014. If you can^{1}t make it to SPNHC, please consider joining us at this event which will focus on the integration of interdisciplinary collections and environmental change research. More details will follow in the coming weeks.

Thank you! ˜Eileen and Ellinor

Eileen Graham, Program Manager Scientific Collections International

e: grahame@si.edu p: 202-633-0256 t: @sci_coll w: www.scicoll.org Dr Ellinor MICHEL Department of Life Sciences The Natural History Museum Cromwell Road SW7 5BD London UK tel: +44-207-942-5516

http://nhm.academia.edu/EllinorMichel www.researchgate.net/profile/Ellinor_Michel Ellinor Michel <e.michel@nhm.ac.uk>

Raleigh Evolution Jun20-24 Deadlines

The deadlines to register at discounted early bird rates, sign up for field trips, and apply for travel awards and other opportunities at Evolution 2014 < http:/-/evolution2014.org/ > in Raleigh, NC, are fast approaching. Please keep the following dates in mind as you plan your trip:

* March 31: deadline to apply for SSE international travel awards < http://evolution2014.org/travel-information/travel-awards/ > * March 31: apply for travel awards for faculty at minority-serving institutions < http://evolution2014.org/travel-information/-travel-awards/ > * April 1: graduate student volunteer < http://evolution2014.org/wpgforms/student-volunteers-2/ > sign-up ends (priority given to graduate students based in North Carolina) * April 1: deadline to apply for the Phylogenomics Symposium and Software School < http://www.cs.utexas.edu/%7Etandy/-symposium-2014.html > * April 1: deadline to sign up for field trips < http://evolution2014.org/conference-information/pre-post-conference-trips/ >

* April 14: undergraduate travel awards < http://-evolution2014.org/travel-information/travel-awards/ > close * April 16: early-bird registration < http://-

evolution2014.org/registration-and-other-costs/ > and presentation submission deadline * May 23: childcare < http://evolution2014.org/childcare/ >registration deadline * May 31: deadline to enter the evolution film festival < http://filmfestival.nescent.org/ > * late-May/early-June: complete program becomes available; stay tuned * June 1: cancellation deadline

We look forward to seeing you in Raleigh in June! Follow or join the conversation on Twitter using #Evol2014. Questions and suggestions? Please email organizer@nescent.org

Robin Smith <ras10@duke.edu>

Raleigh Evolution Jun20-24 EarlyBirdDeadline

Dear colleagues,

The earlybird registration deadline is rapidly approaching – 16 April. After that, registration rates increase by $50.

Also, please submit your presentation title and abstract by 16 April to be sure of making it into the program.

We look forward to seeing you in Raleigh in June!

Follow or join the conversation on Twitter using #Evol2014.

Questions and suggestions? Please email organizer@nescent.org

Allen Rodrigo Chair, Evolution 2014 Organizing Committee

a.rodrigo@nescent.org

Raleigh Evolution Jun20-24 UndergradDiversity Deadline

Undergraduate Diversity at Evolution 2014 - DEADLINE LESS THAN ONE WEEK AWAY!

We are pleased to announce an undergraduate travel award to bring talented and diverse undergraduates to the Evolution meetings this June 20-24 in Raleigh, NC (www.evolution2014.org). For the 12th year in a row we will fly a cohort of undergraduates from throughout the US and Puerto Rico to present a poster at the meetings, receive mentoring from graduate students, postdocs and faculty, and participate in a career-oriented 'Undergraduate Futures in Evolutionary Biology' panel and discussion. The program covers the costs of travel, registration, food and accommodation at the meetings.

The application deadline is Monday, April 14th, and decisions will be announced by Monday, April 21st. Applications are welcomed from all undergraduates, and the admissions goal is to create a diverse pool of students.

An overview of the program and student eligibility, and a link to the online application can be found at:

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

In addition, we will be soliciting names of graduate students, postdocs and faculty members who would like to serve as mentors during the meetings. Mentors meet with pairs of students and attend talks with them, introduce them to colleagues, network and generally make the meetings a welcoming place for them. Although costs are not covered for mentors it is an unusually rewarding experience. Contact Richard Kliman (rmkliman@cedarcrest.edu) if you are interested in serving as a mentor.

For inquires contact one of the organizers:

Jory Weintraub - jory@nescent.org

Richard Kliman - rmkliman@cedarcrest.edu

Scott Edwards - sedwards@oeb.harvard.edu

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

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

Raleigh iEvoBio Jun20-24 RegistrationDeadline Apr16

The early registration and abstract submission deadline for the 2014 Informatics for Evolutionary Biology conference is Wednesday, April 16. Registration and abstract submission is being done jointly with Evolution:

http://evolution2014.org/registration-and-other-costs/ iEvoBio is a forum bringing together biologists working in evolution, systematics, and biodiversity, with software developers, and mathematicians. The goal of iEvoBio is both to catalyse the development of new tools, and to increase awareness of the possibilities offered by existing technologies.

April 16 is the deadline for lightning talks and for software bazaar submissions. Submitted talks and software demos should be in the area of informatics aimed at advancing research in phylogenetics, evolution, and biodiversity, including new tools, cyberinfrastructure development, large-scale data analysis, and visualization. If a submission concerns a specific software system, that software must be licensed with a recognized Open Source License.

For more information, including details of the open source requirement, see http://ievobio.org . Karen Cranston, PhD Training Coordinator and Informatics Project Manager nescent.org @kcranstn http://orcid.org/0000-0002-4798-9499 Karen Cranston <karen.cranston@nescent.org>

Roscoff France EvolutionDiseases Sep6-10

Dear Colleagues,

We are pleased to announce the Jacques Monod Conference Infectious Diseases as Drivers of Evolution: the Challenges Ahead which will take place at Roscoff (Brittany, France) from the 6th-10th September 2014. We welcome proposals for papers on any aspect of the ecology and evolution of host-parasite interactions. The deadline for applications is the 2nd May.

For more info on the conference and how to apply please go to http://www.cnrs.fr/insb/cjm/2014/-Milinski_e.html We look forward to seeing you in Roscoff!

Manfred Milinski (Chairman) Ana Rivero (Vice-Chairman)

Infectious diseases as drivers of evolution: the challenges ahead

Invited speakers (provisional titles)

ALIZON Samuel (Montpellier, France) Multiple infection and virulence evolution BONNEAUD Camille (Exeter, United Kingdom) Evolution of host resistance and pathogen virulence following an emerging infectious disease outbreak BOOTS Mike (Exeter, United Kingdom) Epidemiological drivers of the coevolution of host parasite diversity BUCKLING Angus (Exeter, United Kingdom) Viruses as drivers of bacterial evolution over ecological time scales CHARBONEL Nathalie (Montpellier, France) Adaptative genomics of bank vole tolerance to Puumala hantavirus in Europe DAY Troy (Kingston, Canada) The evolutionary dynamics of drug resistance DOBSON, Andy (Princeton, US) [to be announced] EBERT Dieter (Basel, Switzerland) The population genetics of red queen dynamics EDWARDS Scott (Harvard, USA) Pathogen evolution and pathogen load in the race between house finches and Mycoplasma gallisepticum EIZAGUIRRE Christophe (Kiel, Germany) Host-parasite interaction - a fuel for speciation GANDON Sylvain (Montpellier, France) Malaria manipulates mosquitoes GIRAUD Tatiana (Paris-Sud, France) Mating types, sexes, sex, no-sex, sex with clones, and mating type chromosomes in fungi GRAHAM Andrea (Princeton, USA) The within-host dynamics of optimal defence GRUNAU Christoph (Perpignan, France) Darwins pangens and Jollos' Dauermodifikation - myth or reality? Lessons from the human parasite Schistosoma mansoni GUPTA Sunetra (Oxford, United Kingdom) The role of epistatic interactions between malaria-protective haemoglobin disorders in determining their epidemiology KOSKELLA Britt (Exeter, United Kingdom) Bacteria-phage coevolution within a long-lived host LAZZARO Brian (Cornell, USA) Complexity in the function and evolution of insect immunity LIVELY Curt (Indiana, USA) Parasite-mediated selection leads to host genetic diversity, but host genetic diversity reduces R0: how does that work? McCOY Karen (Montpellier, France) Evolution of host specialisation and circulation of vector-borne disease agents MILINSKi Manfred (Ploen, Germany) Olfactory signalling of immunogenetics for mate choice MORET Yannick (Dijon, France) Evolutionary ecology and mechanisms of trans-generational immune priming in insects REECE Sarah (Edinburgh, United Kingdom) Plasticity in parasite phenotypes: evolutionary and ecological implications for disease RIVERO Ana (Montpellier, France) More than just flying syringes: evolutionary ecology of Plasmodium-infected mosquitoes SCHMID-HEMPEL Paul (Zurich, Switzerland) Do infections drive the evolution of microbiota in social insects? SCHNEIDER David (Stanford, USA) Infected hosts take a long view and plan for recovery SCHULENBURG Hinrich (Kiel, Germany) Lessons from C. elegans as a model host: fast and complex adaptations

SIVA-JOTHY Mike (Sheffield, United Kingdom) Symbionts and insect cellular immunity SORCI Gabriele (Dijon, France) Immune evasion and the evolution of host defence VARALDI Julien (Lyon, France) Infected viruses as key players in host-parasitoid interaction WEBSTER Joanne (London, United Kingdom) Schistosome evolution in a changing

Prof. Dr. Manfred Milinski Department of Evolutionary Ecology Max-Planck-Institute for Evolutionary Biology August-Thienemann-Strasse 2 D-24306 Ploen, Germany, milinski@evolbio.mpg.de

milinski@evolbio.mpg.de

Seattle EvolutionPlasticity AWARDdeadline

2014 American Genetic Association Presidential Symposium - Evolution and Plasticity: Adaptive responses by species to human-mediated changes to their ecosystems

27-29 June 2014 University of Washington, Seattle

STUDENT AWARD APPLICATIONS AND ALL POSTER ABSTRACTS DUE APRIL 15

Awards are available to cover registration ($150), and a limited number to cover both travel and registration ($650). See the Symposium website for details - http://www.theaga.org/sample-page/aga2014/ AGA meetings are small and friendly, offering students a great opportunity to interact with top international researchers.

Early Registration till May 15 only $150 for students, $200 general includes 2 hosted receptions

SCHEDULE:

Friday 27 June 6 - 9 PM Hosted reception and poster session Saturday 28 June 8 AM - 5 PM Symposium, Day 1

Key Lecture by David Reznick, UC Riverside, “Hard and soft selection revisited:How evolution by natural selection works in the real world”

Saturday 28 June 6 - 9 PM Hosted reception and poster session Sunday 29 June 8 AM - 5 PM Symposium, Day 2

Noon brown-bag discussion, “What should conservation biologists and evolutionary biologists know about epigenetics?” moderated by Katie Peichel, AGA president-elect. This will follow a special presentation by Michael Skinner, WSU, “Epigenetic transgenerational inheritance of phenotypic variation in evolution: Lessons from Darwin’s finches”

Please visit the AGA website to register and book housing:

http://www.theaga.org/sample-page/aga2014/ Robin Waples, AGA President

agajoh@oregonstate.edu

Seattle EvolutionPlasticity Jun27-29

2014 American Genetic Association Presidential Symposium - Evolution and Plasticity: Adaptive responses by species to human-mediated changes to their ecosystems

27-29 June 2014 University of Washington, Seattle

STUDENT AWARDS: Awards are available to cover registration ($150), and a limited number to cover both travel and registration ($650). See the AGA website for details - http://www.theaga.org/sample-page/aga2014/ Poster abstracts due April 15

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Friday 27 June 6 - 9 PM Hosted reception and poster session Saturday 28 June 8 AM - 5 PM Symposium, Day 1

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Including: Noon brown-bag discussion, “What should conservation biologists and evolutionary biologists know about epigenetics?” moderated by Katie Peichel, AGA president-elect. This will follow a special presentation by Michael Skinner, WSU, “Epigenetic transgenerational inheritance of phenotypic variation in evolution: Lessons from Darwin’s finches”

Registration includes all the above activities: General is $200 until May 15th

Please visit the AGA website to register and book housing:

http://www.theaga.org/sample-page/aga2014/ Robin Waples, AGA President agajoh@oregonstate.edu

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Turku EvolutionaryPhylogenetics Aug11-14

Dear all,

We are organising a symposium on evolutionary phylogenetics and Lepidoptera biodiversity (see details below) at the International Conference on the Biology of Butterflies, 2014 in Turku, Finland (August 11-14th). http://nymphalidae.utu.fi/icbb2014/index.html We encourage submission for talks and posters: http://nymphalidae.utu.fi/icbb2014/abstract.html Deadline for abstract submission is May 1.

Thanks, and hope to see many of you in Turku,

Marianne Elias and Karina Lucas Silva Brandao Evolutionary phylogenetics and Lepidoptera biodiversity: diversification, adapations and community ecology

Why are there so many species on Earth, and why are they so concentrated in a small number of hotspots? More specifically, what are the processes underlying diversification and what are those permitting multiple species to coexist? These questions have intrigued biologists since the acceptance of Darwin's theory of evolution and still represent a major challenge for modern evolutionary biology. The insect order Lepidoptera is an excellent model group to answer these questions, using recent approaches based on molecular phylogenies. The purpose of this symposium is to present original research on diversification, adaptation and community ecology of Lepidoptera, using phylogenetic tools.

Marianne Elias CNRS Researcher UMR 7205 - CNRS Museum National d'Histoire Naturelle 45 rue Buffon, CP50, 75005 Paris phone: +33 1 40 79 37 90 http://www.mnhn.fr/oseb/elias-marianne,279 melias2008@gmail.com

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Turku Finland ButterflyEvolution Aug11-14 AsHosts

Butterflies as Hosts: what do they face and how do they face it?

at the 7th International Conference on the Biology of Butterflies in Turku, Finland - 11th - 14th of August 2014.

http://nymphalidae.utu.fi/icbb2014/index.html

Butterflies serve as hosts to an extremely large range of organisms, from endo- and ecto-parasitoid wasps, pathogenic fungi and viruses, to endosymbiotic bacteria exhibiting phenotypes in the spectrum between parasitism and mutualism. Such interactions can have profound consequences for the biology of butterfly hosts. The consequent co-evolutionary arm races might, indeed, lead to modifications in the hosts^1 immune strategies, demography, behaviour and important ecological and life-history traits. It is critical that we acknowledge the presence and impacts of parasites, pathogens and symbionts in shaping the biology of their butterfly hosts. This symposium will bring together an exciting mix of researchers to examine some of the best-studied interactions and their consequences for butterfly species, for a broader understanding of the butterflies.

The Keynote speaker for this session is Associate Professor Sonia Altizer from University of Georgia, USA (http://saltizer.myweb.uga.edu/). Other invited speakers are Dr. T. Huigens (Netherlands), Dr. M. Gibbs (UK) and Dr. E. Hornett (USA/UK).

Deadline for abstract submission is the 1st May 2014

Each talk = 12 min + 3 min questions. Presenters not offered talks, may present posters. Poster info: Regular A0 poster size (841 x 1189 mm, portrait orientation ONLY)

The whole conference promises additional exciting symposia including sessions on various aspects of butterfly Biology, Conservation and Genetics, with plenary speakers by Prof. Ilkka Hanski (Finland), Naomi Pierce (USA), Antonia Monteiro (USA) and Felix Sperling (Canada)

For the conference draft programme see: http://nymphalidae.utu.fi/icbb2014/symposia.html Submission must include: 1) The type of presentation Oral/Poster

2) The title of the presentation

3) The name of all authors (underline the presenting author)

4) The institution of each author (short description, not the complete postal address)

5) The Abstract

Registration information can be found here: http://-

nymphalidae.utu.fi/icbb2014/registration.html Follow updates on Facebook: https://www.facebook.com/-events/812109435470412/ Sincerely, Anne Duplouy

Dr. Anne Duplouy Academy of Finland Postdoctoral researcher The University of Helsinki PO Box65 Viikinkaari 1 00790 Helsinki Finland

email: anne.duplouy@helsinki.fi web: www.anneduplouy.net anne.duplouy@helsinki.fi

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Turku Finland ButterflyEvolution Aug11-14 BehaviourSymp

ICBB.2014_Symposium:Butterfly.behaviour

We are organising a symposium for the International Conference on the Biology of Butterflies, 2014 in Turku, Finland (August 11-14th) and encourage submissions for talks and posterson 'Behavioural and neurological aspects of ecological adaptation and speciation'

Symposium theme: A major goal of evolutionary biology has been to characterize the adaptations between populations that contribute to ecological divergence and speciation. Although most studies have concentrated on structural adaptations, such as colour pattern, shifts in behaviour may be especially important in generating both reproductive and ecological isolation. These behavioural differences may be genetically determined or acquired (learnt), may involve sensory adaptations, changes in life history, or adaptive changes in brain size, structure or connectivity. This symposium will take a broad approach to examining the role of behavioural and neurological change in ecological adaptation and speciation.

We hope to attract talks spanning the following topics: The role of behavioural plasticity in ecological diversification The genetic architecture of adaptive behaviours Behavioural aspects of reproductive isolation Neural basis of adaptive behaviours Ecological correlates of neural diversification

During abstract submission please select 'BEHAVIOURAL ECOLOGY' from the drop down box for the main topic area of your abstract.

Invited Speakers: Prof. Steven Reppert (U. Massachusetts): Neuroethology of monarch butterfly migration Prof. Emilie Snell-Rood (U. Minnesota): Nutrition as a constraint on life history and brain evolution: a comparative study across butterflies Dr. Erica Westerman (U. Chicago): Perceptual biases and visual attraction: the role of perception in reproductive isolation Dr. Maaike De Jong (U. Bristol): Ecological genetics of life history and host plant adaptation in the Glanville fritillary butterfly

More details: Conference information: http://nymphalidae.utu.fi/icbb2014/index.html Abstract submission: http://nymphalidae.utu.fi/-icbb2014/abstract.html Many thanks and we hope to see you in Turku, Stephen Montgomery (Stephen.Montgomery@cantab.net) & Richard Merrill (R.Merrill@zoo.cam.ac.uk)

Dr. Stephen Montgomery

Research Fellow The Royal Commission for the Exhibition of 1851 Dept. of Genetics, Evolution and Environment University College London www.SHMontgomery.co.uk Stephen Montgomery <stephen.h.montgomery@ucl.ac.uk>

UAveiro HerpetologyConservation Sep30-Oct4

We have the pleasure to invite you to participate in the XIII Iberian Congress of Herpetology, about the topic Risk Assessment and Conservation in Herpetology, which will take place at the University of Aveiro Campus, from September 30th to October 4th 2014.Organizing Committee:Isabel Lopes. CESAM, Univ. Aveiro

Manuel Ortiz-Santaliestra: Univ. Koblenz-Landau Amadeu Soares: CESAM, Univ. Aveiro Enrique García Muñoz: CESAM, Univ. Aveiro Miguel Ãngel Carretero: CIBIO, Univ. Porto Neftalí Sillero: CICGE, Univ. Porto Sérgio Marques: CESAM, Univ. Aveiro Eduardo Ferreira: CESAM, Univ. Aveiro

Scientific Committee:

Isabel Lopes: CESAM, Univ. Aveiro Manuel Ortiz-Santaliestra: Univ. Koblenz-Landau Amadeu Soares: CESAM, Univ. Aveiro Miguel Ãngel Carretero: CIBIO, Univ. Porto Ãñigo Martínez-Solano: CIBIO, Univ. Porto Neftalí Sillero: CICGE, Univ. Porto

Confirmed Invited Speakers:

Jan W. Arntzen: Naturalis Biodiversity Center Claudia Corti : Univ. Firenze Armando Loureiro: Inst. ConservaçÃ£o da Natureza e das Florestas Albert Martínez-Silvestre: Ctre. Recuperació d'Amfibis y

Rèptils de Catalunya Rui Rebelo: Univ. Lisboa Xavier Santos: CIBIO, Univ. Porto Neftalí Sillero : CICGE, Univ. Porto

We will provide short advanced courses (3 h) to be taught on September 30th:

- Ecotoxicology of amphibians and reptiles - Modelling in Herpetology - Scientific illustration in Herpetology

Important deadlines:

Abstract submission: 15 April - 31 July 2014 Registration deadline (advanced courses & field trip on last day): 1 September 2014

Fees:

Up to September 1st: General - 150; Member of AHE/SPH - 125; Student - 60; Student University of Aveiro - 35 After September 1st: Corresponding reduced fee + 50

For any information or questions contact: BIO-herpe2014@ua.pt or go visit our website: herpe2014.web.ua.pt

Emanuele Fasola Msc PhD student at Department of Biology of Aveiro University (DeBio, Universidade de Aveiro),CESAM (Centro de EstudoS do Ambiente e do Mar), applEE (applied Ecology and Ecotoxicology r&d group).

CESAM webpage: http://www.cesam.ua.pt/emanuelefasola Campus Universitário de Santiago, Universidade de Aveiro, 3810-193 Aveiro, Portugal. Mail: emanuele.fasola@ua.pt or vanderfas@alice.it

Member of: Italian Society for Evolutionary Biology SIBE www.sibe-iseb.it and Member of: Student Affairs Committee of European Society for Conservation Biology SCBEuroSAC http://scb-students.wikispaces.com/ "vanderfas@alice.it" <vanderfas@alice.it>

UIllinois UC ArthropodGenomics Jun12-14

ARTHROPOD GENOMICS 2014

The deadlines for abstract submission and early-bird registration for the 8th Annual Arthropod Genomics Symposium are coming up soon! Register and submit your abstract soon to enjoy the reduced registration rate and take advantage of this opportunity to present your work.

The schedule of speakers for AGS 2014 is now available on the website (link below.)

Important Dates:

Friday, April 4, 2014: Deadline to submit Travel Grant Application for Vector Biologists

Thursday, April 17, 2014: Deadline to submit poster abstracts

Monday, April 21, 2014: Early-bird registration deadline

The 8th Annual Arthropod Genomics Symposium will be held Thursday, June 12 – Saturday, June 14, 2014, hosted by the Institute for Genomic Biology at the University of Illinois at Urbana-Champaign. The link for conference registration and abstract submission is below. Two speakers for each session of the symposium will be selected from among the submitted abstracts.

The symposium will feature sessions on the i5k consortium, vector biology, social insects, microbiomes, and population and comparative genomics. Patricia Wittkopp (University of Michigan) will give the keynote lecture on the evolution of promoters and gene regulation in /Drosophila/ on Thursday evening. Judy Willis (University of Georgia) will give a retrospective lecture on 50 years in insect genomics on Friday evening.

All are also invited to register for a pre-symposium Epigenomics Workshop to be held on-site on June 12.

To register for the Arthropod Genomics Symposium or view more information visit: _http://conferences.igb.illinois.edu/arthropod/_ Arthropod Genomics Symposium 2014 <ags@igb.illinois.edu>

UIllinois UC ArthropodGenomics Jun12-14 Deadline

One week remains to submit abstracts for the 8th Annual Arthropod Genomics Symposium! The deadline for early-bird registration is also coming up fast, on the following Monday. Register and submit your abstract soon to enjoy the reduced registration rate and take advantage of this opportunity to present your work.

The schedule of speakers for AGS 2014 is now available on the website (link below.)

Important Dates:

Thursday, April 17, 2014: Deadline to submit poster abstracts

Monday, April 21, 2014: Early-bird registration deadline

The 8th Annual Arthropod Genomics Symposium will be held Thursday, June 12 Saturday, June 14, 2014, hosted by the Institute for Genomic Biology at the University of Illinois at Urbana-Champaign. The link for conference registration and abstract submission is below. Two speakers for each session of the symposium will be selected from among the submitted abstracts.

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To register for the Arthropod Genomics Symposium or view more information visit: _http://conferences.igb.illinois.edu/arthropod/_ ags@igb.illinois.edu

GradStudentPositions

BaylorU EvolutionaryBiology

The Danley Lab at Baylor University (http://www.baylor.edu/Patrick_Danley) seeks a Ph.D. student broadly interested in evolutionary biology using East African cichlid fish as a model system. The exact nature of the research will be developed by the student in collaboration with Pat Danley though it should relate to the lab's previous research on sexual selection (mate choice, aggression), phylogeography, and speciation.

Applicants with a background in behavioral, phylogenetic, and genomic methods are encouraged to apply. Applicants experienced with R, Perl, and Python are a plus. Applicants are expected to have completed (or will soon complete) either a BS/BA or Msc. by the start of the 14-15 academic year.

The successful applicant will be admitted to the Department of Biology's Ph.D. program which provides 5 years of 12 month stipend ($21,000, plus possible enhancements for outstanding students), tuition remission, and benefits.

The Baylor's Department of Biology has an active graduate community of over 50 students and possesses strengthens in the areas of integrative organismal biology and aquatic ecology. Waco, home of Baylor University, is conveniently located 90 minutes from both Dallas and Austin and was recently ranked as one of America's Awesomest (sic) Cheap Cities making it a perfect home for would be graduate students. http://www.wisebread.com/10-of-americas-awesomest-cheap-cities To apply, please send a cover letter, CV, unofficial transcripts, and GRE scores to patrick_danley@baylor.edu.

Patrick_Danley@baylor.edu

Bielefeld Vancouver 5 GenomeComputations

Dear members of evoldir,

5 PhD positions are available within the bilateral Bielefeld-Vancouver Research Training Group on 'Computational methods for the analysis of the diversity and dynamics of genomes',

http://wiki.techfak.uni-bielefeld.de/didy/-Announcement/ The individual projects are here:

http://wiki.techfak.uni-bielefeld.de/didy/-Announcement/Projects2014 Deadline for application is May 18.

Best regards Ellen Baake Bielefeld

ebaake@techfak.uni-bielefeld.de

BoiseStateU MolecularEvolution

PhD opening

The lab of Dr. Eric Hayden at Boise State University is seeking PhD students (and postdocs) to study the molecular evolution of non-protein-coding RNA molecules. Research topics include robustness and evolvability of RNA molecules, empirical RNA fitness landscapes, and experimental evolution of RNA. In addition to traditional molecular biology techniques, the research utilizes next-generation sequencing and provides opportunities for computational biology approaches. Students are encouraged to develop a project to match their learning and career objectives. Students will enter our interdisciplinary Biomolecular Science PhD program designed to offer students the opportunity to take classes and conduct research at the interfaces of Biology, Chemistry and Physics. Mentoring and resources are available from faculty in all three disciplines. Students and postdocs with an interest in developing skills around RNA molecular biology and sequence analysis/computational approaches are encouraged to apply. Previous experience with one of the approaches is preferred, but exceptional applicants without experience will be considered. PhD students will be guaranteed funding throughout their PhD based on a combination of Teaching assistantships and Research Assistantships. The city of Boise offers a unique combination of a very livable urban environment as well as access to numerous outdoor experiences, which landed it as #12 on the Best Places to Live in the U.S.A. (livability.com).

Please email a brief description of why you are interested in the position and your past experiences to: erichayden@boisestate.edu

Eric J. Hayden Assistant Professor Biological Sciences Boise State University Boise, Idaho, USA 83725

Office Number: 208-426-4625 *Office Fax*: 208-426-1040

Eric Hayden <erichayden@boisestate.edu>

ClarkU AnnelidEvoDevo

The lab of Dr. Néva Meyer at Clark University is looking for a PhD student to study central nervous system (CNS) evolution using the annelid Capitella teleta. The molecular mechanisms underlying annelid development are not well understood and multiple features (phylogenetic position, spiral cleavage) make annelids a great group of animals to study evolution of animal body plans. Potential research topics include deciphering the CNS neurogenic gene regulatory network, understanding whether or not Capitella has neural stem cells and if so how these cells are developmentally regulated (i.e., neurogenesis), and understanding how the dorsal-ventral axis is specified. In addition to using traditional techniques in molecular and cellular biology, the research program is expected to utilize next-generation sequencing.

Students are encouraged to develop a project that matches their learning and career objectives and will enter Clark University's Biology PhD program. Previous experience in molecular biology is desirable. PhD students will be guaranteed funding for five years, with a possible extension through teaching and research assistantships. Possible start dates are September 2014 or January 2015.

Clark University is a small liberal arts research university located in Worcester, MA. Worcester has a nice combination of urban and outdoor activities and is in close proximity to a variety of New England destinations.

Please email a brief description of why you are interested in the position and your past experiences to: nmeyer@clarku.edu

Néva P. Meyer, Ph.D. Assistant Professor Clark University Department of Biology 950 Main Street Worcester, MA 01610

NMeyer@clarku.edu

GLIER UWindsor Salmon Genetics LH Variation

Funded Ph.D. position to investigate the genetics of early life history variation in Pacific salmon (immediate start)

We are offering an exciting opportunity for an outstanding doctoral student (preference for Canadian citizen and landed immigrants) to address a question central to our understanding of the evolution of life history variation and local adaptation in salmon: does life history variation reflect traditional adaptation to local conditions, or have salmon evolved novel forms of life history plasticity? The successful candidate will use molecular, population, and quantitative genetic methods combined with captive breeding experiments and field-based measurements to partition the relative contribution of genetic, epigenetic, GxE interactions and environmental effects to early life history trait variation in Pacific salmon. Your fieldwork would take place on coastal British Columbia, and your lab work would take place primarily in GLIER's innovative Environmental Genomics Facility, where you would have hands-on experience using diverse and cutting edge genetics technologies such as nano-fluidic qRT-PCR and NextGen RNAseq. You will collaborate with salmon farms, scientists at the Department of Fisheries and Oceans as well as researchers at government agencies in BC and Ontario.

Join us at the Great Lakes Institute of Environmental Research (GLIER) for a unique interdisciplinary doctoral experience where you will be mentored by our team of internationally renowned researchers and have unmatched hands-on access to cutting edge genetics facilities. All inquiries should be directed to Dr. Daniel Heath, Director of GLIER, at 519-253-3000 x3762 (dheath@uwindsor.ca).

saraj@uwindsor.ca

GriffithU Bioinformatics

A Ph.D. scholarship in Bioinformatics is available at Griffith University, Nathan, Australia. We have a world class Ancient Genomics laboratory and have sequenced the genomes of ancient penguins, ancient Australians and the extinct moa. We are looking for an enthusiastic student with immense interest in the bioinformatics analysis of next generation sequence data from Illumina, FLX and ion-torrent platforms. The prospective student could work on one of the following project:

1. Ancient human population genomics

2. Evolutionary genomics of ancient and modern penguins

An honors or master's degree in biological, physical or computational science is required. Persons with a non-biology degree should have some basic understanding of genetics, evolution and molecular biology.

Essential skills include:

[We wouldn't expect a starting PhD student to have many of these skills, but an ability and desire to learn them is obviously essential]

Scripting: Perl/Python

Unix command line (particularly to use parallel computing clusters)

Programming: Java/C/C++ (OOPS concept)

Database: maintenance and design; MySQL/PosgreSQL/SQLite or similar

Familiarity with sequence databases and genome browsers (eg. NCBI/EMBL/DDBJ, UCSC)

Familiarity with the following software is desirable:

Read mapping: BWA; Bowtie; GSMapper (454); SOAP

De novo assembly: Velvet; SOAP de novo; Newbler (454)

Assembly summary: Samtools; GATK

Population genetic software: PLINK; EIGENSOFT

For further details please contact Prof. David Lambert (d.lambert@griffith.edu.au)

Regards Sankar

Sankar Subramanian Research Fellow Environmental Futures Centre Griffith University Nathan QLD 4111 Australia

Email: s.subramanian@griffith.edu.au Ph: 61-7-37357495 Fax: 61-7-37357459

Sankar Sankarasubramanian <s.subramanian@griffith.edu.au>

Krakow Poland EcoEvo

Master studies in Ecology and Evolution

EcoEvo is a two year Master of Science programme for students interested in the functionning and evolution of the biosphere offered by the Institute of Environmental Sciences at Jagiellonian University in Krakow,Poland. The participants will investigate the mechanisms underlying ecological and evolutionary processes and will develop practical skills related to carrying out research and conservation projects. They will undertake a range of multidisciplinary courses (consisting of lectures, seminars, laboratory work and field classes) as well as carry out group and individual research projects.

Starting date: October 2014

Admission: the application for the programme is a continuous process; additional application rounds start until there are no more places available or the last application round is over. The dates of application rounds for 2014 are: 19 March V 6 May, 7 May V 24 June, 25 June V 19 August and 20 August V 17 September.

Tuition fees: (1) EU citizens and non-EU citizens with documented Polish background - no tuition fee; (2) non-EU citizens V 1st year: £á 2200, 2nd year: £á 2000.

For more information see: www.ecoevo.uj.edu.pl – – Dr. Zofia Prokop Molecular and Behavioral Ecology Group Jagiellonian University Gronostajowa 7 30-387 Krakow, Poland tel. +48 12 664 5151 e-mail: zofia.prokop@uj.edu.pl *Google Scholar profile < http://scholar.google.co.nz/citations?user=-58lKo7IAAAAJ&hl=en&oi=ao >*

Zofia Prokop <zofia.prokop@uj.edu.pl>

LavalU EvolGenomics

PhD position-Laval University-Ecological Genomics

A four year PhD position in ecological genomics is available at Laval University. The project will exploit a new study system we recently developed for the study of adaptation and ecological speciation using the budding yeast Saccharomyces paradoxus. The candidate will use genomic tools (whole-genome sequencing, high-throughput phenotypic profiling, QTL analyses, association mapping) to study the molecular bases of phenotypic divergence between incipient species and identify genes involved in hybrid incompatibilities. The project will combine experimental molecular biology, bioinformatics approaches and possibly field work.

See recent publications: Leducq et al., Proc Soc B (2014); Charron et al., FEMS Yeast Research (2014); Leducq et al., PLoS Genetics (2012); Landry and Aubin-Horth, Adv Exp Med Biol. (2014); Verta et al., Molecular Ecology (2013); Pavey et al., Trends in Ecology and Evolution (2012); Fontanillas et al., Molecular Ecology (2010); Brown et al., Molecular Ecology (2008); Lynch et al. PNAS (2008); Landry et al., Molecular Ecology (2006); Landry et al. Heredity (2007); Landry et al. Science (2007);

Applicants must have i) a strong background in evolutionary genetics and/or evolutionary ecology plus a strong interest for using genomics and bioinformatics tools and ii) a MSc degree in any relevant field of the life sciences.

The Landry laboratory is a dynamic, international and interdisciplinary research group with broad interests in integrative biology, systems biology, molecular evolution, bioinformatics and ecological genomics. Laval University is one of the most important research universities in Canada and is located in Quebec City, a lively city with a vibrant culture that offers an exceptional quality of life.

Interested applicants should send a CV with a list of publications and accomplishments, a low-resolution copy of official academic transcripts, a statement of interests (1 page) and the names of three referees in a single PDF file to Christian.landry@bio.ulaval.ca.

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

LavalU SystemsBiology

PhD position-Laval University-Systems Biology

A four year PhD position in evolutionary systems biology is available at Laval University. The project will be tailored to the candidates interests and will have to touch upon current research interests of the laboratory, which include i) evolution and robustness of protein interaction networks; ii) evolution of signalling networks and crosstalk among posttranslational modifications; iii) gene duplication and the evolution of network complexity.

See recent publications: Landry et al. Cell (2013); Diss et al. Cell Reports (2013); Freschi et al. PLoS Genetics (2013); Diss et al. Current Opinion in Biotechnology (2013); Freschi et al. Molecular Systems Biology (2011); Gagnon-Arsenault et al. J Proteomics (2013); Moses and Landry, Trends in Genetics (2010); Diss et al. JEZ B (2014); Leducq et al. PLoS Genetics (2012); Levy et al. Phil Trans Roy Soc (2012); Landry et al. Trends in Genetics (2009); Tarassov et al. Science (2008);

Applicants must have i) a strong background in genetics or molecular biology or biochemistry or proteomics or bioinformatics (or their combination), and an expertise in or a strong interest for evolutionary biology and ii) a MSc degree in any relevant field of the life sciences.

The Landry laboratory is a dynamic, international and interdisciplinary research group with broad interests in integrative biology, systems biology, molecular evolution, bioinformatics and ecological genomics. Laval University is one of the most important research universities in Canada and is located in Quebec City, a lively city with a vibrant culture that offers an exceptional quality of life.

Interested applicants should send a CV with a list of publications and accomplishments, a low-resolution copy of official academic transcripts, a statement of interest (1 page) and the names of three referees in a single PDF file to Christian.landry@bio.ulaval.ca.

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

LeidenU MicrobialEvolution

4-year PhD studentship, Microbial Evolution and Ecology

Institute of Biology, University of Leiden, The Netherlands

A 4-year PhD position in microbial evolution and ecology is available at the University of Leiden in The Netherlands. This NWO funded project, run jointly by Daniel Rozen and Gilles van Wezel, will study the evolution and ecology of antibiotic production and resistance in the soil, with the broad aim of understanding the role of antibiotics in nature. Focusing on the prolific antibiotic producing genus, Streptomyces, the student will test the idea that the control of antibiotic production and resistance is tied to competitive and social interactions between coexisting bacteria. The project will integrate methods from microbial and chemical ecology and use high-end mass spectrometry to identify compounds that modify antibiotic production or resistance.

Interested applicants should ideally have experience in microbial ecology and a strong background in evolutionary biology. Experience with molecular genetics and an interest in chemical ecology is also desirable.

Applications will reviewed until the position is filled.

Informal enquiries can be addressed to: Daniel Rozen, Tel: +31 (0)71 527 7990, Email: d.e.rozen@biology.leidenuniv.nl

d.e.rozen@biology.leidenuniv.nl

McGillU HumanPopulationGenomics

Graduate position in mathematical and population genetics

Graduate student positions in mathematical and population genetics are available in Simon Gravel's group at McGill University in Montreal, Canada. The group focuses on creating mathematical and statistical methods to understand human history and evolution through the analysis of high-throughput genomic data. Students will be involved in conceptual methods development, implementation, and applications to exciting datasets. This is unique opportunity to be involved in work that is relevant and interesting from a mathematical, biological, and historical perspectives.

We welcome applications from qualified candidates from diverse backgrounds, including biology, anthropology, mathematics, physics, computer science, and related fields.

The position offers an exceptional opportunity for collaborative research in a quantitative and theoretical lab with access to cutting-edge data. McGills Department of Human Genetics, the Genome Quebec Innovation Center, and the numerous nearby institutes in downtown Montreal provide a thriving research environment.

Applications and queries should be sent to gravellab@gmail.com. Please include a statement of interest (1 page), a CV with a list of publications, contact information for three references, and a low-resolution scan of official transcripts.

simon.gravel@gmail.com

MonashU EvolutionaryTheory

An opportunity is available for a PhD student to join Tim Connallon's research group in the School of Biological Sciences at Monash University, in Melbourne, Australia. We are seeking creative and motivated students who wish to carry out original research in evolutionary theory. Individuals with strong interest in evolutionary biology, and a background in biology or other relevant field (e.g., mathematics, physics, computer science), are invited to apply. Those with strong quantitative and computational skills are particularly encouraged.

Specific projects are flexible, and may potentially address (but are not limited to) topics in: sexual dimorphism, fitness tradeoffs, the genetics of adaptation, the maintenance of genetic variation, sex chromosome evolution, gene duplication, gene expression evolution, and/or the evolution of genome organization. Research plans will be developed in collaboration with the successful candidate, and tailored to match their individual interests and strengths.

Successful candidates will be fully funded for 3.5 years, for full time research, with no teaching requirements. The annual stipend is approximately $25,000 AUD, tax-free, and additional expenses for research, coursework, and conference attendance will also be covered. Both Australian/NZ domestic and international students are eligible to apply. Domestic candidates will be invited to apply for an Australian Postgraduate Award (approximately $25,000 AUD), with potential for a competitive top-up scholarship (additional $5,000).

Monash University is a member of Australia's Group of Eight coalition, and is internationally recognized for excellence in research and teaching. The School of Biological Sciences (http://monash.edu/science/about/-schools/biological-sciences/) is home to a collegial and interdisciplinary research environment, with strengths in ecology, genetics and evolutionary biology. Monash is located in Melbourne, one of the most liveable cities in the world and a cultural and recreational hub.

To apply, please send a CV, academic transcript, contact details for two academic references, and a brief outline of research interests to tmc233@cornell.edu. Informal inquiries are also welcome at the same address. Applicants must hold a Bachelor's degree with first-class honours, or a master's degree. Review of applications will begin immediately, and short-listed candidates will be contacted to set up phone/Skype interviews.

tmc233@cornell.edu

MonashU EvolutionSexualDimorphism

An opportunity is available for two PhD students to join Tim Connallon's research group in the School of Biological Sciences at Monash University, in Melbourne, Australia. We are seeking creative and motivated students who wish to carry out original research on the evolution of sexual dimorphism. Individuals with a background in biology or a related field are invited to apply, and those with strong quantitative and computational skills are particularly encouraged. Specific projects are flexible, potentially interdisciplinary, and include opportunities to carry out new research in theoretical, experimental, or computational evolutionary biology. Specific research plans will be developed in collaboration with each successful candidate, and tailored to match their individual interests and strengths.

Successful candidates will be fully funded for 3.5 years, for full time research, and with no teaching requirements. The annual stipend is approximately $25,000 AUD, tax-free, and additional expenses for research, coursework, and conference attendance (once per year) will also be covered. Both Australian/NZ domestic and international students are eligible to apply. Domestic candidates will be invited to apply for an Australian Postgraduate Award, with a top-up scholarship awarded to successful recipients (approximately $25,000 AUD, with top-up of $5000).

Monash University is a member of Australia's Group of Eight coalition, and is internationally recognized for excellence in research and teaching. The School of Biological Sciences (http://monash.edu/science/about/schools/biological-sciences/) is home to a collegial and interdisciplinary research environment, with strengths in ecology, genetics and evolutionary biology. Monash is located in Melbourne, one of the most liveable cities in the world and a cultural and recreational hub.

To apply, please send a CV, academic transcript, and a brief outline of research interests and goals to tmc233@cornell.edu. Informal inquiries are also welcome at the same address. Applicants must hold a Bachelor's degree with first-class honours, or a master's degree. Review of applications will begin immediately, and short-listed candidates will be contacted to set up phone/Skype interviews.

tmc233@cornell.edu

MonashU GenomeConflict Ageing SexualSelection

A PhD position in the field of evolutionary ecology / evolutionary genomics is available, for a high achieving student, in the research group of Dr Damian Dowling at Monash University.

The topic of the project can be flexible, and discussed with Dr Dowling in advance of the application. The successful applicant will have the capacity to develop their own interests within the general field of experimental evolutionary biology for the duration of the PhD candidature. Projects that draw on the following areas of interest to the Dowling lab, will be particularly encouraged:

Evolutionary coadaptation and conflict between mitochondrial and nuclear genomes

The evolution of ageing

Sexual selection and adaptation

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 successful applicant will nominate for a scholarship to cover salary. Students who hold a four year undergraduate degree with strong academic performance, and a first-authored publication, stand an excellent chance of obtaining a scholarship. The tax-free 2014 rate of a scholarship is A$25392.

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

Monash University is a member of Australia's "Group of Eight" " a coalition of research-intensive universities, and is internationally recognized for its excellence in research and teaching. The School of Biological Sciences (http://monash.edu/science/about/schools/biological-sciences/) is home to a collegial and world-class research environment, with key strengths in evolutionary ecology and genomics. Monash is located in Melbourne, a vibrant cultural and recreational centre (http://en.wikipedia.org/wiki/World's_most_livable_cities).

The deadline for scholarship applications in the current round is 31st May 2014.

Interested students should contact damian.dowling@monash.edu for further information, 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, http://damiandowlinglab.com damian.dowling@monash.edu

MonashU TelomereEvolution

PHD POSITION WITH TOP-UP AWARD: TELOMERE DYNAMICS OF FREE-LIVING FAIRY-WRENS Organization: Monash University Location: Melbourne, Australia Deadline: 15 April 2014

In my research group in behavioural ecology at Biological Sciences, Monash University I have available a PhD top-up scholarship (a $5000 bonus) for a talented and motivated PhD student to study telomere dynamics in fairy-wrens. The student will need to secure a Monash post-graduate scholarship stipend (and tuition waiver in the case of international students). The stipends include all course fees plus ~$25,000 AUD per annum tax-free, with no teaching requirements, for 3.5 years. Should the applicant be successful, the funding of top-up, project costs and research support including the costs of attending at least one conference will be provided by the research group.

Requirements: We are looking for enthusiastic student with a passion for life-history in evolutionary ecology and for studying wild animals. Experience in molecular genetic techniques and/or advanced quantitative skills are highly desirable, and experience with fieldwork and/or birds a bonus. Starting date is negotiable. To express interest, contact Dr. Anne Peters (anne.peters@monash.edu), with a brief CV detailing relevant experience, an expression of interest and contact details of three referees before 15 April 2014 or earlier to meet the Monash application deadline of 31 May.

Further details:https://sites.google.com/site/petersresearchgroup/

anne.peters@monash.edu

Sheffield Macroevolution Birds

Understanding evolutionary rates on the avian tree of life Keywords: rates of evolution, birds, macroevolution, phylogeny, morphometrics, plumage colour

A fully funded PhD position supported by the European Research Council is available at the University of Sheffield, in the Department of Animal and Plant Sciences. The candidate will work under the supervision of Gavin Thomas (http://www.shef.ac.uk/aps/staff-and-students/acadstaff/thomas), and will investigate the rates of phenotypic evolution in birds.

The project is focused on modelling phenotypic evolution of species traits in birds at broad phylogenetic and spatial scales. The aims are to test how and why phenotypic evolutionary rates vary and to ask how that variation has shaped both the avian tree of life and global distributions of species and traits. The successful applicants will join a new research team collecting novel, high-resolution morphometric data on bird bill shape using 3D structured white-light digitisation and plumage colour using visible and UV spectrum digital photography.

The student will integrate into a thriving department and will receive training in morphometrics, phylogenetic comparative approaches to study macroevolution, and museum collection based research. Applications are invited from candidates with interests in macroevolution and collection based research to address questions in evolutionary biology. Prior experience in R would be an advantage.

The deadline for applications is 9th May 2014. The project is open to UK/EU students.

Informal inquiries can be addressed to Gavin Thomas: gavin.thomas@sheffield.ac.uk

Formal applications should be made using our online application form: https://www.shef.ac.uk/postgradapplication/ and should be accompanied by a CV and cover letter (max 1 page) explaining your interests in the studentship.

In addition to the above studentship, four postgraduate research assistant < http://goo.gl/A1sudm > and two postdoctoral research associate < http://goo.gl/ZPkrN3 > jobs are available.

Gavin Thomas gavin.thomas@sheffield.ac.uk

SimonFraserU BritishColumbia EvolutionaryBiol

Opportunities for Graduate Study on Speciation, Ecological Genomics, and Behavior, in Timema walking-sticks. We invite applications for several graduate positions (MSc or PhD) to join an international team that uses Timema walking sticks as research systems to address several of the primary outstanding questions in evolutionary biology, ecology and genomics, with emphases of questions related to species formation, climate adaptation, genomics of adaptation, asexuality, mating systems, and cuticular hydrocarbons. The successful candidates will be based at Simon Fraser University in Burnaby, British Columbia, Canada, and conduct fieldwork in southern California. Positions would begin in Fall 2104, or in early 2015. Candidates who have secured NSERC PGS funding, or other fellowship funding, are preferred. Please send a CV and letter of interest to Dr. Bernard Crespi, Biosciences, Simon Fraser University, crespi@sfu.ca

Bernard Crespi <crespi@sfu.ca>

UAdelaide PlantDomestication AncientDNA

Graduate position: UAdelaide.PlantDomestication.AncientDNA

PhD scholarships at the Australian Centre for Ancient DNA, Adelaide, Australia

A PhD position is currently available at the Australian Centre for Ancient DNA, School of Earth & Environmental Sciences, at the University of Adelaide (http://www.adelaide.edu.au/acad). The position is open to both international and domestic students with a strong academic achievement in either molecular biology, evolutionary and plant biology or Bioinformatics.

Project: The Fertile Crescent region of the Near East (encompassing Iran, Iraq, Kuwait, Turkey, Syria, Jordan, Palestine, Lebanon) was an important region for the development of human civilisation and agriculture. Many of the founding crops (such as wheat, barley and rye) and livestock (cattle, sheep, pigs, etc) were first cultivated there. But as crops were selectively bred for characteristics such as height and yield, many unique phenotypes and their underlying genomic counterparts were lost over time. Now, as genetic diversity is extremely reduced in crops like wheat and barley, breeders are turning to wild cultivars to introduce new traits to continue to improve agricultural populations. With the improvement of next-generation genome sequencing (NGS) technology and ancient DNA extraction methodology it is now possible to directly access ancient alleles from 5,000-year-old wheat and barley seeds, preserved in ancient storage jars buried in a cave in Armenia. This project a ims to investigate ancient wheat and barley genomes and identify lost genes and alleles through comparison with modern breeds.

Experience: This project will ideally suit an enthusiastic student who is interested in learning more about ancient DNA experimental work and Next-Generation Sequencing (NGS), and investigating the mechanisms of plant domestication and evolution by using these unique ancient samples. A good level of molecular biology is essential, and computational knowledge (especially in UNIX systems) is desireable.

Competitive scholarships are available via the University of Adelaide Graduate Centre for domestic (https://www.adelaide.edu.au/graduatecentre/scholarships/research/) and international students (http://www.adelaide.edu.au/graduatecentre/scholarships/research-international/opportunities/). To be eligible for these, applicants should have a 1st Class Honours or MSc degree and high undergraduate academic record. Both the Australian Department of Immigration and University of Adelaide expect international applicants to meet the English Language Proficiency (ELP) requirements. The ELP is based on high scores in IELTS (International English Language Testing System) or TOEFL (Test of English as a Foreign Language). For further information please refer to http://international.adelaide.edu.au/apply/admission/ . There is the potential for fieldwork, and training in ancient DNA, bioinformatics and next-generation sequencing. Interested applicants are encouraged to send a resume and a cover letter to Dr Jimmy Breen (jimmy.breen@adelaide.edu.au)

jimmy.breen@adelaide.edu.au

UAlaskaFairbanks AvianSpeciation

SEEKING A GRADUATE STUDENT IN AVIAN SPECIATION, under the supervision of Kevin Winker at the University of Alaska Fairbanks. Students with demonstrated lab abilities, decent grades and GRE scores, experience with museum specimens, and capable of data analysis and writing are preferred and encouraged to apply.

Alaska is a remarkable state in which to study birds. Situated at the confluence of the Old and New world avifaunas, and with a deep interglacial history of refugia and the Bering land bridge, Alaska's rich avifauna provides a fertile ground for avian studies. The Winker lab is also involved with research in the New and Old world tropics (see the publications associated with this lab here: http://kevinwinker.org/). The University of Alaska Fairbanks is renowned for its strengths in wildlife, ecology, and evolutionary biology research. Fairbanks itself is a great place to live. Details about the University, the Museum, and the Department of Biology and Wildlife can be found at www.uaf.edu, www.uaf.edu/museum, and www.bw.uaf.edu.

Interested students are invited to send letters of interest, curriculum vitae (including summaries of grades and GRE scores), and the names of references to: Kevin Winker, University of Alaska Museum, 907 Yukon Drive, Fairbanks, Alaska 99775-6960, kevin.winker@alaska.edu.

kswinker@alaska.edu

UEssex EvolutionaryGenomics

3-YEAR FUNDED PhD POSITION ON EVOLUTIONARY GENOMICS

TITLE: How the loss of genes has shaped the genome as we know it SUPERVISOR: Antonio Marco ORGANIZATION: University of Essex LOCATION: Colchester, United Kingdom DEADLINE: April 30th, 2014

DESCRIPTION: Genomes are the product of a long evolutionary process. Many genes have multiple copies, reflecting the importance of gene duplication during genome evolution. The duplication of genes with regulatory functions has been associate with the development of novel functions. However, there is strong evidence that the loss of gene functions has also influenced the evolution of species. Gene loss is often associated with redundant functions, but the loss of non-redundant regulatory genes also happens with relative frequency. In recent years, the characterization of novel types of regulatory genes, such as microRNAs or long-non-coding RNAs, showed that gene loss is much more important that previously thought. Nevertheless, gene loss as a driving evolutionary force has not been systematically explored.

This project aims to understand how gene losses have shaped genomes. A PhD student will compare the genomes of related species and characterize which genes have been lost in specific lineages. The work will focus in transcription factors as well as in other regulatory genes such as microRNAs. By analysing the function, evolutionary age and regulatory connections of lost genes, we will be able to generate a model of genome evolution by gene loss. The candidate will be trained in computational biology / bioinformatics, with a focus on evolutionary genetics and comparative genomics. No prior knowledge of computer programming is required, but the candidate will have the chance to learn one programming language and state-of-the-art computational approaches. Depending on the interest of the student, the project may also involve molecular genetics in Drosophila melanogaster.

REFERENCES: - Marco A, Ninova M, Ronsaugen M, Griffiths-Jones S (2013) Clusters of microRNAs emerge by new hairpins in existing transcripts. Nucleic Acids Res, 41:7745-7752. - Marco A (2012) Regulatory RNAs in the light of Drosophila genomics. Brief Func Genomics, 11:356-365. - Hahn MW, Han MV, Han S-G (2007) Gene family evolution across 12 Drosophila genomes. PLoS Genetics 3:e197.

CAMPUS: The School of Biological Sciences at University of Essex is one of the largest science departments in the University, with some 52 teaching and academic staff working in the areas of environmental microbiology, plant productivity, biophysics, biochemistry, organic chemistry, cell/molecular biology and evolution. This broad-based structure provides for a strong multidisciplinary environment involving collaboration between chemists, biochemists and biologists.

Colchester campus is located in Wivenhoe Park, a picturesque and historic 200 acres parkland. The park was originally landscaped in the eighteenth century and was painted by celebrated landscape artist John Constable. The campus is only two miles from the historic centre of Colchester - England's oldest recorded town, and one hour from London. It is a vibrant and international campus, hosting more than 9,000 students from more than 130 different nationalities.

FUNDING: This scholarship will be to the value of £12,500 per annum plus UK tuition fees.

Apply from the University web page at: http://www.essex.ac.uk/study/pgr/how_to_apply/default.aspx For any query, please, contact me at: amarco.bio@gmail.com http://amarco.net – Antonio Marco School of Biological Sciences University of Essex

Web: http://amarco.net Blog: http://eblogution.wordpress.com Twitter: http://twitter.com/amarcobio amarco.bio@gmail.com

UGlasgow VirusEvolution

PhD Studentship, University of Glasgow

A genomic approach to uncovering the mechanisms driving host restriction and virulence in louping ill virus

Why particular viruses are able to infect and to cause disease in some host species but not others are fundamental questions that are critical for controlling viral pathogens. This project aims to uncocver the molecular and evolutionary mechanisms underlying host restriction and virulence of louping-ill virus (LIV), one of several closely related tick-borne flaviviruses in Europe that exhibit high phenotopic variability: whereas LIV mainly causes disease in British sheep and grouse, other LIV strains and related viruses elsewhere in Europe tend to affect other livestock species or human hosts. Using a combination of whole genome sequencing, bioinformatics, in vitro experiments and reverse genetics the project aims to 1) examine the genome-wide diversity and evolutionary history of LIV across its current range; 2) compare the ability of different LIV strains and related virus species for in vitro growth in a range of host species; 3) to experimentally verify putative genotype-phenotype relationships through a reverse genetics system. Through the application of powerful new technologies and analytic approaches, the project will provide novel insights about the biology of a significant animal pathogen in the UK and advance our general understanding of the factors governing virus-host interactions.

This exciting studentship opportunity will draw on expertise from academics within the University of Glasgow and The Moredun Research Institute. The student will spend an equal percentage of their time at both locations.

BBSRC WestBio DTP studentships will follow a 4-year PhD model. The financial package will include a 4-year stipend, approved University of Glasgow fees and a consumables budget per annum. The successful student will participate in the robust MVLS College skills training programme throughout their studies. Please follow URL for further information regarding the programme structure: http://www.gla.ac.uk/colleges/mvls/graduateschool/bbsrcwestbiodtp/ (please note that this project will not involve the Mini-Project rotations as detailed in the programme structure).

Supervisors: Dr Roman Biek, Dr Colin J McInnes, and Dr Alain Kohl

Stipend: £13,726 per annum (2013/14 rate) Start date: 1 October 2014

Application Deadline: 28 April 2014

For informal enquiries contact the main supervisor (Roman.Biek@glasgow.ac.uk).

Eligibility

This position is restricted to UK and EU nationals who meet the residence criteria below.

Qualifications criteria: Applicants applying for a BBSRC WestBio DTP studentship must have obtained, or be about to obtain, a first or upper second class UK honours degree or the equivalent qualifications gained outside the UK, in an appropriate area of science or technology.

Residence criteria: The BBSRC DTP grant provides funding for tuition fees and stipend for UK and *EU nationals that meet all the required eligibility criteria. *Note that EU nationals must be able to demonstrate that they have resided in the UK for three years prior to commencing the studentship. If not, EU nationals are still able to apply to the programme, but would be eligible to receive a 'fees only' award. Full qualifications and residence eligibility details are available here: BBSRC Guide to Studentship Eligibility - http://www.bbsrc.ac.uk/web/FILES/Guidelines/studentship_eligibility.pdf Roman.Biek@glasgow.ac.uk

UGraz CichlidsEvolutionaryBiology

A four year position as 'University assistant without doctorate' is available at the Institute of Zoology, University of Graz (Austria), in the group of Kristina Sefc. Applicants interested in completing a doctoral thesis in the framework of this position are particularly encouraged to apply.

The applicant will join our ongoing research on behavioral ecology and evolutionary biology of cichlid fishes, and is invited to participate in the design of research in line with his or her specific interests. Applicants must have a MSc degree in a relevant field, and be knowledgeable in behavior, ecology and physiology of fish. Experience or interest in fish keeping is also essential, as the applicant will be responsible for the management of laboratory fish stocks. Furthermore, experience with field work, particularly in tropical aquatic ecosystems, is a plus, as the position may require the planning and realization of field work at Lake Tanganyika.

The position also involves teaching in zoology, evolutionary biology or ecology.

Interested applicants are referred to the University?s website (http://jobs.uni-graz.at/en/MB/74/99) for information on the application process. Please contact me if you have any questions (kristina.sefc@uni-graz.at). The application deadline is May 7, 2014.

Kristina Sefc <kristina.sefc@uni-graz.at>

UGuelph SalmonGenomics

Three graduate student positions that apply information from high-density single nucleotide polymorphism (SNP) chips to Atlantic salmon breeding are available in Dr. Elizabeth Bouldings laboratory in the Department of Integrative Biology at the University of Guelph in collaboration with Kelly Cove Salmon Ltd. beginning in May or September 2014.

1) Ph.D. or M.Sc. in applied Atlantic salmon disease genomics/ animal breeding for genetic resistance in commercial strains of Atlantic salmon. The project would involve: a. assisting with annual disease trials in eastern Canada for Infectious salmon anemia (ISA) and Bacterial kidney disease (BKD); b. extractions of high molecular weight DNA from fin clips using modern high-throughput techniques; c. quantitative trait loci (QTL) mapping of ISA and BKD within families of Atlantic salmon using a custom 11K SNP chip; d. calculation of heritabilities and genetic correlations among different disease/parasite-resistance traits; e. assisting a research associate with the calculation of genomic breeding values for the two traits using a proprietary 200 K SNP chip; f. searching the salmon genome for candidate mutations associated with large amount of the variance in disease/parasite resistance. Ideal candidates would have a background in several of: bioinformatics, fish diseases, fish physiology, comparative genomics, molecular laboratory techniques or statistical animal breeding.

2) M.Sc. in applied Atlantic salmon genomics for salmon louse resistance in commercial strains of Atlantic salmon. The project would involve: a. assisting with annual salmon louse parasite challenges in eastern Canada; b. extractions of high molecular weight DNA from fin clips from challenges using modern high-throughput techniques; c. quantitative trait mapping of salmon lice resistance within families of Atlantic salmon using a custom 11K SNP chip d. searching the salmon genome for candidate mutations associated with large amount of the variance in disease/parasite resistance. Ideal candidates would have a background in several of: bioinformatics, fish diseases, fish physiology, comparative genomics, molecular laboratory techniques.

3) M.Sc. in Bioinformatics. Development of new algorithms and R scripts for manipulating data from high density SNP chips and massive phenotypic trait files, developing algorithms and scripts to locate errors in very large pedigrees. Candidates must meet the admission requirement of the University of Guelph M.Sc. program in Bioinformatics. http://www.bioinf.uoguelph.ca/ Preference will be given to Canadian citizens or residents. Interested candidates should send an email to Professor Elizabeth Boulding boulding@uoguelph.ca with the following attachments, preferably as pdf files: 1) All their unofficial university and college transcripts 2) a short version of their resume 3) the names, emails and telephone numbers of 3 referees including at least one previous employer.

Elizabeth Grace Boulding Professor University of Guelph, Ontario Canada Department of Integrative Biology 50 Stone Road East University of Guelph Guelph, Ontario N1G 2W1 Canada Email: boulding@uoguelph.ca webpage: http://www.uoguelph.ca/ib/people/faculty/boulding.shtml boulding@uoguelph.ca

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UNeuchatel EvolutionaryGenomics

PhD position in plant population genetics available at the Laboratory of Evolutionary Botany, University of Neuchatel http://www2.unine.ch/cms/lang/en/pid/11440 The main objective of this PhD project is to infer the evolution of selected diploid/polyploid Aegilops wild wheats in space and time. Dated phylogenies will provide a robust framework to address the comparative phylogeography of their genomes and their inhabiting transposable elements.

The work combines knowledge from high-throughput sequencing, genotyping, bioinformatics, population genetics and evolutionary ecology. Field work will be conducted to complement existing data.

We seek a highly motivated student with strong interest in evolutionary genomics. Skills in treating large datasets with varied statistical tools are relevant. The fellow will interact within a network of researchers and particularly with Prof. N. Salamin at the University of Lausanne, and needs to have collaborative abilities.

For more information please contact Christian Parisod (christian.parisod@unine.ch)

Please send your complete application (letter describing motivation and ideas for this project, CV incl. publication list and contact details of at least two references) as one single pdf to christian.parisod@unine.ch

Application received before April 28th will be given full consideration. Expected start date is June 1st 2014 or at earliest convenience thereafter.

Christian Parisod and Fran?ois Felber

Christian Parisod Evolutionary Botany, University of Neuchatel Rue Emile-Argand 11, 2000 Neuchatel, Switzerland Phone: +41 (0)32 718 2344, Fax: +41 (0)32 718 3001 e-mail: christian.parisod@unine.ch http://www2.unine.ch/evobot/page-11460.html
Christian Parisod <christian.parisod@unine.ch>

UNeuchatel Switzerland HostParasiteEvolution

A 3-year PhD position for the mathematical modelling of the evolutionary ecology of host-parasite interactions is available immediately in the group of Jacob Koella at the University of Neuchatel, Switzerland.

The general research of the group is to integrate evolutionary and ecological thinking into the epidemiology and control of infectious diseases. We develop the theoretical basis of this integration and test empirically assumptions and predictions of the theory, using malaria, microsporidians and their mosquito hosts as experimental systems.

The PhD-project will develop mathematical models to integrate resource ecology with the within-host dynamics of parasite to obtain a better picture of the evolution of the host-parasite interaction. This approach explicitly takes into account a fundamental, yet largely neglected, aspect of parasites: that they steal resources from their host to support their own development. Resource ecology thus gives a mechanistic basis of the host's and the parasite's development. The project will be done in close contact with an experimental project on the same topic, which uses the microsporidian Vavraia culicis and its host, the mosquito Aedes aegypti as an experimental system

The position requires an independent, enthusiastic, and scientifically curious person with a strong background (at the level of an MSc) in theoretical evolutionary biology or applied mathematics and an interest in parasitology. The position requires some teaching of undergraduate and graduate biology labs. The generous salary is in accordance with the standards of the Swiss National Science Foundation.

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

To apply, send a 1-2 page cover letter (in English) indicating research interests, your CV, and the names and email addresses of two referees by email to: jkoella@gmail.com

Applications will be considered until the position is filled.

Jacob Koella

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

jkoella@gmail.com

UNevada EvolutionaryBiology

The Parchman lab in the Biology Department at the University of Nevada, Reno is recruiting PhD students for Fall 2014 or Spring 2015. Most research in the lab utilizes high throughput DNA sequencing approaches to address questions involving landscape genomic variation, the genetic basis of adaptation, speciation and hybridization, and other general questions involving population genetic analysis of geographic, genomic, and phenotypic variation in natural populations. The research typically aims to address questions of both ecological and evolutionary significance in natural populations, and focuses on a diverse array of organisms. You can read more about research in the lab at: http://-wolfweb.unr.edu/˜tparchman/Home.html . I am looking for students broadly interested in evolutionary biology, evolutionary ecology, population genetics and genomics, and/or computational approaches for genomic analysis. Ideal applicants would have experience in basic laboratory genetics approaches for population genetics and some familiarity with programming in R, Perl, and Unix based systems. Potential research topics for PhD students include landscape genomic variation in conifers, population genomic analysis of hybrid zones, and population genomic variation across the adaptive radiation of crossbills. This list serves only as an example, and students interested in alternative, but related research topics are encouraged to apply. UNR has a strong interdisciplinary PhD program in Ecology, Evolution, and Conservation Biology (http://environment.unr.edu/eecb/). Graduate students accepted into the EECB program are guaranteed financial support through Teaching Assistantships (TAs) which includes health insurance and an out-of-state tuition waiver. In addition, funds are available to seed doctoral dissertation projects, for example through paying for high throughput sequencing costs.

University of Nevada, Reno (UNR) is Tier I research university located in a spectacular environment at the confluence of the Great Basin and the Sierra Nevada Mountains. The faculty and graduate students at UNR are highly interactive and include an internationally known group of evolutionary biologists and ecologists. A complete renovation of the Parchman lab has just been finished, and we are now equipped with ample (and new) molecular and computational resources for modern genome sequence analysis. We are also located in an ideal setting for field-based projects in the Great Basin and Sierra Nevada regions, allowing enviable access to spectacular montane and desert ecosystems. Reno is only 45 minutes from Lake Tahoe, offers a high quality of living, an excellent climate, and is a large enough city to offer diverse activities and amenities. World class rock climbing, skiing, and mountain biking opportunities are in extremely close proximity.

Those interested should contact me at tparchman@unr.edu with a description of your interests, qualifications and preliminary application materials (CV, GRE scores, names and contact information for three references).

Thomas L. Parchman Assistant Professor Department of Biology, MS 314 University of Nevada, Reno Max Fleishman Agriculture Building 1664 N. Virginia Street Reno, NV 89557-0314 tparchman@unr.edu

Thomas L Parchman <tparchman@unr.edu>

UNevadaReno BioinformaticsGenomics

GRADUATE STUDENT POSITIONS IN BIOINFORMATICS AND GENOME EVOLUTION AT THE UNIVERSITY OF NEVADA, RENO

The new Bioinformatics and Genome Evolution lab at the University of Nevada, Reno, is accepting applications for Ph.D. students with a strong interest in bioinformatics and molecular evolution.

Research areas in the lab include the evolution of molecular pathways and networks (e.g., protein-protein interaction networks, metabolic pathways/networks, signal transduction pathways/networks, etc.), and organisms genomic adaptation to different temperatures.

More information on the lab can be found at www.genomeevol.wordpress.com The ideal candidates have: - A strong commitment to high-quality research. - A strong interest in Molecular Evolution. - Experience with bioinformatics analyses, including programming in any scripting language (e.g. PERL or Python). - Good communication skills. - Good interpersonal skills. - The requirements to be accepted in the graduate program, listed here: http://environment.unr.edu/eecb/apply/index.html Informal applications should be addressed to Dr. David Alvarez-Ponce (david.alvarez.ponce@gmail.com) as a single PDF, including: - An application letter, addressing the applicants motivation for the position, and how her/his experience and skills fulfill the requirements listed above. - A full CV. - Contact information for 3 potential referees.

The University of Nevada, Reno offers an interactive and productive research environment, including outstanding core facilities in proteomics, genomics, and bioinformatics. The Biology Department has a growing evolutionary genomics research community. Reno is located in the Sierra Nevada mountains near Lake Tahoe, and has been recently rated as one of the best small cities in the US for outdoor recreation and overall quality of life.

Please circulate this post among suitable candidates.

david.alvarez.ponce@gmail.com

http://www.unco.edu/mcglaughlinlab
Mitchell.McGlaughlin@unco.edu

UNorthernColorado PlantEvolution

Graduate positions (MS or PhD) in Plant Evolution in the lab of Dr. Mitchell McGlaughlin, School of Biological Sciences, University of Northern Colorado.

I am seeking MS or PhD students interested in the population genetics, conservation, speciation, and phylogeography of plant species. Research is my lab is focused on using population genetics to understand plant speciation and to inform the conservation of rare and endangered taxa. We employ a wide range of genetic data types, including low copy nuclear sequence, chloroplast sequence, nuclear microsatellite, and next generation sequence data. Current research projects include, phylogeography of the California Channel Islands, ancestral polymorphism in Acmispon, hybridization in endangered Sclerocactus, and conservation genetic research with several native Colorado taxa. Doctoral students are encouraged to develop projects within the scope of research in my lab and masters students can develop their own projects or work on research already initiated in the lab. Funding is available to support graduate students through teaching and research assistantships. I am looking for stu dents to start in Fall 2014 or Spring 2015.

For more information please visit my lab website: http://www.unco.edu/mcglaughlinlab/ or the department website: http://www.unco.edu/nhs/biology/index.htm The University of Northern Colorado is a public institution with about 11,000 undergraduate and 1,500 graduate students, located in Greeley, Colorado. Greeley is situated 50 miles northeast of Denver and 20 miles east of the Rockies, with easy access to Rocky Mountain National Park and other outdoor activities.

Interested applicants should send a letter of interest and CV to Dr. Mitchell McGlaughlin (Mitchell.mcglaughlin@unco.edu). To apply, students will need to submit a complete application to the UNC School of Biology (http://www.unco.edu/nhs/biology/students/gradapp-instructions.html) and Graduate School (http://www.unco.edu/grad/index.html). There is no fixed application deadline. Applications are reviewed when they are received.

– Mitchell McGlaughlin, Ph.D. Associate Professor School of Biological Sciences 501 20th Street, Ross Hall 1560 University of Northern Colorado Greeley, CO 80639 970-351-2139 Mitchell.Mcglaughlin@unco.edu

UPenn Paleobiology Macroevolution

PhD Fellowship in Paleobiology/Paleontology at the University of Pennsylvania

A PhD fellowship in Paleobiology is available in the Department of Earth and Environmental Science at the University of Pennsylvania. Prof. Lauren Sallan seeks a graduate student to address major paleobiological questions, such as how global change has affected life over time, how life evolves at high levels (macroevolution), and the origins of living biodiversity. Specific topics include, but are not limited to: the causes and consequences of the end-Devonian mass extinction and similar events, the role of predation in setting marine biodiversity, the origins of $B!H(Bliving fossils,$B!I(B the effect of the Late Paleozoic Ice Age on the evolution of major groups, and early vertebrate evolution. The student can also develop a new project that address the same major questions using quantitative, phylogenetic and descriptive methods. While research in the lab has focused on fishes, any suitable and well-preserved group of fossil animals may be used.

Interested students should contact Prof. Sallan directly (laurensallan@gmail.com; arriving at Penn in July 2014) for details.

Lauren Sallan, PhD Assistant Professor, Ecology and Evolutionary Biology & Michigan Fellow, Michigan Society of Fellows University of Michigan Office: 1076 Ruthven Museums Bldg Phone: (954) 895-9192 or (734) 764-7797 Websites: www.lsa.umich.edu/directory/faculty/lsallan www.LaurenSallan.com Lauren Sallan <lsallan@umich.edu>

UQuebec Montreal SexualSelection

Graduate Research in Sexual Selection and Ecological Immunology

Funded PhD and MSc positions are available under the supervision of Dr. Clint Kelly at the Université du Québec à Montréal (http://thekellylab.wordpress.com) beginning August 2014. I am seeking motivated students to study questions related to sexual selection including, but not limited to, 1) alternative mating strategies in New Zealand tree weta (funded by Canada Research Chairs Program); or 2) the physiological and reproductive costs of investment in immunity in insects (funded by NSERC). My lab uses an empirical approach in the field and laboratory to examine a broad set of topics in behavioural and evolutionary ecology and we employ a variety of techniques and procedures to address research questions, including: molecular genotyping, immunological assays, phylogenetic comparative studies, geometric morphometrics and meta-analysis. The Kelly Lab belongs to the large, research-active Département des Sciences Biologiques at UQAM (http://bio.uqam.ca). If interested in pursuing a graduate degree in the Kelly Lab please send a brief description of your research interests and a CV to clintdkelly@icloud.com.

clintdkelly@icloud.com

USheffield MathModelling

http://www.findaphd.com/search/-ProjectDetails.aspx?PJID=54179&LID=1381 Thanks, James

Mathematical modelling of key transitions in social insect systems

Our research is about trying to understand the functioning of biological systems through the use of mathematical models. Dr Childs is a population biologist who develops data-driven models to understand population dynamics and natural selection. Dr Marshall is a computational biologist with interests in social evolution and social insect behaviour. We have been awarded a studentship to facilitate a new collaboration. Research pursued by the student may address any topic that lies at the interface of our interests, though we are particularly interested in the following two questions:

1) Can we detect critical transitions in social insect systems? Ecologists have become increasingly interested in using ideas from nonlinear dynamics to forecast qualitative changes in the behaviour of natural communities (e.g. via critical slowing down). Using this framework, we would like to develop methods to forecast the occurrence of economically important phenomena in social insect systems (e.g. colony collapse disorder). 2) What influences the evolutionary stability of unicolonial ant species? Some ant species form huge unicolonial populations. The existence of such supercolonies is surprising: since the relatedness of individuals within them is nearly zero, kin selection theory predicts they should be evolutionarily unstable. We would like to develop models to explore the demographic and ecological factors that favour such colonies in evolutionary time.

The studentship is fully funded and open to residents of the UK/EU. We are looking for students with a strong background in mathematics, physics, or computer science. Contact Dr Childs for further information.

James A. R. Marshall Behavioural and Evolutionary Theory Lab Department of Computer Science and Kroto Research Institute University of Sheffield http://-/staffwww.dcs.shef.ac.uk/people/J.Marshall/ James Marshall <James.Marshall@sheffield.ac.uk>

USouthampton WildlifeConservation

This MRes in Wildlife Conservation is a collaborative programme, run jointly by the Centre for Biological Sciences at the University of Southampton and Marwell Wildlife, an action-oriented conservation organisation based at nearby Marwell zoo. The ultimate aim of the MRes is to produce individuals who have skills, experience and academic credentials required for employment as conservation biologists. We believe there shouldn't be a choice between gaining experience or a qualification, this MRes allows you to achieve both.

The taught element of the course, including a field trip to Kenya, runs from October to January, with the extended research project running from February to September. Candidates must select their preferred project are upon application.

For more details on the course and how to apply, please visit our course website http://southampton.ac.uk/-wildlifeconservation Best wishes,

Judith

Dr Judith Lock Centre for Biological Sciences, Life Sciences B85, University of Southampton, Southampton SO17 1BJ Tel: 02380594312 Twitter: @Judith_Lock MRes Wildlife Conservation, Joint Programme Manager http://www.southampton.ac.uk/-wildlifeconservation J.E.Lock@soton.ac.uk

USouthernMississippi ElasmobranchEvolution

Salary: $19,200 - $19,800; tuition waiver Two MS Graduate Assistantships in the laboratories of Drs. Andrew Evans and Jay Grimes at the University of Southern Mississippi Gulf Coast Research Laboratory are available beginning in Fall 2014. Selected students will participate in a collaborative research project characterizing the elasmobranch microbiome and potential interactions between bacteria and their elasmobranch hosts. The project will include tissue collection, 16S rRNA gene sequencing and bioinformatics, bacterial culture and fluorescence in-situ hybridization. Successful applicants will participate in project design, data collection and analysis, and will develop an independent line of research for their MS thesis.

Applicants should have a B.S. in biology, microbiology, physiology or a closely related field and a strong desire to study elasmobranch physiology, microbiology, bioinformatics, molecular biology and/or microbial-vertebrate symbiotic relationships. Preference will be given to applicants with experience in one or more of the following areas: culture-based and non-culture-based (e.g. microbiomics, PCR/qPCR) methods for the identification of bacteria associated with tissues and organs, fluorescence in-situ hybridization or immunohistochemistry, and elasmobranch physiology/molecular biology. Minimum academic qualifications include a GPA of 3.0 and verbal and quantitative GRE scores in the upper 50th percentile.

Please send to andrew.n.evans@usm.edu, preferably as a single .pdf document: 1. Cover letter highlighting interest and qualifications 2. CV including GRE scores (unofficial OK) 3. Unofficial transcripts

Andrew N. Evans Assistant Professor Dept. of Coastal Sciences University of Southern Mississippi 703 East Beach Drive Ocean Springs, MS 39564 (228) 872-4298

Andrew Evans <andrew.n.evans@usm.edu>

UtahStateU EvolutionaryGenetics

The Gompert lab at Utah State University (Department of Biology) is recruiting PhD students for Fall 2014 or Spring 2015. In our research we seek to better understand adaptation, speciation, and the determinants of genetic and phenotypic variation in nature. We work with a variety of organisms and use diverse approaches to investigate these topics. Most projects in the lab involve generating large, genome-scale DNA sequence data and applying existing or new statistical analyses to these data to test alternative hypotheses. You can read more about research in the Gompert lab here, https://gompertlab.wordpress.com/research/ . We are looking for students broadly interested in evolutionary genetics, genomics, or computational biology, and students with academic training in biology, statistics or applied math, or computer science are encouraged to apply. Potential research topics for these PhD students include (i) fluctuating selection and the maintenance of genetic variation in the wild, (ii) adaptation from standing variation in phytophagous insects, (iii) polygenic adaptation, (iv) hybridization and speciation, (v) the repeatability and predictability of evolution, and (vi) computational analyses of genome sequence variation. This is not an exhaustive list and students interested in alternative, but related research topics are also encouraged to apply. You can learn more about my expectations for graduate students and my mentoring approach here, https://gompertlab.wordpress.com/join-us/ . Graduate students accepted into the lab are provided financial support through Teaching Assistantships (TAs) or Research Assistantships (RAs). Interested students are also strongly encouraged to apply for graduate research fellowships, such as the National Science Foundation Graduate Research Fellowship. Importantly, students are eligible to apply for this and other fellowships in their final year as undergraduates. Additional funding exists for graduate student research and travel to scientific meetings.

Utah State University (USU) is a first-class research university located in the US Rocky Mountains. The faculty and graduate students at USU are highly interactive and include a great and diverse group of evolutionary biologists. The Gompert lab has ample computational and molecular resources for modern genome sequence analysis. We are also well-equipped for field work and lab or field experiments. Logan is a small town in northern Utah with a strong sense of community. The town is just minutes from great opportunities for outdoor recreation including mountain biking, rock climbing, cross-country and downhill skiing, and back-packing. Logan is also within a few hours of several national parks, major ski resorts, and world famous slickrock mountain biking.

Interested students are encouraged to e-mail me (zach.gompert@usu.edu). Please include a short description of your academic background and research interests and your CV. Please contact me by May 10th for full consideration. USU and the Gompert lab are committed to providing equal educational and employment opportunities regardless of race, color, religion, sex, sexual orientation, national origin, socio-economic background, age, disability, or veteran status.

Zach Gompert Assistant Professor

Department of Biology Utah State University Phone: 435 797-9463 e-mail: zach.gompert@usu.edu Website: https://gompertlab.wordpress.com/ zachariah.gompert@aggiemail.usu.edu

UTulsa Oklahoma EctoparasitePopGenet

Graduate research opportunity to study ectoparasite population genetics and metapopulation dynamics. Department of Biological Sciences - University of Tulsa

A graduate student at the M.S. or Ph.D level is sought to work with Drs. Charles Brown and 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 metapopulation dynamics and population structure of swallow bugs (Oeciacus vicarius: Cimicidae), a disease vectoring ectoparasite of cliff swallows (Petrochelidon pyrrhonota). The PIs have amassed a large collection of swallow bugs from cliff swallow colonies varying in size, geographic location, and patterns of occupation, and have recently identified hundreds of microsatellite markers specifically for swallow bugs using next-generation sequencing. The work will draw on a long-term (32-year) study on social behavior and reproductive ecology of cliff swallows in western Nebraska.

The study aims to examine the following objectives: nest fidelity and dispersal patterns, inbreeding dynamics, metapopulation structure and population differentiation; relationships between host and parasite genetic structure and diversity; and the potential of blood-fed bugs as indirect indicators of cliff swallow demography and social structure. Additionally, the student may explore the evolution of extreme phenotypes exhibited by the study species through comparative transcriptomic methods.

Applicants for this position should have a strong background in population genetics, molecular ecology, evolutionary biology, or ecology, be willing to undertake seasonal field research at the study site in western Nebraska, 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)

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 three academics/researchers willing to provide a letter of recommendation 4) Copies of undergraduate/postgraduate transcripts 5) Electronic copies of published manuscripts, if any.

For more information about this opportunity, contact Drs. Brown (charles-brown@utulsa.edu) or Booth (warren-booth@utulsa.edu). Anticipated start date is mid-August 2014.

Additional information regarding our research can be found at our current departmental webpages: Brown - http://www.utulsa.edu/academics/colleges/college-of-engineering-and-natural-sciences/departments-and-schools/Department-of-Biological-Science/Our-Faculty-and-Staff/B/Charles-Brown.aspx Booth - www.booth-lab.org < 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 > - TU academic Lab website < http://www.booth-lab.org/ >

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

UWesternAustralia 2 Biodiversity

Two PhD opportunities: Marine and terrestrial invertebrate diversity and evolution in the Pilbara region, Australia

The Western Australian Museum has secured funding from the Net Conservation Benefits fund (NCB) to undertake a five year project on the Conservation Systematics of the western Pilbara fauna. In this project we are using molecular tools to provide a systematic framework for understanding the diversity, evolutionary relationships, and distributions of marine and terrestrial fauna in the Pilbara region. Included under this broad objective are specific questions pertaining to evolutionary history, understanding the drivers of speciation, species delimitation, phylogeography, taxonomy, and co-speciation.

This project has funding to support two PhD projects that broadly align with the NCB project objectives.

The PhD projects will be aimed at using molecular markers to investigate biodiversity in invertebrates from the Pilbara region, and surrounds. One project will focus on marine invertebrates (eg, sponges, soft corals, nudibranchs, crinoids, or other groups) and the other will focus on terrestrial invertebrates (eg, trapdoor spiders, opiliones, millipedes, or other arachnid or insect groups). The PhD students will be enrolled in the School of Animal Biology at the University of Western Australia, and based jointly at the new Molecular Systematics Unit laboratory, Western Australian Museum, Welshpool, Perth, where the successful applicants will have the opportunity to work directly with specialists in these fields. The specific project aims, questions, design and methods will be developed collaboratively by the students and supervisors.

The work will include opportunities for field work in the Pilbara region, and lab costs will be generously supported by the NCB project.

Currently, this opportunity is open to domestic students (Australia and New Zealand). Although the position is fully funded, students will be expected to put in an application for an Australian Postgraduate Award (APA or University Postgraduate Award (UPA) (http://www.scholarships.uwa.edu.au/-search?sc_view=1&id=341&page=1&q=-Australian+Postgraduate+Award&s=1&old_key=0) through UWA. The NCB funding will provide an additional top-up scholarship of $5k per year, bringing the total stipend to approx. $34k per year (tax free). Any international student should contact personnel below.

Applications open 2 June, and close 11 July for a 1 Aug 2014 start. However, we encourage any applicants to contact us and begin discussions as soon as possible. Those interested in marine invertebrates should contact Nerida Wilson (Nerida.Wilson@museum.wa.gov.au) and cc Jason Kennington (jason.kennington@uwa.edu.au). Those interested in terrestrial invertebrates should contact Joel Huey (Joel.Huey@museum.wa.gov.au) and cc Raphael Didham (raphael.didham@uwa.edu.au).

hueyjoel@gmail.com

UZurich 2 Biodiversity

The Altermatt lab at the Institute of Evolutionary Biology and Environmental Studies (IEE) of University of Zurich and the Department of Aquatic Ecology of Eawag, Switzerland, has a vacancy for:

Two PhD Studentships in Ecology

Project title: Bridging biodiversity and ecosystem functioning in dendritic networks: a meta-ecosystem perspective

Understanding the causes and consequences of biodiversity is among the most challenging goals in ecology. Recent results indicate a generally positive effect of diversity on ecosystem processes. Up to now, almost all work on biodiversity-ecosystem functioning has been conducted in a non-spatial, one-patch perspective. Natural ecosystems, however, are spatially explicit, and there is substantial flow of material and organisms among patches and ecosystems. This project aims at applying the concept of meta-ecosystems to empirical data in spatially explicit dendritic networks.

In a project including two complementing PhD theses and a Postdoc fellow, we will use a laboratory protist microcosm system to experimentally test interacting effects of habitat network structure and ecosystem functioning (PhD Project 1). We will extend these findings to mesocosm experiments and large-scale field studies with amphipods to study ecosystem functioning in Swiss river networks (PhD Project 2). Finally, we will synthesize the findings. In the whole project, diversity and ecosystem functioning will be studied in spatially explicit dendritic networks in a highly consistent framework. Ultimately, we want to get a comprehensive understanding of biodiversity and ecosystem functioning in riverine systems.

Competitive applicants will have previous experience in ecology, biodiversity and spatial dynamics and be interested in participating in this extensive new research project. They will be highly motivated, enthusiastic and independent persons with a passion for science. Candidates should have a good conceptual understanding of ecological theory, excellent experimental skills and/or a background in quantitative modeling. Excellent communication and writing skills in English, good work ethics, and creative thinking are desired. A Masters level degree (or equivalent) in Ecology or related subject is necessary for admission. The working language in the Altermatt lab is English.

The Altermatt lab has a shared base at University of Zurich and at Eawag. It offers a stimulating and international research environment, excellent research facilities and a lively and social working place. Zurich hosts many other research groups in ecology and biodiversity research, and is among the world's leading cities in terms of science, culture and quality of life. The positions will be for a period of three years, and could start in August 2014 or soon thereafter. The PhD students will be enrolled at University of Zurich and be part of the PhD Program in Ecology.

The project is financed by the Swiss National Science Foundation (SNSF Research Professorship to Florian Altermatt from August 2014 onwards).

For further information, consult

http://homepages.eawag.ch/ ˜ altermfl/Home.html http://www.ieu.uzh.ch/index.html www.eawag.ch or directly contact Dr. Florian Altermatt: Tel: +41 58 765 55 92, E-mail: florian.altermatt@eawag.ch

Applications must be submitted by 10th May 2014 and should include a motivation letter with a description of pertinent experience, a complete CV (incl. publication list), the names (with e-mail addresses) of three academic references, and copies of certificates of academic qualifications. The application should be submitted as one single pdf-file.

We look forward to receiving your application through the online application form at:

http://internet1.refline.ch/673277/0267/++publications++/1/index.html Any other way of applying will not be considered.

florian.altermatt@eawag.ch

VictoriaU NZ InvasiveSpeciesEvol

PhD Position for 2014 (3 years) at Victoria University of Wellington

Do human actions select for traits that promote invasiveness in animals?

*Project Description: * Are humans driving the evolution of invasive species to our own detriment? Humans unwittingly and routinely transport invasive animals and plants around the globe. We hypothesise that this process leads to selection for behavioural traits that enhance invasiveness. The proposed project will test this hypothesis with the Argentine ant, which is listed among the world's worst invasive species, and considered the 'Genghis Khan' of the ant world. The project will study populations from the native and introduced range to assess if: 1) variation in novelty-seeking behaviour exists among populations of ants; 2) this variation in behaviour has a molecular basis; 3) humans have exerted selection pressure on this behaviour; and 4) novelty-seeking promotes invasiveness. The project will combine surveys of ecological communities, behavioural experiments, studies of population genetics, and gene and neurochemical expression. The scale of this analysis - from genes to communities, across four continents - is novel and integrative. This novel research will elucidate an underlying mechanism of how evolution and ecology interact to facilitate invasion success.

The Ideal Candidate: The ideal candidate will possess experience and ability with molecular genetics techniques, ecology, and statistics. In addition they will be motivated and organized, with a demonstrated capacity to master the broad skill set necessary for the successful completion of a research project. The candidate will be enrolled at Victoria University of Wellington in New Zealand, co-supervised by Dr. Monica Gruber and Prof. Phil Lester. Students will also spend time sampling and undertaking experiments in Argentina, California and Australia. Our national and international team of world-class researchers includes Prof. Alison Mercer (University of Otago), Prof. Gene Robinson and Assoc. Prof. Andy Suarez (University of Illinois at Urbana-Champaign), Dr. Dave Chapple (Monash University) and Dr. Ben Hoffmann (CSIRO Darwin). The project offers a tremendous opportunity to undertake research with world-leaders.

Eligibility and funding: This opportunity is open to all nationalities. However, candidates must satisfy the English Language Requirements of the University to be eligible for study, and New Zealand criteria for PhD entry. See http://www.victoria.ac.nz/fgr. The project has sufficient funds for travel, consumables, and international conference attendance. Students will be encouraged to seek funding for personal support and fees through a Victoria University Postgraduate Scholarship.

How to Apply: Interested applicants are encouraged to make informal enquiries to Dr. Monica Gruber. Please send your Curriculum Vitae, a copy of your academic transcript, a sample of your written scientific work and the names of three referees with a covering letter to: Dr Monica Gruber (monica.gruber@vuw.ac.nz)

Applications will remain open until the position is filled. It would be desirable if the successful applicant were able to start in mid-late 2014. Dates will be flexible for the ideal candidate.

Monica Gruber Post-doctoral Research Fellow School of Biological Sciences Victoria University of Wellington PO Box 600, Wellington 6140 New Zealand ph: +64 4 463 5026 / 027 658 9903

Monica.Gruber@vuw.ac.nz

WestVirginiaU BobcatEvolution

Ph.D. Graduate Research Assistantship -

Bobcat Molecular Ecology, Division of Forestry and Natural Resources, Wildlife and Fisheries Resources Program, West Virginia University

STARTING DATE: August 2014 or negotiable.

CLOSING DATE: Position is open until filled and pending final approval of funding.

DESCRIPTION: Student will be supported by 12-month Research Assistantship for 4 years.

Biological data on bobcats in West Virginia have not been updated since the late 1970s. Improved data are needed to update the harvest models due to increasing pelt prices and harvest demand, changing habitat quality and abundance, and unreliable harvest data. The student will coordinate with West Virginia Division of Natural Resources personnel to: 1) coordinate statewide hair snare sampling protocol for bobcats; 2) collect genetic data to use in estimating the population and identify potential migration barriers in the landscape; 3) estimate and compare relative abundance of bobcats among ecological regions in West Virginia; 4) refine and or verify the existing bobcat population model to evaluate and determine the bobcat population and use in conjunction with harvest data to evaluate potential changes in bag limits; and 5) collaborate with an MS student who will obtain productivity, age, and condition data that will contribute to the population model. The student will be working toward a Ph.D. in Forest Resources Science with an emphasis in Wildlife and Fisheries Resources at West Virginia University (http://wildlife.wvu.edu/).

QUALIFICATIONS: B.S. and M.S. in Wildlife, Ecology, Genetics, or closely related field. Minimum GPA of 3.0 and combined quantitative/verbal GRE scores of 300 (~1,100 old scoring system). A strong interest in population genetics, predator ecology, and modeling is required.

STIPEND: $19,848/year plus health insurance and complete tuition waiver.

CONTACT: Student will be co-advised by Dr. James T. Anderson and Dr. Amy Welsh. Interested individuals should send a letter of interest, resume, a 500-word statement of purpose (why do you want to work on this project, your research interests, and long-term career goals), unofficial copy of transcripts and GRE scores, and contact information for 3 references to jim.anderson@mail.wvu.edu and amy.welsh@mail.wvu.edu

Amy B. Welsh, Ph.D. Assistant Professor Wildlife and Fishery Resources Program West Virginia University P.O. Box 6125 Morgantown, WV 26506 Phone: 304-293-0718 Office: 311B Percival Hall Website: http://wildgenomics.forestry.wvu.edu Amy Welsh <Amy.Welsh@mail.wvu.edu>

Jobs

Bergen Norway EvolutionaryVertebrateZoology

Associate Professor in Vertebrate Zoology (anatomy/evolution) A permanent position as associate professor in vertebrate zoology is open at the University Museum of Bergen, the Natural History Collections (http://www.uib.no/universitymuseum).

We are seeking a researcher within vertebrate zoology with special competence in vertebrate skeletal morphology (osteology). The successful applicant should also have competence in one or several of the new scientific methods; i.e. isotopes, trace elements or DNA and be able to apply these in research on modern as well as sub-fossil skeletal material. The comprehensive collections of skeletal material from prehistory and present time are important data for research within faunal- and environmental history, morphological adaptation or evolutionary relationships. The successful applicant is expected to document research at international level in zoology/osteology at in least one of these methods. He/she is supposed to work within faunal- and environmental history.

The position is connected to the osteology collections. The University Museum of Bergen hold two comprehensive collections of vertebrate skeletons; one recent collection of c.15000 specimens (fish, amphibians, reptiles, birds and mammals) from Norway and a national collection of sub-fossil bones, mainly from the post glacial and from archaeological excavations. The successful applicant will have scientific responsibility for the modern skeletal collection. He/she is expected to participate in developing the collections through own research, but also by national and international cooperation as well as improvement of databases and home pages. The successful applicant is also expected to participate in teaching and in the development of zoological exhibitions at the University museum.

A more detailed description of the position and information about necessary documentation which must be enclosed in the application can be found further down on this page. Additional information can be obtained from the head of the Natural History Collections, associate professor Kari Loe Hjelle, phone (+47) 55583323 / e-mail kari.hjelle@um.uib.no.

http://www.jobbnorge.no/en/available-jobs/job/101820/associate-professor-in-vertebrate-zoology
Bjarte Henry Jordal <Bjarte.Jordal@um.uib.no>

Bergen Norway SystematicBotany

Associate Professor in Systematic Botany A permanent position as associate professor in systematic botany is open at the University Museum of Bergen, the Natural History Collections (DNS),(http://www.uib.no/universitymuseum).

We are seeking an active researcher focusing on plant evolution, who has expertise in systematics of vascular plants and phylogenetics. Relevant fields of research are evolutionary relationships, taxonomy and species diversity of vascular plants, and evolutionary processes generating biodiversity. Applicants must be able to document research with international standards within one or more of these fields.

This position entails the scientific responsibility for a botanic garden that is more than a century old; the Museum Garden. The successful applicant will also be scientifically responsible for the botanical exhibitions at the museum, and will take part in the development of new natural history exhibitions which are currently being planned. He or she will also be expected to take part in the teaching of botany at UiB.

A more detailed description of the position and information about necessary documentation which must be enclosed in the application can be found further down on this page. Additional information can be obtained from the head of the Natural History Collections, associate professor Kari Loe Hjelle, phone (+47) 55583323 / e-mail kari.hjelle@um.uib.no.

http://www.jobbnorge.no/en/available-jobs/job/-101821/associate-professor-in-systematic-botany
Bjarte Henry Jordal <Bjarte.Jordal@um.uib.no>

CanadianParks Edmonton ConservationManager

The Canadian Parks and Wildness Society in Edmonton is seeking a conservation manager to head up their operations in Northern Alberta, please see below:

Exceptional Opportunity to Lead an Alberta Conservation Organization CPAWS Northern Alberta - Conservation Manager/Executive Director

The Canadian Parks and Wilderness Society, Northern Alberta chapter (CPAWS NAB) is seeking a dynamic, results-oriented individual to provide strategic leadership to the chapter. This position reports directly to the chapter's Board of Directors and has a strong conservation focus in its daily work. The chapter is exploring two different operational models for this position. Only one of the two positions will be hired based on the qualifications of the 'best fit' candidate.

1. Full-time Conservation Manager Candidate has a minimum of 3-4 years of progressively responsible experience, a strong conservation background, proven leadership and communication skills, some experience with strategic planning and fund development, and the potential to grow into an Executive Director role over time. In this model, the Board will work with the Conservation Manager to develop targeted skill-gaps. Applicant's related work experience should not be limited to summer/co-op term positions.

2. Part-time Executive Director (3-4 days/week) Candidate has 5-7 plus years of leadership experience, a strong conservation and strategic planning background, and proven experience with fund development, stakeholder and media relations, and the non-profit sector (management-oriented preferred).

Position Focus Areas The Board will work with the right candidate to shape the position to the candidate's strengths in relation to the organization's gaps and a manageable workload. The final job description, position expectations, and operational model will be determined once the position is filled in consultation with the best candidate. CPAWS NAB is small chapter with limited administrative and staff support requirements for the leadership position. 1. Providing vision and strategic leadership to achieve CPAWS NAB's conservation goals. 2. Ensuring that CPAWS NAB is an influential voice on conservation and parks in Northern Alberta. 3. Representing the organization in multi-stakeholder discussions and to the public, government, and other stakeholders as needed. 4. Working within existing organizational structures and financial frameworks to guide day-to-day operations. 5. Supervising and leading the organization's small contract staff and working with the Board to ensure volunteers remain engaged in key support roles and Board-lead committees. 6. Supporting the chapter's fund development and outreach efforts (led by the Board's Fund Development and Outreach/Special Events committees) 7. Fostering strong relationships within the CPAWS Pan-Canadian Network particularly with the Southern Alberta Chapter and the National office.

Desired skill-sets for both operational models: The Board recognizes the level and depth of experience with the targeted skill sets will differ between the two operational models under consideration. . University degree in a conservation or environmental planning related field or equivalent related work experience. . Knowledge and experience working with environmental issues, in particular those regarding conservation, the boreal forest, and parks. . A demonstrated passion for wilderness and conservation. . Leadership experience, including experience working with and leading teams. . An understanding of the public policy and political process in Alberta and Canada. . Strategic planning experience and a capacity to understand and respect the often contrasting needs of the various stakeholders . Successful history of working with stakeholders and partner organizations and building networks. . Excellent verbal and written communications skills . Assets include experience with GIS, media relations, and working with First Nations.

About the Organization CPAWS NAB is a well-established, conservation group that engages with governments, industry, and the Canadian public, and is the pre-eminent voice for protecting wilderness and biodiversity in the northern two-thirds of Alberta. The ED will work collaboratively with the Board, staff, key volunteers, the CPAWS national network, and other key stakeholders to achieve our conservation goals. For more information on our chapter visit: www.cpawsnab.org . About Edmonton If you are passionate about wilderness, then Edmonton is the city for you! The city boasts the longest connected urban parkland in North America, offering up over 97 km of trails for biking, hiking, skiing and running. Elk Island National Park is less than an hour away, and weekend trips to the Rocky Mountain parks are a must. Edmonton has fantastic

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Cornell LabManager AvianGenomics

The following position is available in the Evolutionary Biology Program at the Cornell Lab of Ornithology. It is currently posted through April 30, 2014 on the Jobs at Cornell web page at https://cornellu.taleo.net/careersection/10164/jobdetail.ftl?lang=en&job=23382 Lab Manager-23382

Research Support Specialist I - Band E Lab of Ornithology, College of Agriculture and Life Sciences Cornell University

The Cornell Lab of Ornithology is the world's leading resource for conservation, research, education, and citizen science focused on birds. The Lab is a vibrant unit within Cornell's College of Agriculture and Life Sciences (CALS), where twelve world-class, mission-driven programs are directed by full-time faculty and other professionals. Lab staff teach undergraduate courses, advise graduate students, collect and disseminate digital resources on biodiversity, and engage with partner organizations and citizens around the world to conduct scientific research and conservation actions. Our management and staff are committed to the highest standards of ethics and excellence in all areas of our work, and our Board leadership includes faculty from Cornell and other universities, successful leaders and managers from the business and non-profit sectors, and conservation-minded citizens from the United States and beyond.

The Fuller Evolutionary Biology Program at the Lab of Ornithology is currently seeking a Lab Manager. Duties include:

* Provide high level technical oversight for an animal molecular genomics laboratory that supports research on a broad variety of organisms and topics using a diverse array of traditional and next- generation technologies. * Oversee the work of the lab's large research community of students, postdoctoral scholars, affiliated faculty, and visiting researchers (25-30 people in total at any given time, with high turn-over among visiting affiliates). * Train and subsequent independent oversight of students and other lab users (including novices) learning traditional and next- generation molecular lab skills, including DNA extraction, PCR amplification, microsatellite and SNP analysis, and DNA sequencing. * Provide equivalent training of lab users in project design and implementation skills. * Provide oversight of lab users in the design, troubleshooting, and implementation of projects using next generation genetic/genomic tools, potentially including GBS, ddRAD, high throughput SNP genotyping, Illumina sequencing, transcriptome analysis, and similar approaches. * Independently generate and analyze next-generation genomic datasets in support of lab-wide research projects. * Manage all day-to-day laboratory operations and infrastructure. * Oversee and ensure long-term security of data and sample archives, including an extensive collection of 30,000+ genomic and tissue samples. * Ensure that laboratory and its users meet all standard laboratory safety guidelines. * Pursue independent research and publications using avian genetics.

Applicants to provide cover letter, resume, contact information for 3 references

Required Qualifications:

* Bachelor's degree in a biology-related field. * 2-3 years of experience in a molecular biology laboratory. * Mastery of routine methods in molecular biology such as DNA sequencing and extraction and PCR amplification. * Ability to prepare reports and analyses for presentation to others. * Must be personable, flexible, possess excellent organizational and communication skills and take pride in their work. * Ability to develop effective working relationships and maintain positive working relationships within a diverse laboratory group. * Visual concentration, attention to detail and manual dexterity required. * Must be able to work independently as well as in a team environment.

* Ability to respond effectively in an environment in which priorities change. * Must exercise sound and ethical judgment when acting on behalf of the University. * Experience using some combination of next generation genetic/genomic tools such as GBS, ddRAD, SNP genotyping, Illumina sequencing, transcriptome analysis, and similar approaches. * Prior supervision experience. * Prior experience with budgets and financial transactions.

Preferred Qualifications:

* Advanced degree in a relevant area and research experience relevant to genetic/genomic studies of any group of organisms. * Previous laboratory management experience strongly preferred. * Applicants to be adept at both traditional and next-generation molecular laboratory and analysis skills, including current

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CSIRO Canberra FruitFlyControl

Applications are invited for an indefinite (permanent) Research Scientist position in molecular biology/functional genomics based at CSIRO Ecosystem Sciences, Canberra, Australia. We are seeking an early to mid-career scientist with an interest in investigating the functional and molecular basis for ecologically relevant traits using knockouts and gene expression analysis. This role will join the Ecological and Evolutionary Genomics team, and will in the first instance work to develop RNAi (gene silencing) methods to improve the Sterile Insect Technique (SIT) to control Queensland Fruit Fly as part of a recently-established Australian consortium (SIT-Plus). We are seeking an enthusiastic, innovative and highly independent scientist with a PhD in molecular biology or functional genomics.

As a Research Scientist, your role will be to design, perform, analyse and communicate results of molecular biology and functional genomics experiments. You will critically evaluate, develop, and improve methods for RNAi gene silencing and targeted mutagenesis (eg. CRISPR, TALEN) in invertebrates, including design and implementation of new methods if required. You will work collaboratively with internal and external collaborators to develop and implement an RNAi-based approach to the Sterile Insect Technique (SIT) to control Queensland Fruit Fly.

Specifically you will:

1) Lead the development of novel approaches that use gene silencing to control invertebrate pests.

2) Generate novel theoretical perspectives by pursuing new ideas and approaches and networking with scientific colleagues across a range of disciplines and organisations.

3) Under broad supervision, undertake planning and preparation of research proposals and carry out investigations requiring originality, creativity and innovation.

4) Communicate findings through seminars, research reports and publication in high-impact international journals.

5) Help build CSIRO's research reputation for integrated and multi- disciplinary science related to understanding ecosystem services.

6) Initiate new research projects aiming to identify the genetic basis of ecologically relevant traits in invertebrates.

7) Work effectively as part of a research team to effectively meet project milestones, and supervise technical staff and students.

Location: Canberra, Australia Term: Indefinite/Ongoing Reference Number: ACT14/00974 Salary: AU$92k - AU$100k plus up to 15.4% super

CSIRO Ecosystem Sciences (CES) is a globally significant centre for sustainability science. The Division applies multidisciplinary science to help ensure the sustainability of Australia's agricultural and forestry systems, built environments, biodiversity, and rural and urban communities and industries. The Evolutionary Biology Program houses the molecular biology, biochemistry, microbiology, analytical chemistry, phylogenetics, and genomics capability in CES. The program aims to document Australia's terrestrial fauna through recognition of species and their distributions, and through the interpretation of their evolutionary origins. The Program examines how Australia's biodiversity has been shaped by evolution, and takes inspiration from evolutionary processes to develop genomics and bio-inspired technologies.

http://www.csiro.au/Organisation-Structure/-Divisions/Ecosystem-Sciences/Evolutionary-Biology.aspx How to Apply for this Job:

To view the position description or to apply online, please visit the following link:

http://csiro.nga.net.au/?jati=3Dc23cca95-3647-d52a-ea14-7fb6949f1cde Applications close May 25th 2014

DrOwain Edwards Program Leader | Evolutionary Biology Principal Research Scientist CSIRO Ecosystem Sciences Underwood Avenue, Floreat WA 6014| Clunies Ross St, Canberra, ACT 2601

Phone: +6189333 6401 (Perth)| +6126246 4514 (Canberra)| Mobile: 0438877 180 owain.edwards@csiro.au

Owain.Edwards@csiro.au

ImperialCollege London ResTech PollinatorEvolution

[Imperial College London] < http://www.jobs.ac.uk/employer/imperial-college-london >

Research Technician Imperial College London - Department of Life Sciences

Faculty of Natural Sciences

Salary scale: Â£25,370 - Â£28,040 per annum (maximum starting salary Â£25,370)

A Research Technician position is available in the research group of Dr Richard Gill to support research looking into the effects of environmental stressors on insect pollinators. The post holder will be based in the Department of Life Sciences at the Silwood Park Campus (near Ascot in Berkshire) of Imperial College London and will become an active member of the Grand Challenges in Ecosystems and Environment initiative

(http://www3.imperial.ac.uk/ecosystemsandenvironment/grandchallenges).

A substantial part of the Research Technician's role will be to support a recently funded NERC project looking at the behavioural and molecular responses to pesticide exposure in bees. You will also be expected to assist in the running of the Gill Research Laboratory. The postholder will take part in leading edge research which will include novel, interesting and important axes of research.

The main duties of the role will include the collection, preparation, processing and storage of bees, plants and chemicals. You will also be expected to assist with the running of manipulation experiments and data collection and be involved with bee and plant husbandry. You will provide assistance in the laboratory to the research group and assist with presentation of results to the group, collaborators, and to the research community in general. You may also be expected to prepare molecular samples such as DNA and RNA extractions and associated optimisation methods.

You must have 2 A-levels in relevant subjects, or equivalent vocational qualifications, plus work experience, preferably in a relevant technical/scientific role. Proven experience in assisting to carry out scientific research in a laboratory and/or field setting, aided with observations of animal behaviour, and experience in providing support for analyses of large data are essential. You must also have experience in collection, preparation, processing and/or storage of animal and plant specimens and a background in a similar work environment.

You should have a methodical approach to your work, good interpersonal and organisational skills, and be able to communicate well within a research group. You will be expected to organise and prioritise your work in response to deadlines, while paying close attention to detail.

This is a fixed-term appointment available for up to 24 months on a full-time basis or up to 36 months on a part-time basis.

Informal enquiries should be directed to Dr Richard Gill at r.gill@imperial.ac.uk.

The preferred method of application is online via our website http://www3.imperial.ac.uk/employment (please select "Job Search" then enter the job title or vacancy reference number including spaces - NS 2014 049 JT - into "Keywords"). Please complete and upload an application form as directed.

Alternatively, if you are unable to apply online, please contact Christine Short by email c.j.short@imperial.ac.uk, to request an application form.

Closing date: 30 April 2014 (midnight BST)

"Gill, Richard J" <r.gill@imperial.ac.uk>

KORA Switzerland FieldAssist LynxPredation

Internship:** Lynx Predation Project** Short title:** Predation of Eurasian lynx in the Northwestern Swiss Alps

Abstract: Eurasian lynx are specialised predators of medium sized ungulates such as roe deer and chamois. The KORA research group (Carnivore Ecology and Wildlife Management) cooperates with the ?Rehprojekt im Simmental? of the University of Zurich in order to better understand the evolution and dynamics of predator-prey relationships.

Tasks: The following topics will be addressed: functional responses, differences in hunting strategy between males and females, use of kills, zones of high risk for prey.

Field assistant will help with on-going field work, organization and data management. Field Tasks will include localization of lynx kills with handheld GPS, identification of species, age and sex of prey, measurements of kill site characteristics. Office tasks include organization of daily work, data entry and reporting to officials.

**Data: **source Data gathered in the field, existing predation data from KORA

Time scale: Continuous fieldwork from Mai to August 2014 (dates negotiable)

Funding: No salary (possibly BNF internship or civil service), field expenses are covered

Job profile: You need a driver?s license, good physical condition and the ability to judge risks and your own limits. The terrain can be steep and dangerous. Skills in reading maps, mountaineering or hiking are of high advantage. Spoken skills in German or French are necessary to communicate with local people. Field days are long and unpredictable; you should have a place to stay in Bern.

It is also possible to combine the internship with a Bachelor or Master Thesis.

Contact: Kristina Vogt k.vogt@kora.ch

Kristina Vogt <k.vogt@kora.ch>

MelbourneU FieldAssist Fairywren

We are looking for field assistants to help monitor a colour-banded population of superb fairy-wrens near Melbourne, Australia for a study on animal personalities.

Time period: start late August or October 2014, finish January 2015 (4-5 months, with mist-netting till end September and nest searching and monitoring Oct-Jan).

Duties include regular censusing of colour-banded birds, searching for and monitoring nests, mist-netting, behavioural observations, video analysis, and data proofing. Working days are long, with early starts six days a week. Enthusiasm, self-motivation, and a strong work ethic are a must. The study is based at Serendip Sanctuary, a small reserve on the outskirts of Melbourne.

Qualifications: experience monitoring colour-banded birds, nest-searching, and mist-netting. Must also be early riser, physically fit, able to work in extreme weather conditions, and enjoy basic shared living conditions. Onsite accommodation in a house with shared dorm-style room is provided, but assistants cover travel to the site and their own food costs. The project will reimburse up to AU$500/mo towards receipted food and travel expenses.

For more information contact: Timon van Asten (t.vanastenATstudent.unimelb.edu.au). To apply, please email a letter outlining previous relevant field research experience, and a resume including names and contact information for 3 referees.

timonv@student.unimelb.edu.au

MNHN Paris InsectAdaptation

Dear Evoldirians,

A lecturer position is opened at the National Museum of Natural History (MNHN) in Paris, France, to work on adaptations, speciation and diversification in Insects. The lecturer will be in charge of curating the Lepidoptera collection of the MNHN. Details (in French only, sorry!) are found here (position n4112). https://www.galaxie.enseignementsup-recherche.gouv.fr/ensup/ListesPostesPublies/-Emplois_publies_Museum_TrieParCorps.html Please note that EU applicants must already have the 'qualification pour les fonctions de maitre de conférence' to be eligible. Non-EU applicants do not need this.

Marianne Elias CNRS Researcher UMR 7205 - CNRS Museum National d'Histoire Naturelle 45 rue Buffon, CP50, 75005 Paris phone: +33 1 40 79 37 90 http://www.mnhn.fr/oseb/elias-marianne,279 melias2008@gmail.com

NorthCarolina MuseumNS Biodiversity

North Carolina Museum of Natural Sciences: Assistant Director, Biodiversity Research Lab

Division Information: This position is located in Raleigh, North Carolina at the NC Museum of Natural Sciences, an award-winning major institution with a prominent State-wide, national and international profile. This key position works in the Biodiversity Research Laboratory, a unit within the Museum's Research & Collections section.

Description of Work: The goal of this position is to develop a research and science communication program in a biodiversity-related field. This position has three primary areas of responsibility: 1. Development of original scientific research programs in biodiversity, animal movement, spatial ecology, urban ecology, or related fields; research programs may have local, regional, and/or international focus and will include pursuit of external research funding, data generation and analyses, and publication/dissemination of results; some aspects of this research should be suitable for display in the Biodiversity Lab (which is on-exhibit at the Museum) and, ideally will include collaborations with local universities and citizen scientists. 2. Operational management and administration of the Biodiversity Research Laboratory in the Nature Research Center wing of the NC Museum of Natural Sciences, including supervision of laboratory with oversight of equipment, budgets, personnel, research programs, and volunteer programs. 3. Participation in science communication initiatives, including participation in Museum educational programming, delivering public science-based presentations, interacting with Museum visitors, serving as a role model for students and citizen scientists, and creating programmatic themes that raise the science literacy of visitors.

Applications due: May 31, 2014

For more information and application instructions, please see: http://tinyurl.com/kodm4ye Jason R. Cryan, Ph.D. Deputy Museum Director, Research & Collections North Carolina Museum of Natural Sciences 11 W. Jones Street Raleigh, NC 27601

Phone: (919) 707-9933 Fax: (919) 715-2614 email: jason.cryan@naturalsciences.org Museum Website: www.naturalsciences.org Research Website: www.planthopper.com "Cryan, Jason R" <Jason.Cryan@naturalsciences.org>

Peru FieldAssist ButterflySpeciation

A field assistant is required to help with research on speciation in Heliconius butterflies. We are studying the genetic basis of traits causing reproductive isolation between a pair of recently diverged sister species (http://www.york.ac.uk/res/dasmahapatra/). The field assistant will help to collect data for QTL mapping of the genomic regions involved in the production of colour patterns, pheromones and host plant choice.

The field assistant will be required from June - December 2014, but the exact dates are flexible and shorter time periods could be considered. The assistant will work with a postdoctoral researcher in Tarapoto, Peru (a medium sized town at the Amazonian/Andean ecotone). The field assistant's primary tasks will be to help run experiments on captive populations of butterflies and to collect wild butterflies to supplement captive stocks. The field assistant will develop an excellent practical knowledge of Heliconius butterflies and their host plants (Passifloraceae). S/he will improve his/her understanding of evolutionary ecology and genetics, be actively involved in experimental design, preliminary data analysis, and likely gain co-authorship on a published study. The project will provide excellent preparation for a PhD on tropical biodiversity.

The field assistant's return airfare to Peru and accommodation will be covered, in addition to a small stipend for food and basic living costs.

Applicants should hold an undergraduate or Master's degree in Life Sciences with an interest in Evolutionary Biology, and have a passion for natural history and biodiversity. The successful applicant will need to be independent and comfortable in a culturally challenging environment. Spanish language skills are highly desirable but not essential. Latin Americans are particularly encouraged to apply. Interested candidates should write to Neil Rosser (neil.rosser@york.ac.uk) before 1st May 2014.

neil.rosser@york.ac.uk

RiceU HuxleyFellow Evolution

HUXLEY FELLOW in ECOLOGY & EVOLUTION: The Ecology and Evolutionary Biology department of Rice University (http://eeb.rice.edu/) seeks to fill a Huxley Fellow position in ECOLOGY or EVOLUTION. The position is a two-year appointment with a third year extension possible, with a start date of July 1, 2014. Our prestigious Huxley Fellow Program aims to recruit outstanding researchers with a PhD and postdoctoral experience, who merge excellence in teaching (25%) and research (75%). The Huxley Fellows receive faculty status, employee benefits, competitive salary, and research funds for independent or collaborative research. Collaborative interests with the existing faculty are a plus and applicants are encouraged to identify a potential faculty host(s) within the EEB department. An application (curriculum vitae, statement of research interests and statement of teaching) and three letters of recommendation should be submitted via e-mail to Diane Hatton, rdh@rice.edu. Please write "Huxley Fellow Application" in the subject line. Application review will begin May, 9, 2014. For further questions and informal inquiries please contact Dr. Volker Rudolf (vr2@rice.edu), Huxley Fellow Search Committee Chair. Rice University is an Equal Opportunity/Affirmative Action Employer and values a diverse faculty. Women and minorities are encouraged to apply.

Diane Hatton

Project Coordinator

Dept of Ecology and Evolutionary Biology

Rice University

Diane Hatton <rdh@rice.edu>

SmithsonianInst DNALabTech

Laboratory Technician - Smithsonian Institution

Center for Conservation and Evolutionary Genetics, Smithsonian Conservation Biology Institute, and Division of Mammals, Department of Vertebrate Zoology, National Museum of Natural History.

We are recruiting at least one technician to conduct DNA analyses in the laboratory at the Center for Conservation and Evolutionary Genetics Laboratory, located at the National Zoo in Washington, DC. The selected individual will be involved in projects on African mammals, their pathogens and associated vectors, with Drs. Kris Helgen (NMNH), Hillary Young (UCSB/NMNH), Jesus Maldonado (SCBI/NMNH) and Rob Fleischer (SCBI).

The position will include the use of basic DNA skills (DNA extraction, PCR and standard DNA sequencing), next-generation sequencing (454 and Illumina) library preparation, ancient DNA, and other molecular methods as required. The work will include pathogen diagnostics, host and vector DNA barcoding, and ancient population genetics.

The position is available initially for 18 months and will begin as soon as possible following the deadline, ideally by 1 June 2013.

Minimum qualification is a bachelor's degree in biology or similar field, or an equivalent combination of education or experience. Demonstrated laboratory experience in one or more of the above areas are required.

To apply, email Rob Fleischer (fleischerr@si.edu) and Kris Helgen (Helgenk@si.edu) with: (1) a brief letter of application detailing your interests and experience in the methods listed above; (2) a current curriculum vitae or resume; and (3) names, addresses and phone numbers of at least three references.

Deadline for applications is 10 May 2014. Please contact Dr. Fleischer and Dr. Helgen if you have any questions concerning the position.

"Fleischer, Robert" <FleischerR@si.edu>

SunYetSenU 6 EvolutionaryBiol

The Ecology and Evolution program at Sun Yet-Sen University (SYSU), a premiere institution in China, is seeking to expand its Ecology and Evolution program by recruiting 6-8 PIs. The positions, open rank, welcome qualified scientists of all nationalities. The EE program at SYSU, recently ranked first in China, plans to recruit in broad areas of modern ecological research and in the interface between ecology and evolution. SYSU has had long-standing ties with major universities in North America and their faculty members have strong research presence on campus. An International center established 2005 will be expanded into a new Open Laboratory in Ecology and Evolution as part of this growth. Salary and start-up package are highly competitive. The university is located in Guangzhou, a major metropolis in southern China. Guangzhou is one of the three most internationalized cities in the country and is home to many international schools from K to 12.

For inquiry, please write to

Hong Pang (Sun Yat-sen University, Lsshpang@mail.sysu.edu.cn) .

For pre-application consultation, interested individuals are welcome to contact

Fangliang He (University of Alberta, fhe@ualberta.ca),

Chung-I Wu (University of Chicago, ciwu@uhicago.edu) or

Antony Dean (University of Minnesota, deanx024@umn.edu).

(SYSU; http://www.sysu.edu.cn/2012/en/index.htm; http://www.sysu.edu.cn/2012/cn/index.htm)

wuci <cw16@uchicago.edu>

TrinityU Texas ResTech LizardEvolution

Research technician position: lizard behavioral evolution

A full-time, NSF-funded, technician position is available in the laboratory of Dr. Michele Johnson at Trinity University in San Antonio, Texas. Projects in the Johnson lab focus on behavioral evolution in lizards, using approaches from the fields of ecology and neuroscience to study the physiological traits underlying social behaviors. We are searching for a motivated, team-oriented technician to join our dynamic research group.

The ideal candidate will have a B.S. or B.A. in biology, biochemistry, or a related field, and a minimum of one year of experience working in a researchlaboratory. The primary duties of the position include data collection in the lab and field (with likely summer fieldwork in the Caribbean), general maintenance of the laboratory, general care of laboratory animals, and training and supervision of undergraduate researchers. Previous research experience with vertebrates and facility with basic molecular and histological techniques are desirable. Facility with basic laboratory equipment, enthusiasm for working in the field, ability to adhere to safety requirements, excellent organizational and interpersonal skills, and the ability to handle multiple priorities are required. This job is ideal for persons who have an interest in gaining additional research skills and experience prior to graduate school.

The Johnson lab is housed in Trinity University's brand new Center for the Sciences and Innovation (http:/-/goo.gl/cLZ8KP). San Antonio is among the fastest-growing cities in the United States, and the low cost of living, many cultural opportunities, and warm climate make the city a wonderful place to live.

To apply for the position, please send the following materials to Dr. Michele Johnson at michele.johnson@trinity.edu: CV or resume, including contact information for 2-3 references, and a cover letter explaining why you are interested in the position. Review of applications will begin immediately, and the ideal start date is May 12, 2014. We strongly encourage women and minority candidates to apply, as we value working with a diverse team. Trinity University is an Equal Opportunity Employer.

Michele A. Johnson, Ph.D. Assistant Professor Trinity University Department of Biology One Trinity Place San Antonio, TX 78212

michele.johnson@trinity.edu office phone: 210-999-8918 lab phone: 210-999-8914 www.trinity.edu/mjohnso9/ mjohnso9@trinity.edu

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UBern EvolutionaryBiol

Reminder

Professor in Evolutionary Biology

The Institute of Ecology and Evolution of the University of Bern, Switzerland, announces a vacancy for a professorship (open rank) in Evolutionary Biology.

Applications are sought from individuals with an outstanding research record in theoretical and/or experimental evolution. Candidates with a strong background in evolutionary genomics are also encouraged to apply. The candidate should have a doctorate in a relevant field, several years of postdoctoral and teaching experience, an interest in developing, testing and teaching evolutionary theory and in collaborating with other researchers of our institute. Senior researchers are also encouraged to apply. Hiring level, from tenure-track Assistant Professor to Full Professor, will be commensurate with experience.

The new faculty member will have responsibility for part of the teaching of evolutionary biology at undergraduate and graduate levels. All graduate teaching and advanced undergraduate teaching are in English.

The application should include a letter of motivation, a CV with a short research plan for the next 5 years, funding history, list of previous teaching and supervised MSc and PhD students, a list of publications, and the names and contact information for three references. Applications from women are strongly encouraged. Appointment will be either to tenure track or tenured, commensurate with experience. The earliest starting date for the position is August 1st 2015.

Applications must be submitted by April 10th 2014 as one PDF file to info@natdek.unibe.ch, and should be addressed to the Faculty of Science, University of Bern, Prof. Silvio Decurtins, Dean, Sidlerstrasse 5, 3012 Bern, Switzerland.

You can contact director@iee.unibe.ch for further information about the position. More information about the institute can be found on iee.unibe.ch

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

UHaifa EvolutionaryBiology

The Department of Evolutionary and Environmental Biology, University of Haifa, Israel (http://eeb.haifa.ac.il), invites candidates for a tenure-track position to begin on October 2014 or October 2015. We shall consider any excellent scientist in the fields of Evolutionary Biology and/or Ecology.

Interested candidates should send a letter of research interests/plans, CV, list of publications, and contact information of at least three referees to Ms. Limor Dvir, ldaniely@univ.haifa.ac.il by April 30, 2014.

Alan R. Templeton Charles Rebstock Professor Emeritus of Biology and Genetics Professor of Evolutionary and Environmental Biology

Department of Biology Washington University St. Louis, MO 63130-4899 USA Institute of Evolution, and Department of Evolutionary and Environmental Biology University of Haifa Haifa 31905, Israel p. 314-935-6868 f. 314-935-4432 e. temple_a@wustl.edu

http://pages.wustl.edu/templeton

templeton@biology2.wustl.edu

UHull Bioinformatics

Bioinformatics Research Fellow in Evolutionary & Environmental Genomics

This is an exciting new Research Fellow position for a bioinformatician to work with staff in Evolutionary and Environmental Genomics. We are looking to work with a bioinformatics colleague and scientist, this is not a technical post. We have quite a number of projects, most already with data, on which you could take the lead. We would additionally welcome the development of new projects in collaboration with staff in the group. We anticipate that for the right candidate this could be a very productive fellowship in terms of publications and collaborations. Please feel free to discuss the position with Dave Lunt. The advert is below:

Reference: FS0093 Campus: Hull Faculty: Faculty of Science and Engineering Department: School of Biological, Biomedical and Environmental Sciences Salary: £31,644 to £36,661 per annum, Post type: fixed term, full time Closing date: Sunday 27 April 2014

Applicants with a strong background in bioinformatics, comparative genomics, or evolutionary and population genomics are invited to apply for the position of Postdoctoral Research Fellow within the School of Biological, Biomedical, and Environmental Sciences at the University of Hull, UK.

The post-holder will work closely with members of the Evolutionary and Environmental Genomics (EEG) group to analyze genomic datasets from a diverse range of projects and develop new collaborative research programmes. Previous expertise of work with eukaryotic genome assembly, RADseq, metabarcoding, or population genomics would be advantageous.

The position is funded by The School of Biological, Biomedical, and Environmental Sciences for two years and will be central to the developing research agenda of this active group. Existing expertise within the EEG Group encompasses phylogenetics, network ecology, bioinformatics, speciation genetics, molecular evolution, and population genetics. It is anticipated that the new Bioinformatics Fellow will complement and extend these existing skills. The EEG Group is very research active and currently comprises six members of academic staff along with postdocs, research students, and technicians.

The post-holder will also be involved in undergraduate and postgraduate bioinformatics teaching. This may include undergraduate metabarcoding practicals, postgraduate training days in bioinformatics, and similar.

This will be an exciting career opportunity for a research fellow wishing to broaden their experience with different research systems, develop methods and novel bioinformatics approaches, forge new collaborations, and maintain a very substantial publication record.

The successful applicant will have completed a PhD in a relevant biological subject area (e.g. bioinformatics, evolutionary biology, population genetics) and have proven ability to carry out large-scale data analysis using bioinformatic approaches. An excellent understanding of the science underlying the work of the EEG group would be advantageous.

This is a full time position for 24 months in the first instance.

Candidates are encouraged to discuss this role informally with Dr Dave Lunt, Tel: +44 (0)1482 465514, Email: dave.lunt@gmail.com

For information about the position and research of the EEG group visit: http://www.evohull.org/-environmental-genomics/ For information about the School visit: www.hull.ac.uk/biosci To apply see https://jobs.hull.ac.uk/FS0093 Dr. Bernd Hänfling Lecturer in Ecology and Evolution Director of Postgraduate Studies Evolutionary Biology Group Department of Biological Sciences University of Hull Hull, HU6 7RX UK

E-mail: b.haenfling@hull.ac.uk Tel: 0044-1482-465804 Fax: 0044-1482-465458 http://www2.hull.ac.uk/-science/biological_sciences/our_staff/academic_staff/-bernd_hänfling1.aspx B.Haenfling@hull.ac.uk

UOslo EvolutionaryGenomics

University of Oslo, Natural History Museum Professor/Associate Professor in Evolutionary Genomics

https://uio.easycruit.com/vacancy/1113731/-71922?iso=no The Natural History Museum (NHM) of the University of Oslo holds extensive collections of animals, fungi, and plants. Besides being the foundation for the classification of organisms, the collections are also important repositories for studying various aspects of geographical and temporal variation in biodiversity. The recent development of sequencing techniques that are suitable for ancient or historical specimens with degraded DNA, has significantly increased the potential to take advantage of the unique documentation of life on Earth preserved through natural history museum collections.

The museumÂs strategy emphasizes the importance of using the collections as a gene bank and to extract the genetic information of specimens for use in science. NHM is also building up collections of fresh DNA/tissue samples and is heavily involved in the global DNA barcoding initiative. The museum has established an ancient-DNA laboratory for extraction of highly degraded DNA from museum samples and from environmental samples, and runs a regular DNA laboratory. Through a strategic collaboration with the Department of Biosciences at our university, NHM has access to central high-throughput DNA sequencing facilities and is partner in a joint effort to establish a new ancient-DNA laboratory which will be hosted by the Department of Biosciences.

We now want to strengthen the museum's focus on collection-based science by increasing our competence in high-throughput sequencing techniques applied to biodiversity research and, in particular, to degraded DNA from museum collections and environmental samples.

The museum has recently reorganized its research department into smaller research groups representing the main research topics within biology at NHM. These include sexual selection and speciation in animals, animal systematics, plant evolution, taxonomy and phylogeny of plants and fungi, and modelling of geo-ecological patterns and processes. More information can be found at the NHM homepages.

Job description

It is expected that the successful candidate should take a lead in coordinating and developing the museumÂs research in evolutionary genomics and biosystematics with emphasis on the use of highly degraded DNA. He/she should be an asset for the whole research department but is expected to associate formally with one of the existing research groups. Additional internal resources, including PhD and postdoc positions, will be made available. The successful candidate will be expected to attract extramural research funding, and a proven record of accessing such funding is essential. The candidate will participate in teaching evolutionary genomics, including courses under the bachelor and master programs of UiO, and should be a capable and enthusiastic supervisor of master and PhD students. Relevant background for taking the scientific responsibility for parts of the museumÂs collections is an advantage, but not a requirement. Duty work may also include providing assistance in phylogenomics and bioinformatics to the research community at NHM.

Qualifications

To qualify for appointment as Professor/ Associate Professor, the applicant must have documented scientific work equivalent to a doctorate, and several years of postâdoctoral experience.

We seek an active researcher in evolutionary genomics with a strong publication record. The successful candidate should be on an upward trajectory and is expected to have strong potential to execute research projects at a high international level and to perform research in areas that will have synergistic effects with current research in the museum. He/she should have the ability to create an attractive research environment and the ideal candidateÂs research would address fundamental questions in evolutionary genomics and biosystematics. The candidate should have a solid background in high-throughput DNA sequencing and in bioinformatics.

Candidates for the position should supply a research plan, which demonstrates how the applicant's research will strengthen or create synergy effects on current research at the museum. Applicants, who at the time of appointment cannot document formal teaching competence, must acquire such competence in the course of two years.

The teaching languages at the University of Oslo are Norwegian and English. The person appointed to the position is expected to be able to teach in Norwegian or English or both.

Personal qualities - Good collaborative skills and social intellect - Strong dedication and motivation - Good command of written and oral English

We offer

- Pay Grade 72-90 (NOK 627 100 -997 000 per year) for appointment as Professor (SKO 1013)

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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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Uppsala Bioinformatics

Dear colleagues,

A permanent position as Bioinformatics specialist/Scientific programmer is available in Thijs Ettema's lab, Cell and Molecular Biology, Uppsala University, Sweden. Applications here: http://www.uu.se/en/jobs/jobs-detail-page/?positionId=36221 We are looking for: A Bioinformatics specialist or Scientific programmer that will work at the lab of Thijs Ettema at the Department for Cell- and Molecular biology, Uppsala University. The position is permanent with a 6-month probationary period beginning June 1st or by appointment.

The Ettema-lab: cutting edge research in microbial and evolutionary genomics Prof. Ettema's lab is applying emerging genomics technologies to analyze microorganisms that defy cultivation under laboratory conditions. These organisms are predicted to comprise up to 99% of all microbes on our planet. By combining such cultivation-independent methods, such as single cell genomics and metagenomics, with next-generation sequencing-based analyses, the Ettema lab aims to study uncultured microorganisms ('microbial dark matter') at the genomic level. Such studies will paint a detailed picture of the overall diversity and origin of life on our planet, and will eventually also reveal important clues about how complex life emerged. For more information, please see: http://www.ettemalab.org/ The Ettema-lab is located at the Biomedical Center (BMC) and will enter brand-new office spaces and a fully equipped genomics lab during the autumn of 2014. Moreover, the lab is well connected to several technology platforms of the SciLifeLab, including platform-based services for next-generation-sequencing, computational support and bioinformatics. We are also actively engaged in a new SciLifeLab platform for single cell genomics (http://www.scilifelab.se/facilities/single-cell/). The research activities in the Ettema-lab are supported by a number of prestigious grants, such as the European Research Council, the Foundation for Strategic Research and the Swedish Research Council.

Job assignment: We are now looking for an experienced bioinformatician that will provide computational support to ongoing research projects within the Ettema lab. The successful candidate will have the following tasks: - In collaboration with the researchers of the lab, design and perform bioinformatics analysis in molecular evolution, phylogenomics, sequence analysis and metagenomics, among others. - Set up and maintain pipelines for the assembly, annotation and analysis of large-scale genome and metagenome sequencing datasets; set up and maintain databases for comparative and evolutionary studies of uncultivated microorganisms. - System administration of the existing local computational infrastructure (server, workstations) and accounts (about 5% of the time). Potentially, the successful candidate might be asked to develop novel bioinformatics applications.

Qualifications:

Requirements: - A PhD or similar research experience in bioinformatics and genomics (within academia or industry). - Extensive experience with the analysis of next-generation sequencing datasets. - Demonstrated experience working in a Linux environment and fluency in at least one programming or scripting language (bash, Perl, python, R, etc.). - Fluent oral and written communication in English. Personal qualities: - Strong sense of organization - Ability to work in cooperation with academic researchers - Excellent communication skills - Pedagogic skills to teach researchers with limited bioinformatics experience - Ability to work independently Merits: - Postdoctoral studies in a related field. - Experience of development and applications of bioinformatics and/or biostatistics methodologies or pipelines for design and analysis of large-scale sequencing datasets (e.g. Galaxy) - Experience of system administration

The positions are permanent with a 6-months trial period. The positions will be placed in the Ettema lab at the Department for Cell and Molecular Biology, Uppsala University. For further details about the position, please contact Thijs Ettema: thijs.ettema@icm.uu.se, +46 18 471 45 21. For more information about the activities in the Ettema-lab, please see http://www.ettemalab.org/ Application: Please send your application marked with ref.nr UFV-PA 2014/1062 as soon as possible, but no later than 2014-04-30.

Lionel Guy Molecular Evolution, Uppsala University, Uppsala, Sweden

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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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Uppsala Sweden Bioinformatician

Bioinformatician in transcriptomics

Full time permanent position. The position is available as soon as possible. 6 months trial period.

Uppsala University is an international research university focused on the development of science and education. Our most important assets are all the individuals who with their curiosity and their dedication makes Uppsala University one of Sweden's most exciting work places. Uppsala University has 40,000 students, 6,500 employees and a turnover of SEK 5,500 million.

Next-generation sequencing (NGS) is a rapidly growing field that provides fascinating new insights into the genetic underpinnings of cellular functions and diseases. However, these new methods place increasing demands on computational expertise and data management. The Swedish Bioinformatics Infrastructure for Life Sciences (BILS; http://bils.se) is therefore seeking a motivated bioinformatician to join their ranks and provide support to projects in the field of transcriptomics and next-generation sequencing.

Job description: The position will be placed at Uppsala University and will be linked to Science for Life Laboratory. Among the main objectives for this newly created post will be the reconstruction of transcripts from read data, using both mapping-based but also denovo assembly algorithms. In addition, the candidate is expected to provide support to projects working with RNA sequencing to study the expression of genes and transcripts. Finally, a major aspect of the study of transcriptomes is the ability to assign functions to individual sequences. Together with the team at the BILS annotation platform, the successful applicant will spend part of the time on the development and implementation of workflows for the functional annotation of genes and transcripts.

Qualifications: We seek a candidate with a PhD in bioinformatics, molecular biology, computer science or any related field who has a strong competence in working with large sequencing data sets and analysis methods in the field of NGS, including but not limited to, RNA-seq. The ability to drive projects and work in a collaborative, yet service-minded environment is a must. Special consideration will furthermore be given to applicants with proficiency in one or more scripting languages (e.g. Perl, Python, Ruby) as well as experience in pipeline design. Excellent communication skills in both written and spoken English are required, since the candidate will collaborate with scientists of very different backgrounds. Emphasis will be placed on personal suitability for the position.

Information: For questions regarding BILS, please check out our website at http://www.bils.se or contact the director of BILS, Bengt Persson (bengt.persson@bils.se). For questions regarding the position, please send an Email to Henrik Lantz (henrik.lantz@imbim.uu.se).

You are welcome to submit your application no later than 12 May 2014. Please see the link below for full details and to access the application form:

http://www.uu.se/en/jobs/jobs-detail-page/-?positionId=3D36290 henrik.lantz@imbim.uu.se

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USussex FieldAssist SpainWasps

VOLUNTEER FIELD ASSISTANT sought immediately for 4-6 weeks (starting mid-April 2014), to help with a study of paper wasp (Polistes) behavioural ecology in southern Spain. The work will involve helping a postdoctoral researcher/PhD student to census and observe colonies as part of experiments to elucidate the basis of helping behaviour in these wasps, which live in small colonies of <20 individuals. The successful applicant must be prepared to work hard and have an interest in behavioural/evolutionary biology and enthusiasm for fieldwork. Successful applicants will obtain excellent experience of cutting-edge insect behavioural ecology. A driving licence and any ability to speak Spanish would be advantages, but neither is essential. Because the work involves recording colour marks on individual animals, the job would not be suitable for someone who is colour-blind. See our research group website for more information about the kind of work we do (http://www.sussex.ac.uk/lifesci/ fieldlab/).

Air fare (from the UK) and accommodation expenses will be provided, with the applicant needing to pay for only their own food/personal expenses, which are relatively cheap in Spain, their travel to/from the airport in their home country, and their travel insurance. A successful applicant will also receive a £250 contribution towards their expenses, on completion of the work. Accommodation will be in a large house shared with the other members of the research group - including shower, cooking facilities, TV, large garden etc. Accommodation is in a medium-sized coastal town with nice beach.

Please send a covering letter and CV, including contact details (including e-mail addresses/tel nos.) for the applicant and 2-3 referees who would be available to provide references. Email as a single Word document to: j.field@sussex.ac.uk

Applicants can come to Sussex University, to discuss the project, either 10/11 April or 15/16th. In your cover letter, please indicate which of these dates you are available. Skype interview may also be possible, but meeting in person is preferred. The position will be allocated as soon as a suitable person is identified.

Informal enquiries: j.field@sussex.ac.uk

Professor Jeremy Field School of Life Sciences, John Maynard Smith Building, University of Sussex, Falmer, Brighton BN1 9QG, UK

J.Field@sussex.ac.uk

UVienna LabTechAssistant PopGenomics

The Research Group of Plant Ecological Genomics of the Department for Botany and Biodiversity Research at the University of Vienna, Austria is recruiting a

Lab Technical Assistant in Molecular Biology

An up to 5-years position funded by the Austrian Science Fund (FWF) is immediately available in a research project on the evolution of wild polyploid orchids (see www.botanik.univie.ac.at/-systematik/projects/dactylorhiza/). Our exciting research makes use of an array of state-of-the-art genomic and epigenomic techniques. Apart from playing a key role in optimizing and performing parts of laboratory protocols, the Assistant will take care of orders and lab equipment. S/he will also maintain databases of protocols and samples.

We are looking for a highly focused and motivated candidate that searches for exciting research opportunities and has an excellent previous record. The successful candidate must have excellent organization and communication skills, and to work in a multinational team. S/he is expected to have a degree in a related discipline (e.g., molecular biology, biochemistry) and to be able to demonstrate previous experience with molecular laboratory duties. Experience with RNA work and/or NGS library preparation will be considered as an important advantage. The Assistant should be willing to learn continuously new methodologies with the support of the rest of the team. The working language in our laboratory is English; German skills are therefore not essential, but they are highly desirable to allow a proper communication with people from outside the team. The position offers a competitive salary (according to experience min. 27,000 per year before tax for full time, including social and health security), and opportunities for career development/further training. If preferable for the successful candidate, 30 hours a week employment is also possible.

To be considered please send your application per email to ovidiu.paun@univie.ac.at including your CV, a cover letter explaining why would this job fit your qualifications, experience and expectations (up to two pages), and the names and contacts of three referees. Please note: Incomplete applications will not be considered. Screening of applications will begin immediately and will continue until the position is filled. The latest preferred start date is June 1st, 2014.

ovidiu.paun@univie.ac.at

UVirginia ResTech EvolutionaryGenetics

The Blackman Laboratory in the Department of Biology is seeking a Laboratory Technician 2 to assist with research in evolutionary and ecological developmental genetics using sunflower and monkeyflower as study systems. Research in the lab focuses on how and why plant developmental responses to environmental cues evolve during domestication, adaptation, and speciation.

The position will involve a combination of research and lab management responsibilities. Research duties will include plant care and phenotyping, molecular and biochemical work (e.g. DNA/RNA extraction, genotyping, qRT-PCR, sequencing library construction), and coordination of large field/greenhouse experiments. Initial projects will be closely supervised with increased independence possible as experience and expertise are developed. Lab management duties will include data and germplasm collection management, oversight of lab organization, ordering supplies and equipment, and supervision and training of undergraduate researchers.

A Bachelor's degree in Biology or a related discipline is required. 1 year's experience working or studying in a research lab setting, including prior conduct of an independent research project is required. Being able to perform sterile techniques, prepare media, carry out basic procedures associated with DNA amplification and sequencing is also required. Strong organizational, computer, and communication skills are essential, and demonstrated experience with basic molecular biology techniques and plant care is preferred.

The position will remain open until filled. Ideal start date is June 2014. This is a one-year appointment; however, the appointment may be renewed contingent upon available funding and satisfactory performance.

To apply, please submit a candidate profile through Jobs@UVA (https://jobs.virginia.edu), search on posting number 0614045. Electronically attach your curriculum vitae, a cover letter, and contact information for three (3) references.

Questions regarding this position should be directed to: Dr. Benjamin Blackman 434-924-1930 bkb2f@virginia.edu http://people.virginia.edu/~bkb2f/Blackman_Lab/

Questions regarding the staff application process or Jobs@UVA should be directed to:

Richard Haverstrom rkh6j@virginia.edu

The University of Virginia is an equal opportunity and affirmative action employer. Women, minorities, veterans, and persons with disabilities are encouraged to apply.

Benjamin Blackman Department of Biology University of Virginia PO Box 400328 Charlottesville, VA 22904

Tel: 434.924.1930 E-mail: bkb2f@virginia.edu Web: http://people.virginia.edu/ ~ bkb2f/Blackman_Lab/ bkb2f@virginia.edu

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UWashington ViralEvolutionSocialNetworks

UW.ViralEvolutionSocialNetworks

Programmer/Researcher UW.ViralEvolutionSocialNetworks

The UW Center for Studies in Demography and Ecology (CSDE) and Department of Microbiology have teamed up to provide an outstanding opportunity for a Scientific Programmer/Researcher (Research Scientist/Engineer 3) to integrate within-host models for viral dynamics into social network models for the spread of HIV within populations.

The Programmer/Researcher will do scientific research and computer programming while providing computer support services for project investigators. The research component will involve developing and testing scientific hypotheses related to one or more of the following subject areas: social network modeling; epidemiology; mathematical modeling of population dynamics; evolutionary biology; population genetics; HIV virulence and pathogenesis; and resistance to anti-retroviral drugs. The programming component requires the candidate to construct, test, and maintain programs written in C and R; create detailed documentation; and publish packages on the Comprehensive R Archive Network (CRAN). Interact with multiple scientists with diverse interests and expertise in order to write papers, develop software, and interact with end-users of the integrated software. The programmer/researcher will also present results at scientific meetings and participate in the development of materials for training workshops on the software.

In the initial phases of the project, the Programmer/Researcher will spend most of his or her time working with social scientists at the CSDE. As the project progresses, he or she will spend increasing amounts of time working with biomedical researchers in the Department of Microbiology.

Requirements:

- MS or Ph.D. in a Quantitative Field (e.g., Computer Science, Mathematics, or Statistics) or a Biomedical/Social Science Field that includes significant mathematical and computational components and three to five years' experience .

- Ability to read, analyze and write scientific papers

- Expertise in the R programming language and package development in R.

- Experience with the C programming language.

- Excellent communication skills

- Willingness to write detailed software documentation for end users.

- Has established technical expertise; serves as a resource to research unit/department.

Equivalent education/experience will substitute for all minimum qualifications except when there are legal requirements, such as a license/certification/registration.

To apply, go to https://uwhires.admin.washington.edu/eng/candidates and enter requisition number 107046 in the required field. If you have questions about this position, you may contact Josh Herbeck (jherbeck@uw.edu), Steve Goodreau (goodreau@uw.edu), or John Mittler (jmittler@uw.edu).

Joshua Herbeck <herbeck@uw.edu>

Vienna ResearchGroupLeader

Applications are invited for outstanding early-career scientists (2-8 years postdoc experience), interested in starting their own independent research group at the Vetmeduni Vienna.

We are aiming to attract exceptional candidates, who will prepare an application together with a professor of the Vetmeduni Vienna for the current call for young investigators by the Vienna Science and Technology Fund (WWTF): http://www.wwtf.at/upload/VRG14_web_v1.pdf In the case of funding through the WWTF, the candidate will receive up to 1.6 million EURO for a period of 6-8 years. After the WWTF funding period and a successful evaluation the candidate will be offered a Senior Scientist position at the Vetmeduni Vienna.

Interested candidates should contact

Prof. Dr. Christian Schlötterer

Christian.schloetterer@vetmeduni.ac.at

Deadline: 15.5.2014

Christian Schlötterer Institut für Populationsgenetik Vetmeduni Vienna Veterinärplatz 1 1210 Wien Austria/Europe

phone: +43-1-25077-4300 fax: +43-1-25077-4390 http://www.vetmeduni.ac.at/en/population-genetics/ Vienna Graduate School of Population Genetics http://www.popgen-vienna.at schlotc@gmail.com

Other

ASN workshop proposals

Are you organizing a workshop for 2015 or the near future?

The American Society of Naturalists provides workshop support to help defray the cost to students for attending. In particular, ASN is interested in sponsoring workshops for graduate students that provide training in modeling, data analysis, or other professional skills. The ASN workshop committee anticipates supporting 1-4 workshops per year at a rate of $1000-2000 each, which can be used towards workshop expenses or deferment of student fees. The application for workshop support should include descriptions of: the workshop (including tangible benefits to participants), venue, procedures for selecting participants, anticipated number of participants, and a budget that includes plans for use of ASN funds. Applications should be submitted as a pdf on or before 15 May 2014 to mbutler@hawaii.edu and should carry the label 'ASN Workshop Sponsorship' in the subject line to assure full consideration. Inquiries should be directed to Marguerite A. Butler at the same address.

Recent workshops (co-)sponsored by the American Society of Naturalists:

2013 - present "Workshop on Molecular Evolution", organized by D. Hillis and M. Sogin at MBL (student applications due 4/15 http://hermes.mbl.edu/education/courses/special_topics/mole.html)

2012 "Mathematical modeling in evolutionary ecology" by H. Kokko - at the Joint Congress on Evolutionary Biology in Ottawa

2012 "Graduate Workshop: The tree of sex - a comprehensive synthesis of sex determination systems in eucaryotes" by D. Bachtrog, J. Mank, and K. Peichel - at the Joint Congress on Evolutionary Biology at Ottawa

2011 - present "Workshop on Evolutionary Quantitative Genetics", organized by S. Arnold and J. Felsenstein at NESCENT

mbutler808@gmail.com

CLUMPP and DISTRUCT answers

"A few weeks ago I posted the following query "Does anyone have a user-friendly way of inputting data into CLUMPP and DISTRUCT? CLUMPP averages results across STRUCTURE simulations once K has been selected, and DISTRUCT produces the STRUCTURE figure.The challenge is that both are command-line programs, and DISTRUCT mac version seems broken (however, I assume PC version is OK).

Dent Earl and Bridgett vonHoldt produced an great solution for processing STRUCTURE output. A similar solution for CLUMPP and DISTRUCT would be most welcome.

(Earl, D. A., vonHoldt, B. M., 2011. STRUCTURE HARVESTER: a website and program for visualizing

STRUCTURE output and implementing the Evanno method. Conservation Genetics Resources 4, 359-361, doi:10.1007/s12686-011-9548-7.)“

Many thanks to those who replied. Their answers are found at http://molecularfisherieslaboratory.com.au/answers-to-technical-query-posted-on-evoldir/“
Thanks, Jenny

Jennifer Ovenden <j.ovenden@uq.edu.au>

CLUMPP and DISTRUCT answers 2

The link in the email is giving problems.

Currently it is http://molecularfisherieslaboratory.com.au/answers-to-technical-query-posted-on-evoldir/“ It needs to be (i.e. With the “ removed at the end) http://molecularfisherieslaboratory.com.au/answers-to-technical-query-posted-on-evoldir/ Can you repost this email?

Thanks, Jenny

“A few weeks ago I posted the following query ”Does anyone have a user-friendly way of inputting data into CLUMPP and DISTRUCT? CLUMPP averages results across STRUCTURE simulations once K has been selected, and DISTRUCT produces the STRUCTURE figure.The challenge is that both are command-line programs, and DISTRUCT mac version seems broken (however, I assume PC version is OK).

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Thanks, Jenny

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** New UQ email address** j.ovenden@uq.edu.au

Jennifer Ovenden http://molecularfisherieslaboratory.com.au http://www.uq.edu.au/sbms/staff/jennifer-ovenden From: Richard Coleman <richard.colema@gmail.com> Date: Thursday, 3 April 2014 6:52 pm To: Jennifer Ovenden <j.ovenden@uq.edu.au> Subject: Fwd: Other: CLUMPP_and_DISTRUCT.answers

Hi Jenny,

Thanks for asking this question! I am going through the exact same issue at this very moment. I was wondering if you had a working link to the answers you compiled? The link that is provided leads to an empty page.

Regards, Richard

—-

Richard Coleman Graduate Research Assistant, Toonen-Bowen Lab NSF Graduate Research Fellowship Program Fellow At-Large Representative, UH Graduate Student Organization Executive-at-Large for Oahu, UH Student Caucus

Hawai'i Institute of Marine Biology University of Hawai'i, Manoa|Department of Biology Coconut Island | PO Box 1346 | Kane'ohe, HI 96744 '916.524.3734 | - rcolema@hawaii.edu | richard.colema@gmail.com

EthidiumBromide alternative answers

Dear EvoDir members:

Please, find here below a summary of the answers I got from all of you about question on DNA stain.

Thank you very much for your very useful suggestions!

Cheers,

Filippo

—–

1. The idea that Ethidium bromide is dangerous, especially at the quantities used to stain gels, is probably false, and is certainly not based on sound mechanism nor strong epidemiological evidence. The article below is very interesting: http://goo.gl/AJKSup For staining DNA on agarose, our labs use Gel red which is no where as toxic as ethidium bromide http://www.bioscience.co.uk/site/user/ page.phtml?page_id 22&search=gel+red&productgrp=OTHER&sid=tgtk74337

Did you try SYBR Safe from Invitrogen? We have been using it for the past 9 months now and it is really reliable (we have even reduced the concentration by half).

4. We use a product called Gel Red. It works well. Not sure who would carry it in Europe, but VWR carries it in the states: http://biotium.com/technology/gelred-gelgreen-nucleic-acid-gel-stains/ 5. Maybe GelRed could help you (http://biotium.com/technology/ gelred-gelgreen-nucleic-acid-gel-stains/). During my last internship, I used it. It is supposed to be non-toxic, but my supervisor was not sure that degradation pruducts were non-toxic.

Have you tried RedSafe? Here is as example: http://www.chembio.co.uk/ product_detail.php?product_id0

We use Midori green it's just as good if not better than ethidium bromide and less toxic.

You may find this blog post helpful: http:// rrresearch.fieldofscience.com/2006/10/heresy-about-ethidium-bromide.html

9. We use GelRed from Biotium. It is quite bright and works with the same filters as ethidium bromide.

10. We use EZ-Vision: http://www.amresco-inc.com/home/products/best- sellers/EZ-Vision.cmsx

I have been using a product called SafeView by NBS biologicals: http://www.nbsbio.co.uk/nbs-sv1 12. In our population genetics lab, we use a product called GelRed, manufactured by Biotium. It gives us very good results. Bands are easily visible on the 1% and 2% agarose gels we use. We use the standard safety and handling procedures as those with ethidium bromide (gloves, gelred only glassware, contamination area, etc), but it is reported to be non-toxic and non-mutagenic. I hope this helps!

I use EZ-vision by Amresco. The RNA version also works.

We use SafeView (www.nbsbio.co.uk/nbs-sv1) and have never had any problems!

My lab uses SYBR Safe with a Blue-Light source. It works nearly as well as Ethidium and is much safer: http://www.lifetechnologies.com/ us/en/home/life-science/dna-rna-purification-analysis/nucleic-acid-gel-electrophoresis/dna-stains/sybr-safe.html

16. We use SybrSafe - it works nearly as well as EtBr: http:// www.lifetechnologies.com/us/en/home/life-science/dna-rna-purification- analysis/nucleic-acid-gel-electrophoresis/dna-stains/sybr-safe.html

Try Nancy-520 from Sigma: http://www.sigmaaldrich.com/life-science/ cell-biology/detection/learning-center/nancy-520.html Nancy seems like a nice alternative to SYBR and ethidium bromide, but I've never used it.

We've had success with SYBR Safe DNA gel stain for >7 years in the Johnson Lab, and, given it produces comparable results while being much safer than ethidium bromide, several other labs use it here on campus at BYU. If there is a chance you could stick with SYBR, maybe you could explain the problem in further detail, and then people could help you arrive at a solution with SYBR. So far, it remains unclear why these other options haven't worked for you.

We use a product called GelRed from Biotum. It works quite wells as an "in-gel" or "post-gel" stain. http://biotium.com/technology/gelred- gelgreen-nucleic-acid-gel-stains/

We use the GelRed Nucleic Acid Gel Stain from Biotium (http:// biotium.com/product/gelredtm-nucleic-acid-gel-stain-10000x-in-water/) and we have satisfactory results. Here is our protocol:

Mix 1

4 mg of BFB (Bromophenol blue)

1 ml of mili-Q Water

Mix 2

174 ul of Mix 1

250 ul of glycerol

576 ul of mili-Q Water

Loading Solution

1 ul of GEL RED

999 ul of Mix 2

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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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EvolutionaryBiol LearningLessons

I have developed a series of active learning lessons in evolutionary biology (undergraduate level). A list and brief description of the lessons are provide at http://spot.colorado.edu/~am/Site/Teaching.html I am interested in having folks test these lessons and provide feedback. There are descriptions of two lessons available for download with more coming depending on interest.

Andrew Martin Professor University of Colorado A mind once stretched by a new idea never regains its original dimensions.

Andrew Martin <Andrew.Martin-1@colorado.edu>

Evolution video

Submit your best evolution-themed video for screening at this year's Evolution meeting

Deadline: May 31

Scientists and science communicators of all stripes are invited to enter the fourth annual NESCent Evolution Video Competition. To enter, please submit a video that explains a fun fact, key concept, compelling question, or exciting area of evolution research in three minutes or less. Entries may be related or unrelated to your own research, and should be suitable for use in a classroom (K-12, undergraduate, graduate...your choice). Animations, music videos, and mini documentaries are all fair game. The finalists will be screened at the Evolution 2014 conference in Raleigh, NC < http://evolution2014.org/ >. You don't need to attend the conference to enter. The first- and second-place winners will receive travel awards to attend the scientific meeting of their choice. All videos submitted by May 31 are eligible to win.

For more information visit filmfestival.nescent.org/

Robin Ann Smith, Ph.D. Science Writing and Communications National Evolutionary Synthesis Center 2024 W. Main Street, Suite A200 Durham, NC 27705 Tel: 919-668-4544 rsmith@nescent.org

http://robinannsmith.com/ http://twitter.com/NESCent www.nescent.org/ ras10@duke.edu

Inclusive fitness

Royal Society Publishing has just published Inclusive fitness: 50 years on, compiled and edited by Andy Gardner and Stuart A West. This content can be accessed at http://bit.ly/PTB1642 A print version is also available at the special price of Â£35.00. You can order online via the above web page (enter special code TB 1642 when prompted) or, alternatively, you can contact debbie.vaughan@royalsociety.org

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Felicity.Davie@royalsociety.org Felicity.Davie@royalsociety.org

Indel aa selection answers

Dear Brian and Evoldir Members,

some time ago, I had asked a question in Evoldir regarding examples of aa indels. The answers were very helpful for me, and I thank everybody.

Here is a compilation of the replies. I also put the emails of the people who gave the replies to facilitate further communications.

all the best pavlos

—

Many examples of conserved insertions and deletions that are evolutionarily highly significant are described in our published work. Most of the conserved indels reported thus far are for different groups of microorganisms, and information for their sequence alignments and group-specificities can be found at the following website (Microbial Evolution and Molecular Signatures < www.microbialevolution.com > and the references described there. You may also look at the Wikipedia page on *Conseved Signature Indel*s, which describes significance and some general characteristics of the Conserved Indels in protein sequences. Further, as shown in the following work "Singh, B. and Gupta, R. S. (2009) Conserved inserts in the Hsp60 (GroEL) and Hsp70 (DnaK) proteins are essential for cellular growth. *Mol Genet Genomics* 281*,* 361-373", conserved indels in a number of proteins have been shown to be essential for the group of organisms where they are found. Hopefully, the information provided will help clarify the evolutionarry/functional significance of conserved indels.

by gupta@mcmaster.ca

—

try the fast-evolving genes for venom proteins in tropical conus snails http://phys.org/news/2012-04-snails-fast-genes-predatory-refine.html also the MHC genes and, as anthropo-selected artifacts, the monoclonal antibodies that have found major medical or industrial success.

by marcos.antezana@gmail.com

—–

The lentivirus (such as HIV-2, HIV-2, EIAV, FIV) envelope protein grows and shrinks in length over very short time spans. The "variable loops" on the surface of the envelope shield the virus from the host immune system. The longer the lops, the more of the of the conserved parts of the envelope are hidden. But those conserved parts are needed to bind to the host cell surface receptors (CD4 and CCR5 host proteins).

You can download alignments of HIV-1 envelope here:

http://www.hiv.lanl.gov/content/sequence/NEWALIGN/align.html Shorter V1-V2 loops are favored at transmission and early in the infection process before the host immune system has created neutralizing antibodies which bind the CD4 receptor-biding site of the envelope. So the loops tend to grow over time in each infected individual and then shorter ones are selected at transmission. Of course this is only on average, and not a solid rule that is always followed.

I did a PubMed search for [amino acid insertion] and found these:

Diversity and Complexity of the Mouse Saa1 and Saa2 genes.< http://www.ncbi.nlm.nih.gov/pubmed/24521869 >

Mori M, Tian G, Ishikawa A, Higuchi K.

Exp Anim. 2014;63(1):99-106. PMID: 24521869

A unique *insertion* of low complexity *amino acid* sequence underlies protein-protein interaction in human malaria parasite orotate phosphoribosyltransferase and orotidine 5'-monophosphate decarboxylase.< http://www.ncbi.nlm.nih.gov/pubmed/24507637 >

Imprasittichail W, Roytrakul S, Krungkrai SR, Krungkrail J.

Asian Pac J Trop Med. 2014 Mar;7(3):184-92. doi: 10.1016/S1995-7645(14)60018-3. PMID: 24507637

The 19-*amino acid insertion* in the tumor-associated splice isoform Rac1b confers specific binding to p120 catenin.< http://www.ncbi.nlm.nih.gov/pubmed/20395297 >

Orlichenko L, Geyer R, Yanagisawa M, Khauv D, Radisky ES, Anastasiadis PZ, Radisky DC.

J Biol Chem. 2010 Jun 18;285(25):19153-61. doi: 10.1074/jbc.M109.099382. Epub 2010 Apr 15. PMID: 20395297

Extension of the hydrolysis spectrum of AmpC beta-lactamase of Escherichia coli due to *amino acid insertion* in the H-10 helix.< http://www.ncbi.nlm.nih.gov/pubmed/17586561 >

Mammeri H, Poirel L, Nordmann P.

J Antimicrob Chemother. 2007 Sep;60(3):490-4. Epub 2007 Jun 22. Erratum in: J Antimicrob Chemother. 2008 Apr;61(4):971. PMID: 17586561

A 59 *amino acid insertion* increases Ca(2+) sensitivity of rbslo1, a Ca2+ -activated K(+) channel in renal epithelia.< http://www.ncbi.nlm.nih.gov/pubmed/10568789 >

Hanaoka K, Wright JM, Cheglakov IB, Morita T, Guggino WB.

J Membr Biol. 1999 Dec 1;172(3):193-201. PMID: 10568789

A novel isoform of rat estrogen receptor beta with 18 *amino acid

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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

Intron evolution

Dear Evoldir Members,

I'm wondering if anyone could point me toward some recent comprehensive reviews, dedicated websites, or specific bodies of work on intron sequence evolution in protein-encoding genes? I am especially interested in conceptual papers and/or any that might include new tools for finding and comparing specific sequence themes independently of intron length, potential miRNA encoding regions, miRNA target sites, etc.

thanks in advance for any help you can give.

Bruce Turner

fishgen@vt.edu

KJT survey txt

* KJT Group is a healthcare market research firm (www.kjtgoup.com) * We are looking to field a study for a large multinational, medical device client, regarding next-generation sequencing (NGS) trends as they relate to target enrichment/sequence. * Target survey respondents include

* Title/role: Principle Investigator, Investigator, Scientist, Research Scientist, Research Associate/Assistant, Director or Co-Director, Genomics Operations Manager * Works in/for: University, Medical school, Pharmaceutical or Biotech company, Agricultural company, Government Laboratory, Clinical Laboratory * Have access to instrument for DNA/RNA sequencing or work using it * Roche, Illumina, Life Technologies, or Pacific Biosciences * Decision maker for capital equipment (reagents and kits) or hands on user of equipment * Number of genes analyzed (to be used for classification purposes. Depending on market size we may adjust as appropriate once we have a better understanding.)

* Number of publications * We follow CASRO (http://kjtgroup.com/about/memberships-affiliations/) guidelines and personal info is not released to client * We only collect personal information in order to send $honoraria to study participants * Participant expectations * 25-minute web-assisted telephone interview * Incentive $amount TBD

Any interested participants would be able to link to a screener/scheduler.

Mike Michael Mooney KJT GROUP, INC. Field Operations Manager

Email: michaelm@KJTgroup.com | Website: http://KJTgroup.com Office: 6 East Street, Honeoye Falls, NY 14472 Telephone: 585.582.5053 | Fax: 585.624.8052

LIMS for EvolBiol

Dear Evol-dir community,

I would appreciate recommendations for laboratory information management systems for academic labs focused on molecular biology. As our lab does mostly population genetics-oriented research on numerous species, we are accumulating more samples and associated information than is easy to keep track of in spreadsheets and our heads. Ideally this LIMS would accommodate the use of barcodes for samples and storage locations (i.e. boxes, freezers), provide easy recording of actions on samples like extraction and library preparation, list the outcomes of those events (degraded, failed, consumed, etc.), and connect to products of those events (e.g. links to NGS fastq files).

I am most interested in relatively simple out-of-the-box solutions or MS Access templates that won't break the bank. Any suggestions or experience would be helpful. Thanks!

Stuart Willis

swillis4@gmail.com

MorphoJ website

Dear all,

My name is Emma Chance and I am a final year student at the University of Manchester working on my dissertation project. I have created a website to help people beginning or switching to using MorphoJ, for analysing geometric morphometric data, get started with fewer difficulties and have a greater understanding into the rationale and purpose behind a few of the key statistical analyses. I would really appreciate it if you could take a look at my website, and spend no longer than 5 minutes of your time to answer a quick survey about how useful you have found my resource and any improvements that I could make.

Thank you very much for your time. Kind regards, Emma Chance

http://personalpages.manchester.ac.uk/student/emma.chance/Homepage/Homepage.htm
emma.l.chance@gmail.com

MouseSamples MD Delaware

Hello all,

I am working on a study of the evolutionary genetics of house mice (Mus musculus), and I am looking for fresh tissue samples from populations of house mice specifically from the eastern shore of Maryland and anywhere in Delaware.

Because the tissue must be relatively fresh, I am specifically looking for anyone who is currently, or will soon be, doing small mammal trapping (whether for research purposes or to remove a nuisance species), and who might be willing to collect some tissue from any house mice collected. I can provide a sampling kit and pay for shipping, so the commitment would mostly be in terms of time (which should be minimal if part of an established trap line or while trying to remove a mouse infestation from a home or farm). If you are interested in helping out with this study, please email me at achunco@gmail.com and I'd be happy to provide more details about this study.

Thank you in advance,

Amanda

Amanda Chunco Environmental Studies Elon University achunco@gmail.com

achunco@elon.edu

Photos population geneticists

For evoldir:

During the 1960s and 1970s I frequently took photos of people in my field, especially theoretical population geneticists.

I have now posted 40 of them, scanned from color slides, in a Flickr album here:

https://www.flickr.com/photos/123558304@N02/sets/72157644164299043# These are many of the best ones, but I do hope to add more later.

Joe Felsenstein joe@gs.washington.edu Department of Genome Sciences and Department of Biology, University of Washington, Box 355065, Seattle, WA 98195-5065 USA

Joe Felsenstein <joe@gs.washington.edu>

Phyloseminar Bastien Boussau Apr22

Bastien Boussau Université de Lyon Gene tree-species tree methods for comparative genomics Tuesday, April 22, 2014 9:00 AM PDT

In this second talk of our series on genome-scale phylogeny, I build upon Gergely's introduction and present the modelling assumptions and algorithmic details behind some of the methods we and others have developed. There will be two parts to this talk. I start with the model of gene duplications and losses implemented in PHYLDOG. I present the assumptions we make and the shortcuts we take to improve the program's efficiency, and show some results on real and simulated sequence data. I notably show problems that arise when the program is confronted with data generated with a model of incomplete lineage sorting (Rasmussen and Kellis, 2012), and present avenues of research to find solutions to these problems. In the second part, I present our current efforts to use our model of gene duplication, loss, and transfer (Szöllosi et al, 2013) to infer a species tree in which speciation nodes are ordered in time. I briefly remind the forgetful viewer of what this model does and how it works, and I then explain how we devise a new MCMC algorithm to use it on data sets containing dozens of species and thousands of gene families. I finish with some perspectives of our plans uniting gene tree-species tree models and databases of gene families and phylogenetic trees.

For more details, see http://phyloseminar.org/ . Frederick "Erick" Matsen, Assistant Member Fred Hutchinson Cancer Research Center http://matsen.fhcrc.org/ ematsen@gmail.com

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Phyloseminar EricTannier Apr30

Evolution of genome organization Eric Tannier INRIA, Université de Lyon

Genome rearrangements were discovered and used to build molecular phylogenies in the 1930s. They are implied in many cancers and their evolutionary role might be of primary importance. But the mathematical and computational tools to model rearrangements are still not as efficient as the ones developed later for local mutations as nucleotide or amino-acid substitutions. In this seminar I will report the attempts to integrate genome organisations in the usual models of genome evolution. I will explain how this can improve the inference of phylogenies, as well as ancestral genomes.

For more information, see http://phyloseminar.org/- . Frederick "Erick" Matsen, Assistant Member Fred Hutchinson Cancer Research Center http://-matsen.fhcrc.org/ ematsen@gmail.com

Phyloseminar Gergely

Mini-course on genome-scale phylogeny, talk 1 of 3.

Inferring gene trees with species trees Gergely Szöllõsi Eötvös Loránd Tudományegyetem Tuesday, April 15, 2014 9:00 AM PDT

Molecular phylogeny has focused mainly on improving models for the reconstruction of gene trees based on sequence alignments. Yet, most phylogeneticists seek to reveal the history of species. Although the histories of genes and species are tightly linked, they are seldom identical, because genes duplicate, are lost or horizontally transferred. Building models describing the relationship between gene and species trees can thus improve the reconstruction of gene trees when a species tree is known, and vice-versa. Several approaches have been proposed to solve the problem in one direction or the other, but in general neither gene trees nor species trees are known. Only a few studies have attempted to jointly infer gene trees and species trees.

I introduce models that describe the relationship between gene trees and species trees. I begin with models that account for gene duplication and loss, and subsequently introduce models that account for the horizontal transfer of genes. I review results from simulations as well as empirical studies on genomic data that show that combining gene tree-species tree models with models of sequence evolution improves gene tree reconstruction. In turn, these better gene trees provide a better basis for studying genome evolution or reconstructing ancestral chromosomes and ancestral gene sequences. I also discuss the possibility of extracting information on the timing of speciation events from ancient horizontal transfer events.

Frederick "Erick" Matsen, Assistant Member Fred Hutchinson Cancer Research Center http://-matsen.fhcrc.org/ ematsen@gmail.com

Plant sequencing projects

Dear EvolDir community:

We are planning an experiment in which we subject plants in the field to specific selective pressures for multiple generations and then use RNASeq on selected and control plants to examine changes in the gene expression associated with selection under these pressures. However, we are having difficulty identifying sequenced plant species on which we can map RNASeq results that are suitable to our requirements (1. Grow in the cool temperate climates found in Scotland; 2. Grow in grasslands; 3. Associate with arbuscular mycorrhizal fungi (e.g. no pines or Brassicas)).

Thus I ask: Do you know of any ongoing sequencing projects for the following plant species (or close relatives of the following plant species)?

Plantago lanceolata, Centaurea cyanus, Daucus carota (carrot), Trifolium pratense, Pisum sativa (pea), Bromus hordeaceus, Avena fatua or any onion species. Any help you could provide or alternatives you could suggest would be greatly appreciated!

If your group, or a group you know, is involved in such a sequencing project we would like to discuss the possibility of using the genome map in 4-5 years. We would, of course, keep all information confidential until publication. Please contact me offlist using the information below to discuss.

Thank you! Alison

Alison Bennett, Ph.D., FRES Research Leader James Hutton Institute née Scottish Crop Research Institute Errol Road Invergowrie Dundee DD2 5DA Alison.Bennett@hutton.ac.uk 044 (0) 1382 568700 ext 7567

Alison.Bennett@hutton.ac.uk

Rearing Chambers

We are looking for an insect rearing chamber and got a great price from Powers Scientific but I am unfamiliar with the company or their chambers. Does anyone have one or know of them? Would you recommend them?

Thank you in advance for your time!

Diane Ramos, PhD

Assistant Professor Natural Sciences Department Daemen College 4380 Main St. Amherst, NY 14226

Duns Scotus 329 (716) 839-8560 dramos@daemen.edu 716.839.8560

dramos@daemen.edu

SelectiveSweep Webserver

Dear Evoldir,

We are developing a web-server for performing selective sweep analyses using either OmegaPlus (LD-based) or SweeD (SFS-based). The user has to upload data (FASTA, VCF, ms or MaCS format), insert analysis parameters and provide his email. Then results will be submitted to his mailbox.

Please visit the page: http://pop-gen.eu/wordpress/server-for-selective-sweep-detection for further information. The tools are described in the following papers:

SweeD: likelihood-based detection of selective sweeps in thousands of genomes. < http://www.ncbi.nlm.nih.gov/pubmed/23777627 > Pavlidis P, Å½ivkovic D, Stamatakis A, Alachiotis N., Mol Biol Evol. 2013 Sep;30(9):2224-34.

OmegaPlus: a scalable tool for rapid detection of selective sweeps in whole-genome datasets. < http://www.ncbi.nlm.nih.gov/pubmed/22760304 > Alachiotis N, Stamatakis A, Pavlidis P., Bioinformatics. 2012 Sep 1;28(17):2274-5.

Kind regards, pavlos

Pavlos Pavlidis, PhD

pavlidisp@gmail.com

Foundation for Research and Technology - Hellas Institute of Molecular Biology and Biotechnology Îikolaou Plastira 100, Vassilika Vouton GR - 711 10, Heraklion, Crete, Greece

Pavlos Pavlidis <pavlidisp@gmail.com>

Software BEAST v2 1 2 released

BEAST v2.1.2

We are pleased to announce the release of BEAST v2.1.2.

The main improvements are: o BEAUti handles multiple partitions more conveniently o improved package management o fix bug in *BEAST template o added functionality (FASTA support, stochastic distributions, *BEAST operator weighting, etc.) o support for more packages.

A more complete list can be found here http://blog.beast2.org/2014/03/30/what-is-new-in-beast-v2-1-2-and-its-packages/ To install, select the package for your operating system at

http://beast2.org/ BEAST core development team

Remco Bouckaert <remco@cs.auckland.ac.nz>

Species Ontology survey

Dear Biologist,

A small collaborative effort has been formed with the goal of exploring contemporary opinions on the nature of species. With competing and sophisticated operational strides in mathematics, techniques and analyses, and data handling, it is an exciting time to once again explore the topic of species ontology. Therefore, we ask for your help with this endeavor as the community of systematic biologists. It would be most appreciated if you would take the brief survey by clicking on the link at the bottom of this letter. The survey deals with opinions on the nature of species, and will take very little time to complete (< 5 minutes). Please read the rest of this information letter thoroughly before proceeding. Thank you for your help.

Auburn University College of Science and Mathematics Department of Biological Sciences

(NOTE: DO NOT AGREE TO PARTICIPATE UNLESS IRB APPROVAL INFORMATION WITH CURRENT DATES HAS BEEN ADDED TO THIS DOCUMENT.)

=== *INFORMATION LETTERfor a Research Study entitled“Species Perceptions: Ontological evidence for a Biological Divide”*

You are invited to participate in a research study to explore contemporary opinions on the nature of species. The study is being conducted by Christopher Murray (PhD candidate), under the direction of Dr. Craig Guyer, Professor in the Auburn University Department of Biological Sciences. You were selected as a possible participant because you participate in evolutionary biology at a professional level and are age 18 or older.

What will be involved if you participate? Your participation is completely voluntary. If you decide to participate in this research study, you will be asked to respond to six opinion-based questions. Your total time commitment will be approximately five minutes. If you are invited to take the survey multiple times, please only complete it once.

If you change your mind about participating, you can withdraw at any time by closing your browser window. If you choose to withdraw, your data can be withdrawn as long as it is identifiable. Once you've submitted anonymous data, it cannot be withdrawn since it will be unidentifiable. Your decision about whether or not to participate or to stop participating will not jeopardize your future relations with Auburn University, the Department of Biological Sciences or the investigators.

Any data obtained in connection with this study will remain anonymous. We will protect your privacy and the data you provide by never recording IP addresses, panel information or identifying information using the Qualtrics survey system options. Information collected through your participation may be published in a professional journal, and/or presented at a professional meeting.

If you have questions about this study, please contact Christopher M Murray at murracm04@gmail.com or Caleb D. McMahan at cmcmah2@tigers.lsu.edu.

If you have questions about your rights as a research participant, you may contact the Auburn University Office of Human Subjects Research or the Institutional Review Board by phone (334) 844-5966 or e-mail at hsubjec@auburn.edu or IRBChair@auburn.edu.

HAVING READ THE INFORMATION ABOVE, YOU MUST DECIDE IF YOU WANT TO PARTICIPATE IN THIS RESEARCH PROJECT. IF YOU DECIDE TO PARTICIPATE, PLEASE CLICK ON THE LINK BELOW. YOU MAY PRINT A COPY OF THIS LETTER TO KEEP.

Christopher M Murray__________4/21/14______________ Investigator Date Caleb D McMahan____________4/21/14________________ Co-Investigator Date The Auburn University Institutional Review Board has approved this document for use from 4/3/14 to 4/2/17. Protocol #14-141 EX1404

===*LINK TO SURVEYhttps://auburn.qualtrics.com/SE/?SID=SV_54HAzRvBFqFv2cJ Caleb McMahan <cmcmah2@tigers.lsu.edu>

UBasel VolFieldAssist ButterflyDispersal

Field assistants in butterfly evolutionary ecology

We are looking for voluntary field assistants to participate in a research project on dispersal and behavioral ecology of butterflies. The project is run by the Research Station Petite Camargue Alsacienne, University of Basel (www.camargue.unibas.ch, PD Dr. Valentin Amrhein). Fieldwork will be done from June to August 2014, at the Research Station Petite Camargue Alsacienne in France, about 10 km north of Basel (Switzerland).

Field assistants will participate in a capture-mark-recapture study and in translocation experiments, and some knowledge on identification and handling of butterflies would be an advantage. We cannot cover travel expenses, but we offer free accommodation and use of the infrastructure at the research station. Field assistants will receive a compensation of 600 Euros for the field season to cover food expenses. Applicants are expected to stay for the entire field season from beginning of June until the end of August.

The positions will be filled as soon as possible. Applications should be in English and should include, in one single pdf or word file, a curriculum vitae and a letter of motivation. Please send applications by email to the following address:

PD Dr. Valentin Amrhein Zoological Institute University of Basel pca.recherche@orange.fr

Valentin Amrhein <pca.recherche@orange.fr>

Undergraduate Evol course

Hi,

Next semester, I will be teaching an undergraduate course on Vertebrate form and function, which will have a large component of functional morphology.

The course will include a weekly 2h 30 min lab, which should complement the lecture part. I would like to make the lab more interesting and practical than just focusing it on a comparative study of bones/skeletons and anatomies.

I was wondering if anyone has suggestions on how I could make the lab more interesting and possibly include some research - based experience for the students.

Thanks in advance, Ylenia

–

Dr. Ylenia Chiari Assistant Professor

Department of Biology University of South Alabama LSCB 123 5871 USA Dr. N. Mobile, AL 36688 USA

Phone: (251) 460-6331 Fax: (251) 414 8220

Email yle@yleniachiari.it

Web http://www.yleniachiari.it http://www.usouthal.edu/biology/faculty/chiari/chiariindex.html Ylenia Chiari <yle@yleniachiari.it>

Undergraduate Summer Research SyracuseU

The lab of Dr. Scott Pitnick at Syracuse University in central New York is looking for a mature, motivated undergraduate for NSF REU (Research Experience for Undergraduates) research in sexual selection and speciation biology. The successful candidate will work with the PI, a technician, postdoctoral fellows and PhD students to conduct experiments on three different model dipteran study systems: (1) the fruit fly Drosophila melanogaster and related species, (2) the yellow dung fly Scathophaga stercoraria and (3) the dung fly Sepsis punctum. Investigations will be conducted in the laboratory, with artificial pastures in a greenhouse and at local cattle and sheep pastures. The successful candidate will potentially participate in projects conceptually related to postcopulatory sexual selection, rapid evolutionary diversification, mechanisms of reproductive isolation between sibling species, mechanisms of ejaculate-female interaction, and alternative male reproductive tactics. She/he will receive training and experience in many to all of the following skills: rearing, maintaining and handling fly cultures; collecting virgins and setting up mating crosses; dissecting male and female reproductive tissues; preparing and staining sperm slides; microscopy and use of camera software to quantify sperm quantity, quality, performance and fate within the female reproductive tract. The student will be on campus from May 26-Aug. 15 (some flexibility allowed) and will receive a summer stipend of $4950. Only US citizens or permanent residents who are fully enrolled in undergraduate institutions are eligible. Please send an official transcript, a brief essay (no longer than one page) on your research interests, career goals and what you seek to gain from an REU experience, and provide contact information for two references to Dr. Pitnick at sspitnic@syr.edu. Deadline for application is April 30.

Dr. Scott Pitnick Professor of Biology Syracuse University Syracuse, NY 13244 USA (315) 443-5128 sspitnic@syr.edu http://biology.syr.edu/faculty/pitnick/pitnick.htm

sspitnic@syr.edu

PostDocs

ArizonaStateU EvolutionaryGenomics

[A pdf of this ad is available at http://cartwrig.ht/postdocs.pdf] The Cartwright Lab at Arizona State University in Tempe, AZ is seeking multiple Postdoctoral Research Associates in the areas of Evolutionary Genomics, Statistics, and Bioinformatics to develop methodologies and study evolutionary questions related to mutation and short-read sequencing. Successful applicants will join a rapidly growing and well-funded lab involved on a variety of active research projects and collaborations. Current projects include (1) the analysis of cilliate mutation accumulation lines, (2) the development of software for de-novo mutation detection from traditional and single-cell sequencing datasets, (3) the analysis of non-pathogenic somatic mutation patterns in mammals and plants, (4) the study of indel patterns across the tree of life, (5) characterizing mutations and fitness-landscapes of metabolically engineered microbes, (6) population genetics of malaria parasites, (7) the construction of phylogenies from short-read, whole genome datasets, and (8) simulation techniques for molecular evolution research.

The Cartwright Lab is part of the Center for Evolutionary Medicine and Informatics (CEMI), one of 10 research centers in 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. Members have the opportunity to develop both dry-lab and wet-lab research programs through interactions with both national and international collaborations.

As part of this project, the Postdoctoral Research Associates are expected to be able to:

1) Assemble microbial or metazoan genomes from short-read sequences and identify variable sites and regions. 2) Develop novel, high-throughput methodolo-

gies to study mutations from next generation sequencing of related individuals and cells. 3) Work closely with collaborators to customize methodologies to specific experimental designs.

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

Desired Qualifications: Experience working with genomes and evolutionary analyses; Knowledge of programming languages including R, Python, and C++; Knowledge of statistical methodologies; Experience with short-read sequencing

Application must contain: (1) Resume, (2) Cover Letter, (3) Names, addresses, and phone numbers of three professional references

Deadline for applications is May 1, 2014. Applications will continue to be accepted and considered until the job is filled/closed.

For more information see http://cartwrig.ht/lab/ or http://labs.biodesign.asu.edu/cartwright/ . 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.

A pdf of this ad is available at http://cartwrig.ht/-postdocs.pdf 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 Website: http://cartwrig.ht/ rcartwri@asu.edu

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BGPI Montpellier InvasiveAdaptations

Postdoctoral Position in modeling the genetics of adaptation of invasive populations

We seek to hire a post-doctoral research associate for a Grand Federative Project funded by the French Agropolis Fondation1 called BIOFIS "Bioagressors and invasive species: from individual to population to species". The project is dedicated to develop, coordinate and communicate research actions on bioagressors in Europe (insects, mites, trees, fungi and virus) and on their associated natural enemies.

Term and location: The position should start in December 2014 at the latest. Support is for one year. This position is co-supervised by E. Klein (INRA - BIOSP, Avignon France) and V. Ravigné (CIRAD - BGPI, Montpellier, France). We encourage the postdoctoral fellow to be based in Montpellier but being hosted in Avignon is also possible.

Eligibility: Agropolis Fondation typically considers applications from candidates that have not resided or carried out their main activity (work, studies, etc) in France for more than 12 months in the 3 years immediately prior to the date of submission of the proposal and that have obtained their PhD degree for no more than 3 years upon the date of application. However, we encourage excellent candidates not entirely fulfilling these conditions to contact us, as these might be funded if no other eligible candidate satisfies scientific requirements for the job.

Project: Bioinvasions have long been considered as purely ecological processes until researchers recognize that evolutionary processes such as drift and selection may play a substantial role in their success. Recently particular attention has been paid to evolutionary processes occurring during spatial expansions. Selection for different life-history strategies at the source and front of invasions is expected to affect the speed of spatial spread. The strong effects of genetic drift associated to the specific demography of an expansion (in particular successive funding effects distributed in space) may as well shape the neutral and selected diversity along invasion waves. To better understand the interaction between drift, selection, and dispersal, we wish to design and analyze spatially explicit simulation models allowing studying the spatial spread of beneficial/neutral/deleterious mutations during a colonization process. We are particularly interested in studying the effect of i) environmental heterogeneity and ii) non-standard mating systems (e.g., mixing sexual and asexual reproduction) on the process. In the end, these theoretical results may be confronted to population genetics data in different species.

This work is mainly theoretical in its present shape but it is expected to produce useful results for approaches aiming at detecting traces of selection during bioinvasions from the analysis of the spatial genetic structure of populations at a large number of loci (genome scan).

We seek a young researcher who combines with a strong conceptual background in evolutionary biology and some modeling skills (mathematics and computer science). Experience with programming, bioinformatics and theoretical population genetics is required. Skills in data analysis are not necessary but will be considered positively. Facility in writing is important. The post-doc will benefit by working as a member of the BIOFIS project team with an extent network of collaborators interested in dispersal, invasion biology, plant pathology, evolutionary biology and population genetics.

Contact: Virginie Ravigné. Virginie.ravigne@cirad.fr

1 Agropolis Fondation: http://www.agropolis-fondation.fr/ Virginie Ravigné Chercheuse CIRAD - Département BIOS - UMR BGPI

UMR PVBMT Station de Ligne-Paradis Pôle de protection des plantes 7 chemin de l'IRAT 97410 Saint-Pierre - Réunion

Tel : 0262 49 92 24 /06 92 32 04 97 Mail : Virginie.Ravigne@cirad.fr http://agents.cirad.fr/-index.php/virginie.ravigne

Virginie Ravigné <virginie.ravigne@cirad.fr>

BiKF Frankfurt BiodiversityModels

The Biodiversity and Climate Research Centre (BiK-F) has been founded by the Senckenberg Gesellschaft fuer Naturforschung, the Goethe-University Frankfurt am Main, and additional partners. It is funded by the Federal State of Hessen through its Initiative for the Development of Scientific and Economic Excellence (LOEWE). The mission of the centre is to carry out internationally outstanding research on the interactions of biodiversity and climate change at the organism level. The working group of Prof. Dr. Katrin Böhning-Gaese invites applications for a

Postdoctoral Researcher on “Intercomparisons of biodiversity models” Ref. #B20b

The project contributes to the EU COST Action “Harmonizing Global Biodiversity Modelling HarmBio (http://harmbio.uom.gr/)”. This action aims for the harmonization of current models and datasets of terrestrial, freshwater and marine biodiversity to improve the reliability of future projections of biodiversity change. This cross community initiative aims to accelerate the development of transparent and scientifically robust biodiversity models, through validation, calibration and inter-comparison of models and data.

Your tasks: â Facilitating systematic inter-comparisons and benchmarking of biodiversity models. Model comparisons will involve comparing outputs of different models among models as well as with biodiversity data. â Facilitating the development of standards for model-model and model-data comparisons â Leading conceptual and original scientific publications as well as preparing grant proposals â Facilitating exchange and collaborations with other members of the COST Action â Organizing and leading international workshops

Your profile: â PhD in ecology, biodiversity modelling, statistics, or a related field â Solid background in biodiversity modelling, advanced statistics and macroecology â Very strong publication record â Experience and interest in working within an international collaborative research group â Very good organizational and excellent written and oral communication skills

Salary and benefits are according to a public service position in Germany (TV-H E13). The contract shall start on July, 1st 2014 and will initially be restricted until December, 31th 2015. An extension of the contract is possible. The Senckenberg Research Institute supports equal opportunity of men and women and therefore strongly invites women to apply. Equally qualified handicapped applicants will be given preference. The place of employment will be Frankfurt am Main, Germany. The employer is the Senckenberg Gesellschaft fuer Naturforschung. Funding of the position is subject to final approval.

Please send your application before April, 23rd 2014 preferentially by e-mail (attachment in a single pdf document), mentioning the reference of this position (Ref. #B20b) and including a letter outlining your suitability for the post, a detailed CV, contact details of 2 references and pdfs of five publications to the Administrative Director: Herrn Dr. Johannes Heilmann c/o Senckenberg Gesellschaft für Naturforschung Senckenberganlage 25 60325 Frankfurt E-Mail: recruiting@senckenberg.de Your application should contain the information on where you found the job advertisement.

For scientific enquiries please get in contact with Prof. Dr. K. Böhning-Gaese (email: katrin.boehning-gaese@senckenberg.de.

Frankfurt, 26.03.2014

Dr. Johannes Heilmann Administrative Director

Jan.Wenner@senckenberg.de

BiKF Frankfurt EvolutionSeedDispersal

The Biodiversity and Climate Research Centre (BiK-F) has been founded by the Senckenberg Gesellschaft fuer Naturforschung, the Goethe-University Frankfurt am Main, and additional partners. It is funded by the Federal State of Hessen through its Initiative for the Development of Scientific and Economic Excellence (LOEWE). The mission of the centre is to carry out internationally outstanding research on the interactions of biodiversity and climate change at the organism level. The working group of Prof. Katrin Böhning-Gaese invites applications for a

Postgraduate Researcher in “Seed dispersal and pollination interactions of birds” Ref. #B61

The project is part of the DFG Research Group Kilimanjaro (www.kilimanjaro.biozentrum.uni-wuerzburg.de).

Your tasks: â Contribute to an ongoing PhD investigation of the impact of climatic factors and land-use intensity on the functional diversity of birds and their mutualistic interactions with plants â Intensive field work on birds and their fruit and flower resources along elevational and land-use gradients on Mt. Kilimanjaro, Tanzania â Monitoring of interactions using visual observations and digital cameras; analyses of camera recordings â If interested, statistical analysis of frugivore - plant interaction networks and publication of research results â Close collaboration with other members of the Research Group Kilimanjaro, in particular with a corresponding project on the functional diversity of bats

Your profile: â Master's degree in ecology or a related field â Solid background in community ecology and/or animal ecology â Experience in field work in a tropical country â Very good bird identification skills, interest in plants â Willingness to learn basics in Kiswahili â Very good organizational and oral communication skills â Ability to work independently; physical and mental endurance

Salary and benefits are according to a public service position in Germany (TV-H E13, 50%). The contract shall start approximately October 2014 and will be restricted to 18 months. The Senckenberg Research Institute supports equal opportunity of men and women and therefore strongly invites women to apply. Equally qualified handicapped applicants will be given preference. The place of employment will be Frankfurt am Main, Germany. The employer is the Senckenberg Gesellschaft fuer Naturforschung.

Please send your application before April, 23rd 2014 preferentially by e-mail (attachment in a single pdf document), mentioning the reference of this position (Ref. #B61) and including a letter outlining your suitability for the post, a detailed CV and contact details of 2 references to the Administrative Director: Herrn Dr. Johannes Heilmann c/o Senckenberg Gesellschaft für Naturforschung Senckenberganlage 25 60325 Frankfurt E-Mail: recruiting@senckenberg.de Your application should contain the information on where you found the job advertisement.

For scientific enquiries please get in contact with Prof. Dr. K. Böhning-Gaese (email: katrin.boehning-gaese@senckenberg.de.

Frankfurt, 26.03.2014

Dr. Johannes Heilmann Administrative Director

Jan.Wenner@senckenberg.de

ColdSpringHarborLabs ComputationalGenomics

MULTIPLE POSTDOCTORAL POSITIONS are available in Dr. Adam Siepel's research group in its new location at the Simons Center for Quantitative Biology at Cold Spring Harbor Laboratory, starting in September, 2014. The Siepel group specializes in the development of probabilistic models, algorithms for inference, prediction methods, and application of these methods in large-scale genomic data analysis. Of particular interest is research relevant to existing, NIH-supported projects in (1) human population genomics, including demography inference using Bayesian coalescent-based methods, inference of natural selection on regulatory and other noncoding sequences, and prediction of fitness consequences for noncoding mutations; and (2) transcriptional regulation in mammals and Drosophila, including the estimation of rates and patterns of transcriptional elongation from the GRO-seq data, prediction of transcription factor binding sites from DNase-seq data, and regulatory network inference based on joint patterns of transcription and binding in inducible systems. The research on transcriptional regulation will continue to be carried out in close collaboration with

Dr. John Lis at Cornell University.

Relevant recent papers including the following:

1. Rasmussen MD, Hubisz MJ, Gronau I, Siepel A. Genome-wide inference of ancestral recombination graphs. PLOS Genet., in press.

2. Freedman AH, Gronau I, Schweizer RM, Ortega-Del Vecchyo D, Han E, et al. (30 co-authors). Genome sequencing highlights the dynamic early history of dogs. PLOS Genet.10(1):e1004016, 2014.

3. Capra JA, Hubisz MJ, Kostka D, Pollard KS, Siepel A. A model-based analysis of GC-biased gene conversion in the human and chimpanzee genomes. PLOS Genet. 9(8):e1003684, 2013.

4. Arbiza L, Gronau I, Aksoy BA, Hubisz MJ, Gulko B, Keinan A, Siepel A. Genome-wide inference of natural selection on human transcription factor binding sites. Nature Genetics 45(7):723- 729, 2013.

5. Danko CG, Hah N, Luo X, Martins AL, Core L, Lis JT, Siepel A, Kraus WL. Signaling pathways differentially affect RNA polymerase II initiation, pausing, and elongation rate in cells. Mol. Cell50(2):212- 222, 2013.

6. Gronau I, Arbiza L, Mohammed J, Siepel A. Inference of natural selection from interspersed genomic elements based on polymorphism and divergence. Mol. Biol. Evol. 30(5):1159-1171, 2013.

7. Guertin MJ, Martins AL, Siepel A, Lis JT. Accurate prediction of inducible transcription factor binding intensities in vivo. PLOS Genetics, 8(3):e1002610, 2012.

8. Gronau I, Hubisz MJ, Gulko B, Danko CG, Siepel A. Bayesian inference of ancient human demography from individual genome sequences. Nature Genetics 43(10):1031-1034, 2011.

The ideal candidate will be enthusiastic, highly motivated, and independent, will have a strong background in comparative genomics, population genomics, or transcriptional regulation, a serious interest in molecular biology and genetics combined with good skills in mathematics and computer science, and a strong record of accomplishment in research. Postdoctoral associates in the group are expected to participate in both methods development and data analysis, to be comfortable in a fast-moving, interactive, and collaborative research environment, and to actively publish and present results.

Required Qualifications

1. Ph.D. in bioinformatics, computer science, statistics, genetics, molecular biology, applied mathematics, or a related field. 2. Research experience (with first-author publications) in computational genomics or a closely related field. 3. Fluency in probabilistic modeling and computational statistics. 4. Proficiency in programming, ideally in C or C++ as well as in scripting languages such as python, perl, matlab, or R. Should be comfortable in a linux environment, with large data sets, computer clusters, and databases.

Term

The term for this position is flexible but most likely will be 2-3 years. The proposed start date is September 2014. As many as 4 positions may be filled, depending on the quality of the applicants.

To Apply

Submit a CV, a short description of research interests and experience, and contact information for three references by e-mail to acs4 at cornell dot edu. Informal inquiries are welcome.

Adam Siepel 102E Weill Hall Cornell University Ithaca, NY 14853

Adam Charles Siepel <acs4@cornell.edu>

CornellU CassavaGenomics

Research Associate: Genomic Selection in Cassava

A Research Associate position is available to work in the area of genomic selection in the Department of Plant Breeding and Genetics at Cornell University. The overall purpose of this position is to serve as a key researcher and assistant to Jean-Luc Jannink, the leader of an international project to implement genomic selection in cassava (http://www.nextgencassava.org). The position requires an experienced scientist to conduct independent research in development and implementation of genomic prediction models, with an emphasis on empirical data from cassava breeding programs. The individual will provide regular advice to PhD students conducting research in genomic selection, and will help them with preparation of research papers. In addition, the individual will work with the project manager to coordinate activities and the flow of information among project partners. The position involves travel to Nigeria and Uganda for meetings with colleagues, visiting field sites, and presentation of workshops.

Anticipated Division of Time Research and writing: 60-70% Teaching (mentoring, preparing and giving workshops): 20-30% Coordination, meetings: 10%

Requirements PhD in genetics, plant breeding, or statistics required Three years of postdoctoral experience desirable Programming experience required Experience with statistical genomics required Excellent writing skills required Mentoring/teamwork experience required Ability to work well with people of different backgrounds and experience required Willingness to travel to Africa required Experience with next-generation genotype data desirable

The position is available 7/01/14. Applications will be reviewed until a suitable candidate is found. The initial appointment will be made for one year, with the expectation of renewal pending satisfactory performance (the project is funded until August 2017). Cornell is an equal opportunity employer. A list of publications from the Jannink group can be found at http://www.ars.usda.gov/pandp/people/-people.htm?personid=40650 Inquiries or applications can be sent to the project manager, Hale Tufan (hat36@cornell.edu). In your CV, please indicate which publications were actually written by you.

"Martha T. Hamblin" <mth3@cornell.edu>

CornellU SymbiosisMetabolicCooperation

"Job: Evolution of Metabolic Cooperation in Insect-Microbial Symbiosis"

A postdoctoral position in animal-microbial interactions is available immediately in the laboratory of Dr Angela Douglas (Cornell University, USA), to investigate the evolution of metabolite exchange between symbiotic bacteria and their animal hosts. The research project funded by NSF will investigate (1) how the coevolved metabolic networks of the interacting organisms are integrated, including network properties that may increase metabolic cooperation and reduce conflict among the partners; and (2) the contribution of systems-level variation in network properties to the functional variation among symbioses involving bacteria with genetically equivalent metabolic capabilities. The research involves metabolic modeling, including metabolic network reconstruction and flux balance analysis, together with genome/transcriptome sequencing and metabolite analysis in the context of coevolved symbioses; prior experience of working with genomes is essential, and experience of metabolic modeling and/or symbiotic associations is strongly preferred. The successful candidates will join an integrated team of researchers committed to understand the evolution and function of animal-bacterial symbioses (http://www.angeladouglaslab.com/).

Applications from candidates with a PhD in a biological discipline should be sent by email to Angela Douglas (aes326@cornell.edu). Please include a CV, statement of research, and details of three referees. The covering letter should include an explanation of how your qualifications and experience make you a good candidate for this position. Informal inquiries are welcome. To ensure full consideration, all materials should be received by May 12, 2012; however, applications will be accepted until the position is filled.

Angela E. Douglas Daljit S. and Elaine Sarkaria Professor of Insect Physiology and Toxicology Department of Entomology and Department of Molecular Biology and Genetics 5134 Comstock Hall Cornell University Ithaca, NY 14853 USA

Tel. +1-607-255-8539 FAX +1-607-255-0939 email aes326@cornell.edu http://www.angeladouglaslab.com/ aes326@cornell.edu

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CSIRO Canberra TephritidaeGenomics

Applications are invited for a three-year OCE Postdoctoral Fellowship in quantitative genetics/genomics of fruit flies. The Tephritidae fruit fly family includes some of the major pests of cultivated fleshy fruits in tropical and temperate regions of the world. In Australia this includes Bactrocera tryoni, B. neohumeralis and B. jarvisi, three species that differ in their distribution, stress tolerance and host rank preference. These species produce fertile hybrids in the laboratory, thereby offering unique experimental strategies. The successful candidate will pursue a genetic dissection of fruit fly natural history traits as part of a research team working more broadly on the molecular biology of Bactrocera species, including full genome sequencing, comparative genomics, RNAi and gene expression, and will build and lead the quantitative genetics component of the project.

Specifically you will:

1) Contribute to the design of laboratory bioassays and common garden experiments to determine whether introgression can change reproductive performance under conditions favouring traits from one species over another.

2) Guided by full-genome sequence, identifying regions of recombination that are preferentially introgressed in hybrid lines under different conditions.

3) Undertake molecular characterisation of the most promising candidate loci using RNAi.

4) Produce high quality scientific and technical outputs including journal articles, conference papers and presentations, patents and technical reports.

5) Develop innovative concepts and ideas for further research, regularly review relevant literature and patents.

Location: Black Mountain, Canberra, Australia Salary: AU$78,000 to $88,000 plus up to 15.4% superannuation Reference Number: ACT13/03745 Term: 3 years

CSIRO Ecosystem Sciences (CES) is a globally significant centre for sustainability science. The Division applies multidisciplinary science to help ensure the sustainability of Australia's agricultural and forestry systems, built environments, biodiversity, and rural and urban communities and industries. The Evolutionary Biology Program houses the molecular biology, biochemistry, microbiology, analytical chemistry, phylogenetics, and genomics capability in CES. The program aims to document Australia's terrestrial fauna through recognition of species and their distributions, and through the interpretation of their evolutionary origins. The Program examines how Australia's biodiversity has been shaped by evolution, and takes inspiration from evolutionary processes to develop genomics and bio-inspired technologies.

http://www.csiro.au/Organisation-Structure/-Divisions/Ecosystem-Sciences/Evolutionary-Biology.aspx How to Apply for this job:

To view the position description and apply online, please visit:

http://csiro.nga.net.au/?jati=3D2a3c87b6-82cc-a685-3737-7713254bc53c

Applications close May 7th 2014

DrOwain Edwards Program Leader | Evolutionary Biology Principal Research Scientist CSIRO Ecosystem Sciences Underwood Avenue, Floreat WA 6014| Clunies Ross St, Canberra, ACT 2601

Phone: +6189333 6401 (Perth)| +6126246 4514 (Canberra)| Mobile: 0438877 180 owain.edwards@csiro.au

Owain.Edwards@csiro.au

FHCRC Seattle HIV molecularEvolution

This postdoctoral position is an opportunity to contribute to the design of the upcoming 701 and 702 HIV vaccine trials to maximize power in subsequent statistical analyses. Specifically, it will be to develop new statistical and molecular evolution methods to design the trials so that infection time and founder sequences can be inferred with maximum fidelity. The scope of the study design includes sampling times and sequencing protocol, and also may afford some opportunities to design novel ways of combining sequencing methodologies. The project will last two years, with some possibility of extension. It may also offer an option to travel to South Africa to help teach a short course at the University of Cape Town, and possibly interact with the Fred Hutchinson Research Institute there.

This position will require significant statistics expertise, programming ability, and of course interest in collaboration. A background in molecular evolution would be very helpful, but isn't strictly required. For more details, see http://matsen.fhcrc.org/general/2014/04/-11/HVTN-postdoc.html Frederick "Erick" Matsen, Assistant Member Fred Hutchinson Cancer Research Center http://matsen.fhcrc.org/ ematsen@gmail.com

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Glasgow EpidemiologicalPhyloDynamicModelling

Research Assistant / Associate in Epidemiological/Phylodynamic Modelling - Ref: 008448

Grade 6/7: £26,527 - £29,837 / £32,590 - £36,661 per annum

The Institute of Biodiversity, Animal Health and Comparative Medicine (University of Glasgow) is looking to recruit a postdoctoral research assistant with excellent computational skills and an interest in epidemiological models to support our research on the transmission dynamics of bovine Tuberculosis (bTB) in British and Irish cattle and badgers. BTB is the most prominent disease of livestock in Britain and Ireland, and an exceptional exemplar for developing general principles regarding the transmission dynamics of multi-host pathogens.

Possessing excellent quantitative skills and academic qualification at Degree and/or PhD you will contribute to this BBSRC funded project by developing novel methodologies to explore the dynamics of bTB spread, exploiting dense demographic data and whole genome sequence data generated from the vast archive of bacterial samples available. The project is led by Prof. Rowland Kao and builds on a broad consortium of collaborators at Glasgow, the AHVLA and AFBI in Northern Ireland. The holder will be embedded within the Boyd Orr Centre for Population and Ecosystem Health (www.glasgow.ac.uk/boydorr), a vibrant research grouping of scientists interested in the application and development of cutting edge quantitative methods to solve real disease problems. The work of the Boyd Orr Centre was recently acknowledged by the award of the Queen's Anniversary Prize to the University of Glasgow, on the basis of the Centre's research excellence and commitment to broader impact on human and an imal health (http://www.gla.ac.uk/news/-headline_297128_en.html).

This position is funded until 31 May 2017.

For more details and online application see: http:/-/www.gla.ac.uk/about/jobs/vacancies/ (Reference: 008448)

Closing date: 9 May 2014

Informal inquiries to Rowland Kao (Rowland.Kao@glasgow.ac.uk) or Roman Biek (roman.biek@glasgow.ac.uk)

Roman.Biek@glasgow.ac.uk

Goiania Brazil EvolutionaryBiology

POST-DOC IN EVOLUTIONARY BIOLOGY (BRAZIL)

*Post-Doctoral Research position *in Goiania, Brazil with a competitive salary (49,200 BRL a year) for one year, extendable to second based on performance, focusing on developing next-generation sequence data and comparing it to fossil pollen data for a population genomics study.

Applicants must have experience in population genomics or phylogenomics, as well as a strong interest in evolutionary biology and ecology. Programming skills are important and should include proficiency working in the Unix environment as well as experience with R, Python/Perl and/or standard sequence analysis tools. Highly enthusiastic applicants with a strong disposition to learn the needed tools to succeed are also encouraged to apply.

*Informal inquiries as well as applications (including a CV, copies of relevant publications, and two names of recommenders) should be emailed to Christine Bacon (**christinedbacon@gmail.com* <christinedbacon@gmail.com>*) prior to May 15th, 2014.*

Starting date: July 1st, 2014, or upon agreement

Project: The de-evolution of diversity in Amazonia

Tropical America (the Neotropics) is recognized as harboring biodiversity hotspots, such as Amazonia, but there are some areas where diversity has decreased over time, particularly in oligarchic (monodominant) forests. This project aims to understand the evolutionary origins and maintenance of oligarchic forests in the context of geologic change and historical climate, thereby improving our predictions of how organisms, habitats, and Neotropical biomes may respond to comparable changes in the face of climate change. The genus *Mauritia *(Arecaceae, the palm family) presents an ideal system for investigating the evolution of oligarchic forests, or the de-evolution of Amazonian biodiversity. The genus has a rich pollen record, the taxonomy of palms is well known, and next- generation sequencing techniques, gene capture probes, have been developed specifically for palms that are appropriate for investigating demographic structure on both ecological and evolutionary time-scales. Furthermore, *Mauritia *is the most widely used and economically important native South American palm. We hypothesize that historical extinctions in *Mauritia *correlate with increased diversification rates in eudicotyledonous plants, the expansion of South American savannas, and/or the constriction of lowland rainforests during the Neogene. The inference of biogeography and diversification is an integral window into the past that enables the investigation of how geographic regions, biomes, and communities assembled through time and how they may evolve in the future. By integrating data across fields, for example from geology, genetics, fossils, species distribution and abundance, and morphology, we can reach a more comprehensive framework for the understanding of biome evolution and extinction.

Keywords: Amazon, biodiversity, fossil, next-generation sequencing, palms, pollen

Institution: Laboratory of Genetics and Biodiversity, Universidad Federal de Goias, Goiania, GO, Brazil (http://lgbio.icb.ufg.br/pages/33272-lgbio)

Remuneration: Monthly, untaxed salary is 4,100.00 Brazilian Reais per month. Moving costs and health insurance are not included. The position is for one year, extendable to two years based on a performance evaluation at the end of the first year. The position is funded by the Conselho Nacional de Desenvolvimento Cientifico e Tecnologico (CNPq; the Brazilian National Science Foundation). The post-doc position includes funding for travel abroad or within Brazil for project development, either for conferences, workshops, or training visits. One trip to the Antonelli Lab at the University of Gothenburg, Sweden is planned for early 2015.

The research project team: The Laboratory of Genetics and Biodiversity at the Universidad Federal de Goias is actively working on various next-generation sequencing projects of key plant taxa from the Cerrado, as well as other organisms (herpetofauna, ichtyofauna, etc.). The core supervisor for this position is Rosane Collevatti (http://scholar.google.com/citations?user=ChqtpzkAAAAJ&hl=en), known for her breadth of research on phylogeography and population genomics. The co-PI on the CNPq grant is Christine Bacon (http://scholar.google.com/citations?user=_p4DcHgAAAAJ&hl=en), who studies evolution and biogeography in palms (Arecaceae). Christine is based on Santander, Colombia and will be at UFG working on the project 1-3 months per year for the duration of the grant. Other associates of the project are Thiago Rangel (

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Goiania Brazil PlantGenetics

The laboratory of Genetics and Biodiversity from de Universidade Federal de Goias, Goiania, Brazil, is supporting researchers wanting to apply to the open FAPEG postdoc scholarships (20 in total - all areas) call. Projects should be in the areas of Plant molecular genetics, Plant genetics of populations, Plant molecular ecology and Plant cytogenetics of species of the Brazilian Cerrado region. Please visit FAPEG site about requirements and Mariana Telles for more information and project details (tellesmpc@gmail.com). Proposal submission closing date 30/05/2014 http://www.fapeg.go.gov.br/sitefapeg/ Fernando Roa <ferroao@gmail.com>

INRA France ChickenEvolution

Job description: The laboratories 'Mathématique Informatique et Génome (MIG)' and 'Génétique Animale et Biologie Intégrative (GABI)' at INRA research center in Jouy-en-Josas, (30 km south of Paris) have an open post-doctoral position funded by the 'Domestichick' ANR grant.

Project description: The objective of the project is to study the evolutionary dynamics of chicken domestication, using a comparative genomics approach. The Gallus genus comprises 4 species. G. gallus is considered as the ancestral species of the domestic chicken. Previous work demonstrated the genomic contribution of G. sonneratii and it is considered that other species may also have contributed to the genomic make-up of the domestic chicken. Our approach relies on (1) deep-sequencing of a representative sample of wild Gallus species (n) and (2) deep re-sequencing of birds from various domestic breeds, to identify the genomic structure of the domestic chicken genome and to detect introgression or other evolutionary events fixed during domestication. The study is three-pronged:

1. The first step deals with genome assembly, using the domestic chicken reference genome, and variant detection (SNPs, indels, structural variants).

2. In the second step, we will build a hidden markov model (HMM) to represent the evolutionary history of both wild and domestic birds and infer local ancestry of domestic birds along the genome.

3. The third step is devoted to the evolutionary dynamics that shaped the Gallus genome at the genus level. We will more specifically develop and implement an Approximate Bayesian Computation by Population Monte-Carlo (ABC-PMC) method to test different demographic scenarios and identify the complex events underlying the current diversity: bottleneck, gene flow, selection.

The post-doctoral fellow will be involved in all steps of the studies but his/her work will focus on the modeling, implementation and use of the statistical models mentioned in steps 2 and 3.

Research Environment: The work will take place in MIG laboratory, an interdisciplinary laboratory that hosts around 40 people in addition to a bioinformatics platform. The work involves close collaboration with MIG and GABI researchers. The candidate will benefit from the bioinformatics expertise of both laboratories, the expert knowledge of GABI researchers about the domestic chicken and the MIGALE computation facility hosted by MIG.

On a broader scale, the candidate will also benefit from the scientific environment of the INRA research center of Jouy-en-Josas, which hosts several research teams working on animal genetics, and the collaboration network of both partners, known for their skills in statistical genetics.

Qualifications: The candidate should hold a PhD in bioinformatics, biostatistics or applied mathematics with applications in molecular biology. (1) Skills and/or knowledge in computational or Bayesian statistics and (2) skills with NGS data analysis would be a plus but not required. The candidate should have a strong interest in data analysis, especially in comparative genomics, and a taste for collaborative work.

Funding: 21 months post-doctoral fellowship, starting as soon as possible and financed by ANR grant Domestichick. Salary will depend on the candidate's background and experience. Additional financial compensation through the AgreenSkills program will be sought for eligible candidate (http://-www.agreenskills.eu/agreenskills-cms/). The job will be located at the INRA research center of Jouy-en-Josas, in the South-West of Paris.

Application: Send a detailed CV, a short motivation letter and references to Frédéric Hospital <frederic.hospital@jouy.inra.fr> and Mahendra Mariadassou <mahendra.mariadassou@jouy.inra.fr>. Applications should be submitted before June 1st, 2014

bertrand.bedhom@jouy.inra.fr

ISTVienna Austria PopulationGenetics

A postdoc position is available to work at the interface between computer science and population genetics. The mathematical tools available to computer science, and in particular to the theory of evolutionary computation, offer many exciting opportunities of application to population genetics. We aim at deploying these tools in many outstanding problems in evolutionary theory, such as the evolution of recombination, analysis and classification of fitness landscapes, and the limits to selection. There is ample freedom in choosing research directions within this framework.

The position is part of SAGE (Speed of Adaptation in Population Genetics and Evolutionary Algorithms), a new European project in the Future and Emerging Technologies scheme. The post involves close collaboration with the other SAGE partners at Nottingham, Jena, IST Austria and Sheffield. For further information about SAGE, please see http://www.project-sage.eu. The position will be based at IST Austria, in the Population Genetics group headed by Nick Barton, and will be available for three years. The salary scale starts at 47.250 p.a. Applicants should have a Ph.D. in a relevant area (including computer science, mathematics, statistical physics, and population genetics), with strong mathematical skills, and an interest in fundamental research. For further details, please contact Tiago Paixao (tiago.paixao@ist.ac.at) and see the group's webpage at https://ist.ac.at/research-groups-pages/barton-group/. Applications should include a CV, a statement of research interests or a motivation letter, and names of two to three referees.

The Institute of Science and Technology is a new multidisciplinary research institute, located just outside Vienna (www.ist-austria.ac.at). The Institute encourages multidisciplinary research, and has strong groups at the interface between biology and physics, and in computer science. There are close links with other evolution groups in Vienna (www.univie.ac.at/evolvienna).

Tiago Paixao <paixao@ist.ac.at>

Lausanne PopulationGenetics

Computational Population Genetics

The Jensen Lab has two open postdoc positions. In both cases, the ideal candidate will work on the intersection of theory development, statistical method design, and data analysis. However, candidates with particular expertise in one of these areas, with an interest to develop the others, will be happily considered.

The first will be centered around the study of cryptic coloration in wild mouse populations - a long-term

Swiss NSF funded collaboration between our group, the Hoekstra Lab (Harvard), and the Excoffier Lab (Berne) - with the possibility of spending time in all three groups. The project has recently undergone a large expansion, and this new hire will work on both novel population genetic method development for the joint inference of selection and demography, as well as the analysis of multiple newly generated datasets. For examples of recent lab publications in this area, please see: 1) Linnen et al. 2009. On the origin and spread of an adaptive allele in Peromyscus mice. Science 325: 1095-98. 2) Domingues et al. 2012. Targeted re-sequencing reveals a single recent origin of a beneficial pigment allele in cryptic beach mice. Evolution 66: 3209-23. 3) Linnen et al. 2013. Adaptive evolution of multiple traits through multiple mutations at a single gene. Science 339: 1312-16.

The second will be centered around the study of viral drug-resistance evolution utilizing both experimental and clinical data, a long-term European Research Council (ERC) funded project. This new hire will work on both theory development related to extensions of Fisher's Geometric Model, method development pertaining to the inference of the distribution of fitness effects, as well as the analysis of large-scale datasets from both Human Cytomegalovirus (HCMV) and influenza virus . For examples of recent lab publications in this area, please see: 1) Renzette et al. 2013. Demography and selection contribute to the rapid evolution of cytomegalovirus within human hosts. PLoS Genetics 9(9): e1003735. 2) Bank et al. 2014. A Bayesian MCMC approach to assess the complete distribution of fitness effects of new mutations: uncovering the potential for adaptive walks in challenging environments. Genetics 196: 841-52. 3) Foll et al. 2014. Influenza virus drug resistance: a time-sampled population genetics perspective. PLoS Genetics 10(2): e1004185.

The Jensen Lab is an active research group, with current postdocs and PhD students coming from backgrounds spanning biology, mathematics, and computer science. We are located in the School of Life Sciences at the Ecole Polytechnique Federale de Lausanne (EPFL) in Switzerland, on the shores of Lake Geneva and at the base of the Alps. The working language of the lab is English. Further information may be found on the lab website: http://jensenlab.epfl.ch Starting dates are flexible, and salaries are highly competitive (newly appointed postdocs begin at CHF 81,000 = EUR 66,000 = USD 92,000 / year). Both positions have available funding for three years, and contracts are renewed annually. Interested applicants should send a CV, contact information for three references, as well as a cover letter stating general research interests as well as fit to the desired position. Applications should be sent to jeffrey.jensen@epfl.ch by June 01, 2014.

jeffrey.jensen@epfl.ch

LMU Munich ComparativeGenomicsPhylogenomicsNon-Bilateria

PostDoc position in comparative genomics and phylogenomics of non-bilaterian animals (LMU Munich, Germany)

We invite applications for a *PostDoc* position in the project MODELSPONGE funded by the LMUexcellent program through the German Excellence Initiative.

The project is located at the *Department of Earth- and Environmental Sciences* (Chair of Paleontology and Geobiology) and the *GeoBio-Center^LMU * of the Ludwig-Maximilians-Universität (LMU) München.

The phylogenetic relationships among non-bilaterian animals (i.e. Porifera, Ctenophora, Cnidaria, Placozoa) and their relationships to the Bilateria are still discussed controversially. This project will build on recently published as well as unpublished in-house sequenced genomes of sponges and other non-bilaterians to comparatively analyse their genomes to further our understanding of early animal evolution. The project is also aimed at contributing to resolve controversies about the branching patterns at the base of the animal tree of life. Key publications in this context from the lab include Philippe et al., 2009, Current Biology; Pick et al., 2010, Molecular Biology and Evolution; Philippe et al., 2011, PLoS Biology; Wörheide et al., 2012, Advances in Marine Biology; Dohrmann & Wörheide, 2013, Integrative and Comparative Biology; Nosenko et al., 2013, Molecular Phylogenetics and Evolution.

We are seeking a highly motivated applicant, ideally trained in evolutionary bioinformatics, with excellent and demonstrated (phylo)genomic skills, bioinformatics expertise as well as a sound background in biology, who is willing to tackle the challenging task of working with the genomes of non-bilaterian animals. The successful candidate will also contribute to the lab's ongoing genome sequencing efforts, contribute to expand the bioinformatic tools available in the lab, and has the opportunity to contribute to teaching specialty courses in the Master's programme. High-performance computing is available in the lab (64-core LINUX cluster) as well as through the Leibnitz Rechenzentrum (< www.lrz.de >).

The successful candidate will join an international and dynamic lab focussing on the geobiology and evolution of marine animals. More information about the lab can be found at < www.geobiology.eu >.

Requirements: PhD in Biology or Bioinformatics or related field; demonstrated expertise and understanding of molecular evolution including phylogenomic methods, demonstrated expertise in processing and analysing Illumina NGS genome and transcriptome data; excellent English language skills; excellent programming skills (e.g., in commonly used bioinformatic languages such Perl, Python, etc.). Evidence of this expertise must be provided through high-ranking international publications. Prior postdoctoral experience is desirable but not essential. German language skills are not necessary, the working language of the group is English.

The position is initially available for 12 months, with possible extension depending on performance. The position will be paid according to the German salary scheme TV-L E13.

Application: Send application including letter of motivation, CV, PDFs of max. 5 of your most significant publications, and contact details of 2 referees in a single PDF (only) by email to Mrs Monika Brinkrolf <m.brinkrolf@lrz.uni-muenchen.de>. Application deadline is 15 May 2014. Informal enquiries may be directed to Professor Gert Wörheide (woerheide@lmu.de).

The Department of Earth- and Environmental Sciences, Palaeontology & Geobiology of the Ludwig-Maximilians-Universität Munich offers an excellent multidisciplinary research environment, one of its particular strength being due to the close interaction between Geosciences and the Faculty of Biology in the framework of the GeoBioCenter^LMU (http://www.geobio-center.uni-muenchen.de).

The LMU Munich is the leading research university in Germany, with a more than 500-year-long tradition, and builds upon its success in the Excellence Initiative, a Germany-wide competition promoting top-level university research. Munich has been repeatedly voted Germany's most livable city and is among the Top 5 most livable cities worldwide.

The LMU Munich is an Equal Opportunity/Affirmative Action Employer and has an affirmative action policy for the disabled.

Prof. Dr. Gert Wörheide Department of Earth and Environmental Sciences, Division of Paleontology & Geobiology & GeoBio-CenterLMU Ludwig-Maximilians-Universität München, and Director, Bavarian State Collections of Palaeontology and Geology Richard-Wagner-Straße 10 80333 München Germany

Phone: +49 (89) 2180-6718 Fax: +49 (89) 2180-6601 E-Mail: woerheide@lmu.de www.palmuc.de | www.mol-palaeo.de

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LMU Munich ComparativeGenomicsPhylogenomicsNon-Bilateria
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The position is initially available for 12 months, with possible extension depending on performance. The position will be paid according to the German salary scheme TV-L E13.

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Lyon France SexChromosomeEvolution

Postdoc position on sex chromosome evolution - Lyon (France)

We offer a 24-months postdoc position on sex chromosome evolution in primates. The postdoc research project will be about studying the effect of X-Y and Y-Y gene conversion on the evolution of the primate Y chromosome. The postdoc will contribute to ongoing methodological developments to identify gene conversion events in phylogenies using a ML framework and to study the molecular evolution of regions undergoing gene conversion using non-homogeneous codon-based models. She/he will apply these methods to an unpublished multispecies sequence dataset. The postdoc will work with Gabriel Marais (http://lbbe.univ-lyon1.fr/-Marais-Gabriel-.html) and Laurent Guéguen (http://lbbe.univ-lyon1.fr/-Gueguen-Laurent-.html). The position will be at the "Ecology and Evolutionary biology"

Department (rated A+ at last AERES evaluation in 2009, see http://lbbe.univ-lyon1.fr), at the Université Lyon 1. Gross salary is 2,500 euros / month, health insurance provided.

Contact: Prof. Gabriel Marais CNRS / Université Lyon 1 Email : Gabriel.Marais@univ.lyon1.fr

MARAIS GABRIEL <Gabriel.Marais@univ-lyon1.fr>

Marseille MarinePopulationGenetics

Dear all

I propose a post-doctoralfelllowship (6 - 24 months)

Marine comparative population genetics and community ecology.

We obtained funds for 24 months of fellowships. The fellowship is financed by a FP7 European program (DEVOTES: Development of innovative tools for monitoring and assessing the good environmental status of the marine environment). *We seek candidates who proved their autonomy in data analyses and in writing international scientific papers.* A solid experience in population genetics is also required. Expertise in community ecology, benthic coastal marine biodiversity, marine currentology, modelisation, as well as scuba-diving is not compulsory but considered as a "plus". Our goal (IMBE) is to evaluate the interest and the limits of intra-specific genetic diversity (of a set of species) as an indicator of the good environment status of a locality. For this, we compare local diversity among species, with species diversity (Shannon or other indices) when possible, and we aim at correcting for (or taking into account) genetic connectivity and physical connectivity.

The post-doc will at first benefit from an already available data set (partly published) of population genetic data from 6-10 invertebrate species (eventually a red alga may also be available) with contrasted dispersal abilities in a common set of localities along the French Mediterranean coast. His first goal will be to combine those data in a global comparative analysis, integrating physical data and models (by collaborations with physical oceanographers), biological data on life history traits(duration and season of dispersal stage), and disentangle factors linked to physics, life history traits. The post-doc is expected to write and submit one scientific article (at least) within the 6 months period with the data that were already available.

A fellowship of 18 months will then be proposed for a combined study comparing community composition and intra-species genetic diversity, focusing on coralligenous habitats. Coralligenous habitats are typically Mediterranean; they are highly complex habitats, based on a biogenic substratum composed of a variety of red algae. Community composition will be obtained from metabarcoding (with controls by classical taxonomy and photo-quadrats). Population genetics will be studied for a few species of the coralligenous habitat: at least one red alga (or a full species complex, providing natural replicates), a bryozoan, etc. (NGS genotyping will be obtained for some species). Samplings are finely contextualized by contrasted ecological parameters (orientation, depths, slope, rugosity, temperature...) within each locality (islets), allowing estimating the relative parts of adaptation and neutrality at both the intra-specific and the community levels (local adaptation, neutral theory of biodiversity). This sampling and ecological study is a strong part of the European ANR "CIGESMED" (an ERANET project of the Seas-ERA call).

Do not hesitate to contact us for more details on the scientific project and the contract.

Contact: anne.chenuil@imbe.fr

www.imbe.fr

*http://www.cigesmed.eu/*** *www.devotes-project.eu/*

– Anne CHENUIL

Email: <anne.chenuil@imbe.fr>

UMR 7263 (CNRS) - IMBE Institut Méditerranéen de Biodiversité et d'Ecologie Marine et continentale (IMBE) (Aix-Marseille Université) Station Marine d'Endoume Chemin de la Batterie des Lions 13007 MARSEILLE

Tel.: +33 (0)4 91 04 16 17 Fax: +33 (0)4 91 04 16 35

Anne Chenuil <anne.chenuil@imbe.fr>

Montpellier WheatTranscriptomicsAdaptation

Dear colleagues,

We have a 18 month postdoc in Montpellier starting in September 2014 on the wheat transcriptomic response to pathogenic and mutualistic bacteria. Details below.

*Postdoc *on Wheat transcriptomics in interaction with mutualistic and pathogenic bacteria

18 month postdoc starting in September 2014 (possibility to change slightly the start date according to eligibility criteria and availability of candidates)

*Lab host:*UMR RPB (Resistance of Plants to Bioagressors), IRD (Institute of Research for Development (www.ird.fr < http://www.ird.fr >), Montpellier, France. The postdoc will be under the direction of Dr Ralf Koebnik, and will interact also with Dr Lionel Moulin and Dr Florence Wisniewski-Dyé. Montpellier is a vibrant, elegant and artistic city in the heart of the Languedoc-Roussillon region, along the shores of the Mediterranean Sea in southern France.

*Project:*MIC-CERES (http://umr-lstm.cirad.fr/-principaux-projets/mic-ceres)

Eligibility criteria:

PhD defense less than 2 years ago on 1^st of September 2014 (possibility to increase if we modify starting date). The candidate should not have spent more than 10 months in France during the last 3 years. Eligibility criteria regarding the date of PhD defense might be reconsidered for best fitting candidates.

Postdoc Profile:

We are looking for an enthusiastic young postdoc researcher to work primarily on the bread wheat transcriptomic response to pathogenic (/Xanthomonas/) or mutualistic bacteria (/Azospirillum /and/Burkholderia/). Activities will include RNA extraction of wheat roots and leaves in different inoculation conditions, preparation of samples for RNA sequencing, analyses of RNAseq data and differential gene expression studies in wheat challenged with /Xanthomonas,/ /Azospirillum/ or /Burkholderia/.

The candidate will have knowledge on plant transcriptomics, DNA sequence technology and downstream analyses. Background in plant response to microbes would be a plus. Candidates with experience in RNAseq analyses (fastQC, Cutadapt, Tophat/bowtie, or others pipelines) and R language for differential expression analyses (DESeq, DESeq2, edgeR, EBseq) will be favored; otherwise attraction to computing and willingness to learn would be OK.

Working language will be English. Basic knowledge of French will facilitate extra-lab communication but is not a must.

*Starting salary:*1750 euros per month including social security, pension and job loss benefits.

*How to apply:*send a CV and a covering letter describing your suitability for the position before *May 15^th , 2014* to ralf.koebnik[at]ird.fr, lionel.moulin[at]ird.fr and florence.wisniewski[at]univ-lyon1.fr.

Lionel Moulin

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Dr Lionel Moulin, Chargé de Recherche IRD Laboratoire des Symbioses Tropicales et Méditerranéennes, TA A-82/J Campus International de Baillarguet, 34398 Montpellier cedex 5, FRANCE Tél: +33 467593763 Fax: +33 467593802 Website: umr-lstm.cirad.fr

Lionel Moulin <lionel.moulin@ird.fr>

Okinawa EvolutionofBiodiversity

The Biodiversity and Biocomplexity Unit (http://-arilab.unit.oist.jp/, PI: Evan Economo) at the Okinawa Institute of Science and Technology, Japan, is seeking applicants for postdoctoral researchers.

Our research investigates ecological and evolutionary processes generating and maintaining biodiversity across spatial scales and levels of biological organization, with an empirical focus on ant biodiversity. Ongoing projects (http://arilab.unit.oist.jp/research/) include understanding the macroevolutionary dynamics of the hyperdiverse ant genus Pheidole, global biodiversity patterns in ants, the island biogeography of Pacific Island ants, genomic approaches to community ecology, biodiversity theory, and high-throughput biodiversity inventory methods. Towards those ends, we integrate a variety of approaches including quantitative theory, phylogenetics, high-performance computing, ecoinformatics, morphometrics, field sampling, and traditional collections-based taxonomy. Within these general research areas, the specific project is flexible and can be adapted to the interests and skills of the postdoc. Previous knowledge and experience with ant biology is not required, and it is possible to work on other taxonomic groups. Applicants having experience with model-based inference of population and evolutionary processes and working with next-generation sequence data are especially encouraged to apply.

The successful candidate will be provided funding to pursue their research and attend meetings, technician support, and access to state-of-the art facilities and equipment on the OIST campus. These resources include a 4000-core computer, a high-throughput ecological genomics pipeline, an X-ray micro-CT, SEM/TEM, confocal microscopes, etc. There will be numerous opportunities to work closely with other research groups at OIST and elsewhere.

To apply, please send your CV, a list of references, and a letter describing your scientific background and interests in a combined document by email to <economo@oist.jp> by April 15. Informal enquiries or questions are also welcome at the same address. The start date is flexible. Applicants must have a PhD in Ecology/Evolution or related field.

About OIST: The Okinawa Institute of Science and Technology (www.oist.jp) is a new interdisciplinary research institute and graduate university located in the seaside village of Onna-son. The institute is international by design; the working language is English and researchers are split between Japanese and foreign nationalities. Knowledge of Japanese is not required, and our relocation staff will assist you with moving to Okinawa and setting up your life. The institute is located in a beautiful ecological setting adjacent to coral reefs and subtropical forest, and offers a competitive compensation package for postdoctoral scientists. For more information on OIST, see recent articles in Nature (http://www.nature.com/news/2011/-110629/full/474553a.html) (http://www.nature.com/-nature/journal/v474/n7353/full/474541b.html), the Economist (http://www.economist.com/node/-21540228), and info on our lab website (http://-arilab.unit.oist.jp/laboist-okinawa-oist/).

Evan P. Economo Assistant Professor Biodiversity and Biocomplexity Unit Okinawa Institute of Science and Technology 1919-1 Tancha Onna-son, Kunigamigun Okinawa, Japan 904-0495 http://arilab.unit.oist.jp/ evaneconomo@gmail.com

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Oxford PopulationGenetics

Population and statistical genetics posts in Oxford Group of Gil McVean, Wellcome Trust Centre for Human Genetics Grades 7 and 8: Salary range £29,837 - £45,053 with a discretionary range to £49,216 p.a.

Up to four posts are available to work on population and statistical genetics theory, methodology and application in the group of Gil McVean at the Wellcome Trust Centre for Human Genetics (WTCHG) Oxford; see http://www.well.ox.ac.uk/gil-mcvean . Posts are available to work across a range from projects including: 1. The comparative study of mutation and recombination rates in vertebrates through whole-genome sequencing of individuals in extended pedigrees. 2. Characterisation of patterns of genetic variation within the HLA region and the analysis of host-pathogen interactions. 3. Methods for analysing patterns of haplotype structure in very large sample sizes (>100,000) with application to large-scale data sets being generated within the UK. 4. Graphical methods for describing genome reference variation with application to improved characterisation of high diversity regions of human and pathogen genomes using high throughput sequencing.

You will help in the design of experiments, the development of statistical and computational methods for analysing data, interpretation of project data, the dissemination of methodology and results, and participate in collaborations with specific partners and international consortia. Where appropriate, more senior appointees with help with the supervision of junior posts.

You will have a PhD with a strong quantitative or computational element, a good publication record and skills in statistical programming (preferentially R). You should have experience of analysing large data sets and experience of scripting (Python or Perl). We are looking for people with a range of skills and expertise, from population genetics theory to software development.

The positions are funded by the Wellcome Trust and are fixed-term for 3 years in the first instance.

How to apply Applications for this vacancy are to be made online. You will be required to upload a CV and supporting statement as part of your online application.

For more information, please see the following sites: Junior posts: https://-www.recruit.ox.ac.uk/pls/hrisliverecruit/-erq_jobspec_version_4.jobspec?p_id=112693 Senior posts: https://www.recruit.ox.ac.uk/pls/-hrisliverecruit/erq_jobspec_version_4.jobspec?p_id=-112808 Please contact mcvean@well.ox.ac.uk for additional information.

Gil McVean Professor of Statistical Genetics Acting Director of the Oxford Big Data Institute Wellcome Trust Centre for Human Genetics Roosevelt Drive Oxford OX3 7BN UK

Tel (WTCHG): +44 1865 287534 Tel (Statistics): +44 1865 281881 PA Emma Jones: emma@well.ox.ac.uk +44 1865 287506 web: http://www.well.ox.ac.uk/gil-mcvean mcvean@well.ox.ac.uk

Paris EvolutionaryEcology Phylogenetics

Postdoctoral positions. Evolutionary ecology - phylogenetics. Ecole Normale Supérieure, Paris

Several postdoctoral positions are available to work with Hélène Morlon (http://www.cmap.polytechnique.fr/ ~ morlon/) on a project supported by a five year grant from the European Research Council (ERC), in the general area of evolutionary ecology and phylogenetics. The project integrates across diverse fields (macroevolution, macroecology, community ecology, ecological networks, paleobiology, microbial ecology) with a focus on phylogenetic approaches. Applicants with very diverse backgrounds are encouraged to apply (e.g. mathematics, physics, ecology, evolutionary biology, bioinformatics). Applicants should have solid quantitative, programming, and/or bioinformatics skills, as well as good writing skills. Speaking French is not mandatory.

The postdoctoral researchers will work in Hélène Morlon's group at the Institute of Biology of the Ecole Normale Supérieure (http://www.ibens.ens.fr/). The IBENS is a multidisciplinary research centre in Biology with more than 300 staff members, conveniently located in the Latin Quarter in downtown Paris. The centre develops research in a wide range of disciplines, including evolutionary biology, ecology, computational biology, genetics, and comparative genomics.

Review of applications begins immediately and will continue until the positions are filled. Starting dates are flexible and salaries depend on experience. To apply, please submit: i) a cover letter summarizing research interests and expertise ii) a Curriculum Vitae (including publications), and iii) the names and contact information for at least two references. Questions and application should be sent to Hélène Morlon (morlon@biologie.ens.fr).

Helene Morlon <morlon@biologie.ens.fr>

QMUL London phylogenomics

A Postdoctoral Research Assistant position is available for three years in the School of Biological and Chemical Sciences at Queen Mary University of London (QMUL) with Dr Richard Buggs, using genome sequencing and phylogenomics methods to identify candidate genes for low pest and pathogen susceptibility in ash trees.

QMUL is one of the UK's leading research-focused higher education institutions, with a budget of £285 million per annum. Richard Buggs' research group works on the evolutionary genomics of trees, and this project collaborates with Stephen Rossiter whose group studies the phylogenomics of mammals.

This project is funded jointly by a grant from BBSRC, Defra, ESRC, the Forestry Commission, NERC and the Scottish Government, under the Tree Health and Plant Biosecurity Initiative.

The PDRA will be responsible for sequencing and assembling the genomes of 35 ash species. Using pipelines developed by the group of co-PI Rossiter to study convergence (Nature 502, no. 7470 (2013): 228-231), the PRDA will use phylogenomic methods to identify genes and alleles associated with low susceptibility to ash dieback and the emerald ash borer. The PDRA will liaise with collaborators at Forest Research (UK) and the United States Forest Service (Ohio) who will experimentally determine the susceptibility phenotypes for each species. The PDRA will also interact with social scientists seeking to understand the attitude of the UK public to the potential use of genus-wide genome diversity in trees to combat tree health threats.

The successful candidate will have a PhD in a relevant area of bioinformatics, molecular systematics, molecular evolution or a related field. Candidates must have experience in genomics, phylogenetics and programming, with a solid grounding in plant systematics, evolutionary biology and/or handling next generation sequence data. Previous post-doctoral experience is essential criteria for this post.

During the project, the PDRA will also have opportunities to develop their supervision, writing, communication, media, and organisational skills, excellent preparation for a career in academia or industry. Duties will also include assisting in the training and supervision of PhD and final year project students.

The position is full time and available for 36 months. The starting salary will be £38,579 per annum, inclusive of London Allowance. Benefits include 30 days annual leave, defined benefit pension scheme and interest-free season ticket loan.

Candidates must be able to demonstrate their eligibility to work in the UK in accordance with the Immigration, Asylum and Nationality Act 2006. Where required this may include entry clearance or continued leave to remain under the Points Based Immigration Scheme.

http://www.jobs.qmul.ac.uk/4725 For informal enquiries via email: r.buggs@qmul.ac.uk

The closing date for applications is 25th April 2014. Interviews will be held soon thereafter.

Dr Richard Buggs | Senior Lecturer | School of Biological and Chemical Sciences, Queen Mary University of London, E1 4NS, United Kingdom | email: r.buggs@qmul.ac.uk | website: http://www.sbcs.qmul.ac.uk/staff/richardbuggs.html | office: +44(0)207 882 8441 | mobile: +44(0)772 992 0401 | twitter: @RJABuggs

r.buggs@qmul.ac.uk

Roscoff France ClimateAdaptation

*Context of the project *(OPOPOP ANR-BIOADAPT January 2014-december 2017)

Global change linked to temperature increase and ocean acidification but also more direct anthropogenic influences, such as aquaculture, have caused a worldwide increase in reports of /Vibrio/-associated illness affecting humans but also animals such as corals and mollusks. In particular, over the last 5 years, /Vibrio splendidus/ and /V. aestuarianus/ have been associated with recurrent mortality outbreaks in oyster beds (/Crassostrea gigas/) in France. Investigating the "emergence of /Vibrio/ pathogenesis events" requires the analysis of microbial evolution at the gene, genome and population level in order to identify genomic modifications linked to increased virulence, resistance and/or prevalence, or to recent host shift.

The aim of the post doc project is to:

/1- Compare the population structure of Vibrio in oysters and surrounding water during oyster mortality outbreaks/

In the water column, vibrios have been shown to assemble into specific populations defined by ecological preferences to attach to different types of particles and/or zooplankton, or to occur free-living. We will determine if /Vibrio/ populations are assembled neutrally in oyster or whether specific colonization processes occur and result in association with specific populations.

/_Method_/: Phylogenetic (PhyML) and population prediction (Adapt ML, BAPS) as described previously (Hunt et al., 2008; Shapiro et al., 2012).

/2- Compare the genome of virulent versus non-virulent strains belonging to different ecological populations/

Preliminary data suggested that not all /Vibrio/ populations harbor potential oyster pathogens.Moreover, within pathogen-containing populations (i.e., closely related, ecologically similar genotypes) pathogenicity potential ranges from non-virulent to highly virulent.We are currently testing how efficiently different strains and genotypes affect host survival.These data will be correlated with genome analyses to build hypotheses of gene function in the context of oyster pathogenesis.

/_Method:_/Genome assembly from short read data using hybrid strategy (scaffolding onto closely related genomes and /de novo/ assembly), comparative genomic, phylogeny (Shapiro et al., 2012; Goudenège et al., 2013)

*/Competences required:/***Bioinformatician: Genome assembly, annotation, comparative genomics, phylogeny, microbial evolution, computational biology, microbial diversity, genotyping, ecology**

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*/Beginning of the post doc:/*mid 2014; 30 months

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*/Salary:/*about 1900 euros/months

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*/Professional address:/*the post doc will be based in the team of Dr Frédérique Le Roux at the station biologique de Roscoff (http://www.sb-roscoff.fr/en-genomic-vibrio.html) and will be co-supervised by Pr Martin F. Polz at the MIT (http://polzlab.mit.edu/). Training in the Polz lab will be funded by the project.

A letter explaining the competences and scientific interests, a CV, a publications list and letter(s) of reference should be send to Frédérique Le Roux by email: frederique.le-roux@sb-roscoff.fr

Le Roux Frédérique Head of the GV team Equipe émergente Ifremer/UPMC: "Génomique des Vibrio" Station Biologique de Roscoff frederique.le-roux@sb-roscoff.fr Tel ext: 33 (0)2 98 29 56 47 Tel int: 416

Frédérique Le Roux <frederique.le-roux@sb-roscoff.fr>

Sheffield Macroevolution Birds

Understanding evolutionary rates on the avian tree of life Two post-doctoral and four postgraduate research assistant positions in macroevolution/trait evolution in birds.

Two postdoctoral research associate positions and four postgraduate research assistant positions are available to work on macroevolution and trait evolution in birds. The posts are funded by a European Research Council consolidator grant to Gavin Thomas in the Department of Animal and Plant Sciences at the University of Sheffield. The successful applicants will join a new research team collecting novel, high-resolution morphometric data on bird bill shape using 3D structured white-light digitisation and plumage colour using visible and UV spectrum digital photography.

Postdoctoral Research Associates (two posts): The project is focused on modelling phenotypic evolution of species traits in birds at broad phylogenetic and spatial scales. The aims are to test how and why phenotypic evolutionary rates vary and to ask how that variation has shaped both the avian tree of life and global distributions of species and traits. The exact directions of the research will be partially dependent on the skills and interests of the successful applicant(s). Applicants must have a PhD with emphasis on macroevolutionary/phylogenetic approaches to evolutionary biology or similar. Expertise in modelling evolutionary processes on phylogenies, 3D surface morphometrics, or measuring plumage colour with digital photography would be advantageous.

Full details are available from, and formal applications should be made, via University of Sheffield job's pages < http://goo.gl/ZPkrN3 >

Postgraduate Research Assistants (four posts): The postgraduate post-holder(s) will be responsible for generating and processing high-resolution morphometric data on bird bills using 3D structured white-light digitisation and plumage colour using visible and UV spectrum digital photography. Data collection will rely on extensive museum collections in the UK and elsewhere. Applicants must have a good first degree in biology, ideally with a substantial evolutionary biology component. However, candidates with other backgrounds will be considered. A masters degree in an evolutionary biology discipline would be an advantage. Potential applicants with a PhD are also eligible to apply. Experience in working with museum collections would be an advantage but is not essential and training will be provided. Up to four positions are available initially as fixed-term one-year contracts with funding available to extend by an additional 1-2 years for suitable candidates.

Further details are available from, formal applications should be made via University of Sheffield job's pages < http://goo.gl/A1sudm >

Informal enquiries for all posts are encouraged and should be sent by email (gavin.thomas@sheffield.ac.uk) with an outline or your research interests, CV and or/link to a personal webpage.

In addition to the above posts one PhD studentship on the same grant is available and details will be advertised very soon.

Gavin Thomas <gavin.thomas@sheffield.ac.uk> Gavin Thomas <gavin.thomas@sheffield.ac.uk>

StLouis GrassEvolution

Post-doctoral position, evolution of plant development Donald Danforth Plant Science Center

The Kellogg lab at the Donald Danforth Plant Science Center has funding for a post-doc interested in the evolution of genes, genomes, and morphology in the grasses. The project will investigate controls of inflorescence development in grasses related to maize and sorghum, and is a collaborative project with the McSteen lab at University of Missouri-Columbia. We are combining studies of genomics, molecular evolution, plant development, and gene expression to translate results from maize to other cereal crops and wild grasses. Specifically, we are investigating the gene suppressor of sessile spikelet1, which controls spikelet pairing, a fundamental aspect of inflorescence architecture in a major clade of grasses. The project will involve studying the molecular evolution of the protein and its genomic context, expression of the gene in the model system Setaria viridis, and construction of transgenic plants to test hypotheses of gene regulation.

The successful candidate should have a strong background in molecular evolution, genomics, and/or evolution of development. Candidates with a Ph.D. in plant biology, with strengths in phylogenomic analysis, plant morphology, and methods of studying gene expression are strongly encouraged to apply.

More information about the Kellogg lab is at kellogglab.weebly.com and at http://www.danforthcenter.org/scientists-research/principal-investigators/elizabeth-kellogg . Send resume and three references to:

Donald Danforth Plant Science Center Human Resources RE: Postdoc/Kellogg lab 975 North Warson Rd. St. Louis, MO 63132

Or by email to: careers@danforthcenter.org with 'Postdoc/Kellogg Lab' in the subject line.

"Kellogg, Elizabeth" <EKellogg@danforthcenter.org>

TexasAM LandscapeGenetics

TEXAS, COLLEGE STATION. Texas A&M University. The Department of Geography invites applications for a non-tenure track Visiting Assistant Professor in Geography with research and teaching interests in landscape genetics and spatial population genetics to begin 1 September 2014. The successful candidate will be required to teach two undergraduate classes per year in the Geography Department and the Environmental Studies Program at Texas A&M University. This position will be responsible for maintaining an active research agenda in coordination with the Biogeography Lab in the Department of Geography. This will include writing proposals, helping with the analysis of genetic/genomic data, and interacting with graduate students. Minimum qualifications include a Ph.D. in Genetics, Bioeography, Landscape Ecology or related discipline. Experience in ecological and landscape genetics and population genetics research is required. Familiarity with bioinformatics, genomics and specific software packages for genetics analysis are preferred (e.g. GeneLand, SPAGeDi, STRUCTURE, R). Preference will be given to candidates with experience working in plant population genetics, especially with conifers.

The Biogeography Lab at TAMU (http://people.tamu.edu/ ˜ cairns) is engaged in using genetics/genomics techniques to investigate gene flow across topographically complex landscapes. One specific project aims to determine the importance of long distance dispersal to the migration potential of the alpine treeline in south central Alaska. More details regarding current and planned research projects are available from Dr. Cairns. The person hired for this position will be expected to work closely with Dr. Cairns to strengthen the landscape genetics research program. The Department of Geography has 20 faculty members with strengths in biogeography, climatology, geomorphology, human geography, human-environment relationships, geographic education and GIST (Geographic Information Science and Technology) (http://geography.tamu.edu). We are based in the College of Geosciences (http://geosciences.tamu.edu) with the Departments of Atmospheric Science, Geology & Geophysics, and Oceanography, and play a major role in the Environmental Programs in Geosciences. The College of Geosciences also includes Sea Grant, the Geochemical and Environmental Research Group (GERG), and the Integrated Ocean Drilling Program (IODP). Texas A&M University houses the Whole Systems Genomics Initiative (http://genomics.tamu.edu) that provides an intellectually vibrant community and state-of-the-art resources for genomics and bioinformatics research. Texas A&M University, a land-,sea-, and space-grant university, is located in a metropolitan area with a dynamic and international community of 175,000 people.

Candidates should submit a letter of application, curriculum vitae, and names and addresses (including e-mail addresses) of three referees to Dr. David Cairns (cairns@tamu.edu) Assistant Department Head, Department of Geography, Texas A&M University, College Station, TX, 77843-3147. We will begin reviewing applications immediately. Texas A&M University is an Affirmative Action/Equal Opportunity Employer committed to excellence through the recruitment and retention of a diverse faculty and student body and compliance with the Americans with Disabilities Act. The University is dedicated to the goal of building a culturally diverse and pluralistic faculty and staff committed to teaching and working in a multicultural environment. We strongly encourage applications from women, underrepresented ethnic groups, veterans, and individuals with disabilities. Texas A&M University also has a policy of being responsive to the needs of dual-career partners (hr.tamu.edu/employment/dual-career.html).

cairns@tamu.edu

UAlabama DrosophilaMetabolomics

Postdoctoral Fellow in Drosophila Metabolomics

A postdoctoral position in the cutting-edge field of metabolomics is available in the laboratory of Laura Reed, within the Department of Biological Sciences at the University of Alabama. The Reed Lab is a highly interactive group that conducts research on the genetic basis of genotype-by-environment interactions contributing to metabolic disease and variation in Drosophila. Major areas of research include QTL mapping of loci interacting with diet to produce obesity and type-2 diabetes phenotypes, evolutionary genetics of complex traits, functional analysis of candidate genes for metabolic phenotypes, whole genome expression analysis of genetic and environmental variation, and metabolomic analyses.

This opening is for a highly motivated postdoctoral fellow with familiarity with Drosophila and some background in bioinformatic methods. The postdoc will work to facilitate the data curation and experimentation goals of the International Drosophila Metabolomics Curation Consortium (IDMCC, http://flygxe.ua.edu/-metabolomics.html) including working to expand publically available tools such as MetScape 2.0 developed by researchers at the University of Michigan (metscape.ncibi.org, Karnovsky et al, 2012) and MetaCyc developed by researchers at SRI International in California (www.metacyc.org, Caspi et al, 2013) to incorporate Drosophila specific data. The postdoc will also work closely with the NIH Common Fund Metabolomics Data Center and Workbench (WDCW) at UC San Diego. While collating relevant data sources the postdoc will help identify critical gaps in the available knowledge needing further empirical work to fill, and would then have the opportunity to conduct some of those studies.

All candidates must have received a Ph.D. in a relevant field.

The position is available for 2 years with the possibility of renewal contingent on securing external funding, and will include a competitive salary and full benefits.

A successful applicant will have:

Extensive research experience

Creativity and independence

Genetic or molecular lab experience

Computational or bioinformatics experience

Excellent communication skills, both written and oral.

Application review will begin May 1, 2014 and will continue until the position is filled. The successful applicant should be able to beginning working in the position August 15, 2014.

Submit an application to the departmental postdoctoral pool https://facultyjobs.ua.edu/postings/33497 . Materials should include:

1. Cover letter with a description of past research accomplishments and future research goals, (maximum of two pages) and the names and contact information for 3 references. 2. Curriculum vitae

Contact Dr. Laura Reed (lreed1@as.ua.edu) with questions regarding the position or application process. For further information about the Reed lab visit flygxe.ua.edu.

About the University of Alabama

The University of Alabama is the flagship campus of the University System of Alabama, with an enrollment of over 35,000 students. The University is committed to achieving excellence as one of the country's primary centers of research and education. It is located in the vibrant college town of Tuscaloosa, AL, which boasts many cultural and athletic activities. The campus also benefits from the close proximity to the Birmingham metropolitan community.

The University of Alabama is an Affirmative Action/Equal Opportunity Employer. Women and minorities are encouraged to apply.

Laura K. Reed Assistant Professor Dept. of Biological Sciences University of Alabama, Tuscaloosa Office: 2330 SEC, Lab: 2322 SEC Mailing address: Box 870344, Tuscaloosa AL 35487

office: 205-348-1345 lab: 205-348-1368

lreed1@bama.ua.edu http://flygxe.ua.edu/
lreed1@ua.edu

UCalifornia Davis 2 MaizeEvolutionaryGenetics

Two postdoc positions are available in the lab of Jeffrey Ross-Ibarra at UC Davis to study the evolutionary genetics of maize and teosinte. We are recruiting for two projects:

An NSF funded project to use population genomics to understand local adaptation and inbreeding depression of teosinte and maize landraces. We are currently sequencing >100 maize and teosinte genomes from multiple populations, which serve as the parents of two large mapping populations for which phenotyping is under-way. Potential projects are flexible and include investigation of inbreeding depression, the effects of linked selection, and local adaptation.

A USDA- and industry-funded project to investigate regions of the maize genome under selection during modern breeding. Using genotype, phenotype, and pedigree data from thousands of maize inbred lines, we will use a number of approaches to understand the effects and targets of selection during the last 80 years of maize breeding.

Opportunities exist for both positions to additionally collaborate on a number of projects, including adaptation to high elevation in maize landraces and the population genetics of centromere evolution. Both positions are for one year, with the potential for a second year of support conditional on performance. Start dates are open-ended, with preference for earlier dates.

UC Davis has extremely strong programs in both plant and evolutionary biology. Candidates would have the opportunity to interact with members of the Center for Population Biology and the Genome Center as well as the Dept. of Plant Sciences.

Preference is for candidates with a strong background in evolutionary biology, proficiency in unix and experience with computational analysis of population genetic data. For more information or to apply, please send a cover letter and a CV with a list of references to rossibarra@ucdavis.edu.

Jeffrey Ross-Ibarra

Dept. of Plant Sciences and Genome Center 262 Robbins Hall, Mail Stop 4 University of California One Shields Ave Davis, CA 95616

Tel: 530-752-1152 Fax: 530-752-4604 www.rilab.org rossibarra@ucdavis.edu

UCalifornia Davis EvolutionaryGenomics

A postdoctoral position is available in Artyom Kopps lab starting in the summer of 2014. Our work focuses on the evolution of developmental pathways, especially with regard to evolutionary innovations and convergent evolution. By focusing on closely related species of Drosophila, we integrate molecular-genetic approaches with phylogenetic, quantitative-genetic, and population-genetic analyses. The main postdoctoral project would involve the identification of genes responsible for convergent evolution of sex-specific color patterns in different (non-model) Drosophila species. Additional projects may focus on the evolution of sex- and tissue-specific transcriptomes. Postdocs will be encouraged to develop independent research reflecting their own interests, within the broad field of developmental evolution and evolutionary genomics.

Initial appointment is for one year, extendable by mutual agreement. Candidates should have demonstrated expertise in genomics and bioinformatics/computational biology. Experience in eukaryotic genome assembly, resequencing, GWAS, RNA-seq, and ChIP-seq is highly desirable. Our lab provides a relaxed and supportive atmosphere. The broader research environment at UC - Davis offers postdoctoral fellows an excellent chance to interact and collaborate with many other people working in the fields of evolutionary genetics and comparative genomics. Northern California, where Davis is located, provides outstanding recreational opportunities. Interested applicants should contact Artyom Kopp (akopp@ucdavis.edu) with a CV, a brief statement of research interests, and the names of three references.

akopp@ucdavis.edu

UCalifornia LosAngeles EvolutionaryGenetics

Postdoc UCLA Bioinformatics and Evolutionary Genetics

University of California, Los Angeles Center for Tropical Research and Department of Ecology and Evolutionary Biology

We seek a highly qualified and enthusiastic individual to join our team to conduct bioinformatic analyses, develop statistical methods, and analyze population-level genetic data of select animals and plants from Central Africa. The overarching goal of the NSF-PIRE funded project is to develop an integrated, evolutionarily informed framework for conserving Central African biodiversity under climate change (for more information see http://www.caballiance.org/).

The successful candidate will be expected to analyze and manage genomic sequence data generated on next-generation platforms, construct and execute bioinformatic pipelines for de novo assembly, alignment, SNP detection, annotation, and assist in the development and implementation of novel methods of statistical analysis for genetic data in molecular ecology contexts. This project will provide an exciting opportunity for the analysis of cutting-edge genomic data from non-model systems. Specific activities will include, but are not limited to:

- Transcriptome assembly and alignment of non-model organisms - Comparing assembled transcriptomes to genomes from model taxa - Assigning locations of sequences identified by RAD-tag within a genome - Inference of population history and natural selection across diverse taxa

The postdoc will work under the joint supervision of Kirk Lohmueller <klohmueller@ucla.edu> (https://www.eeb.ucla.edu/Faculty/Lohmueller/) and Thomas B. Smith <tbsmith@ucla.edu> (http://www.environment.ucla.edu/ctr) at UCLA, but will be expected to collaborate closely with other PIRE collaborators, including Katy Gonder, Nicola Anthony, and other members of the PIRE team. The postdoc will also be encouraged to develop her/his own research focus on some aspect(s) of the project.

Application: Please send a single PDF containing a CV, a statement of research interests, and contact information for three references to Christa Gomez, cgomez@lifesci.ucla.edu with a subject of Bioinformatics Postdoc. Review of applications will begin June 1st, 2014. The postdoc is for two years with the possibility of renewal. Salary will be determined based on experience level.

tbsmith@ucla.edu

UCollegeLondon CooperationImprinting

Postdoctoral Research Fellowship University College London

1. The regulation of cooperation and cheating in the evolution of multicellularity 2. The evolution of genomic imprinting

A 2-year postdoctoral research fellowship funded by the EPSRC is available in the Department of Genetics, Evolution and Environment, UCL. We seek an enthusiastic and highly motivated postdoc, with experience in population genetics, game theory, mathematical modelling and computer simulation. The post holder will join the research group of Professor Andrew Pomiankowski working with Dr Nick Lane (UCL) or Dr Francisco Ubeda (Royal Holloway University of London). They will be a member of CoMPLEX (www.ucl.ac.uk/complex) and the 2020 Science Programme (www.2020science.net). They will join several other 2020 fellows appointed on this programme at UCL Oxford University and Microsoft Research Cambridge.

Suitable candidates will be highly motivated researchers with a PhD in a relevant area of science, such as: mathematical or computational biology, computer science or biology. Research experience of mathematical or computational modelling of complex natural systems is essential, as well as the ability to conduct and complete research projects, as witnessed by published peer-reviewed work. The post-holder is expected to be exceptional early-stage scientists who will apply for further research fellowship funding during the period of the award.

Please send expressions of interest & CV to ucbhpom@ucl.ac.uk. Further details and formal applications should use the following link http://www.2020science.net/news/2-x-research-fellow-positions-ucl Closing Date: 21 Apr 2014, 5pm

1) The regulation of cooperation and cheating in the evolution of multicellularity (with Nick Lane, UCL).

Projects in this theme will extend existing theoretical work on the transition from relatively simple prokaryotic forms of life to complex, multicellular eukaryotes. Research could focus on the origins of sexual reproduction, symbiosis with the proto-mitochondrion, multicellularity and the evolution of a germline, gene and protein interactions between mitochondria and the nucleus, or related topics.

2) The evolution of genomic imprinting (with Francisco Ubeda, Royal Holloway University of London).

Imprinted genes are either maternally expressed and paternally silenced or show the reverse pattern of gene expression. This project will develop a mathematical framework of the co-adaptation theory of genomic imprinting, the idea that imprinting coordinates expression of positively interacting loci in different individuals. The model will be integrated into the existing body of theory, in particular the kinship theory of imprinting.

Andrew Pomiankowski Professor of Genetics UCL ucbhpom@ucl.ac.uk ucbhpom@ucl.ac.uk

UFedSaoCarlos Brazil QuantGenetics

Another postdoctoral position (up to two years funding) is now available at the Universidade Federal de Sao Carlos (UFSCar) working with Reinaldo A. de Brito, in collaboration with Jason Wolf (University of Bath). The collaboration offers the opportunity for the postdoc to spend time in both Bath (UK) and Sao Carlos (Brazil), with empirical components being done in Sao Carlos and computational work being split between institutions.

The project is focused on understanding the genetic architecture of species differences in South American fruit flies of the group Anastrepha fraterculus (Diptera: Tephritidae). The primary goal of the project is to understand the nature of variation underlying traits that distinguish species (including major ecologically relevant traits as well as traits potentially involved in mate recognition) and how the species differences relate to within species variation.

The postdoc will contribute to empirical and computational components of the project. Empirical work will involve implementation of multigenerational breeding schemes, phenotyping and next-generation genotyping. Computational work will involve genome scale analysis of associations using marker and sequence data.

This is a second post-doc opportunity associated with the project previously advertised. We expect that this position will be filled by July (to ensure that the full two years of funding is available). We are looking for people interested in discussing the details of the project and the application process. If you expressed interest in the previously advertised position and would like to be considered for this second position, please let us know and send an updated CV.

Please contact either one of us for more information or to express interest.

Reinaldo A. de Brito brito@ufscar.br CCBS- Depto de Genetica e Evolucao Universidade Federal de Sao Carlos

Jason B. Wolf Jason@evolutionarygenetics.org Dept. of Biology & Biochemistry University of Bath

brito@power.ufscar.br

UFlorida EvolutionaryEcology

Postdoctoral Researcher position in butterfly evolutionary ecology at University of Florida

A Postdoctoral Researcher position is available at the Florida Museum of Natural History's McGuire Center for Lepidoptera and Biodiversity, University of Florida. The postdoc will form an integral part of the multi-institution team working on the NSF-funded project "Dimensions: Collaborative Research: Connecting the proximate mechanisms responsible for organismal diversity to the ultimate causes of latitudinal gradients in species richness". In particular, the postdoc will be responsible for conducting and coordinating ecological studies of Adelpha butterfly communities in several Neotropical field sites.

The deadline for applications is May 16th, 2014, with the position available from January 2015 (or earlier) for three years. Information on the position and application instructions are available here: http://www.flmnh.ufl.edu/butterflies/-neotropica/postdoc2014.html Please contact me (kwillmott@flmnh.ufl.edu) with any questions.

Keith Willmott Associate Curator for Lepidoptera

McGuire Center for Lepidoptera and Biodiversity Florida Museum of Natural History 3215 Hull Road, Powell Hall PO Box 112710 Gainesville, FL 32611 (USA) Tel: (1 352) 273 2012 Fax: (1 352) 392 0479

kwillmott@flmnh.ufl.edu

UIllinois FungalEcolEvolutionMetagenomics

Postdoctoral fellow in fungal metagenomics and ecology

A postdoctoral position is available in the department of Plant Biology, in the School of Integrative Biology, at the University of Illinois in Urbana-Champaign. PIs Astrid Ferrer (aquatic mycologist), Katy Heath (plant and microbe evolution), and Jim Dalling (plant and fungal community ecology) are looking for a highly motivated postdoc to work on a NSF-funded Dimensions of Biodiversity project aimed at understanding the ecological and genetic controls on fungal community assembly and decomposition function in tropical wood-decomposing aquatic fungi. Both the Heath and Dalling labs are lively, highly-collaborative environments with students and postdocs working on a range of topics in ecology and evolution of plants, bacteria, and fungi.

The duties of the project postdoc will include preparing libraries for metagenomic sequencing of aquatic fungi communities from environmental DNA samples, RNAseq of cultured fungi in response to various environmental treatments, downstream bioinformatic and statistical analyses, and writing manuscripts based on these results.

Expertise in some or all of the following areas is desired: Molecular biology, (meta)genomics, bioinformatics, statistical analysis, ecology, evolution.

Strong candidates will also possess the following attributes:

- A strong publication record from their PhD (papers published, in press, or submitted).

- Creativity, independence, and the desire to learn new things.

- Excellent communication skills, both written and oral.

All candidates must have received a Ph.D. in a relevant field. The position is available for 2 years, with the first year as a probationary period, and will include a competitive salary and full benefits.

Application review will begin May 1, 2014 and will continue until the position is filled. Start date is flexible, with a rough target date of August 2014. All materials should be submitted to the PIs below for consideration. Applications should include a brief cover letter, curriculum vitae, a brief description of past research accomplishments and future research goals (under two pages), and the names and contact information for three references.

Contact Dr. Katy Heath regarding the position or application process. For further information about the Heath lab, visit the lab webpage accessible at: http://www.life.illinois.edu/heath Katy Heath

Assistant Professor

Department of Plant Biology

University of Illinois

kheath@illinois.edu kheath@illinois.edu

UInnsbruck NextGenerationSequencing

EVOLUTIONARY SYSTEMATICS, INSTITUTE OF BOTANY, UNIVERSITY OF INNSBRUCK PostDoc position

The Evolutionary Systematics group of the Institute of Botany seeks to hire a PostDoc with experience in Next Generation Sequencing (wetlab and bioinformatic analysis of restriction site associated DNA [RAD] sequencing data). The position starts in autumn 2014 (exact starting date flexible; 40 h/week employment for 26 months). Centering on the Alpine Space, the group's mission is interdisciplinary research, embedded in international collaboration networks. A list of research topics can be found at: http://www.uibk.ac.at/botany/research/biodiversity/vascular_plants/index.html.en . The successful candidate will conduct NGS-based phylogeographic studies of a range of steppe organisms, including both plants and animals. The project consortium is international and includes members of the Universities of Innsbruck and Vienna (Austria), Lausanne (Switzerland) and the Real Jardín Botánico in Madrid (Spain). The project addresses the following issues: (1) Did the steppe biota colonize each Alpine dry valley independently or is there evidence for genetic exchange among the insular steppe habitats of different valleys? (2) What are the biogeographic connections of steppe biota from the Alpine dry valleys with other areas of steppe vegetation in Eurasia? (3) Are the phylogeographic patterns seen in steppe plants and animals congruent, implying range shifts of entire communities, or rather idiosyncratic, suggesting individualistic responses to climatic oscillations? (4) Our phylogeographic approach will unravel intraspecific patterns of spatial differentiation and temporal diversification across steppe plant and animal lineages. These will then not only be compared with each other, but also with data from independent sources. Changes of distribution ranges of our study taxa through time will be hindcasted using environmental niche modeling. A description of the project can be found at http://www.uibk.ac.at/botany/research/biodiversity/vascular_plants/steppe-flora.html.en).

Responsibilities 1. optimization of a double digest RAD sequencing protocol for the study species, barcoding of individuals for pooled analyses 2. processing raw Illumina data and filtering of SNPs 3. phylogeographic and phylogenetic (BEAST, ABC-approaches, etc.) data analyses 4. species distribution modeling with Maxent 5. leading role in manuscript writing 6. contact and collaboration with scientists and laboratory technicians at the Molecular Ecology group, Institute of Ecology, Innsbruck University, as well as at other Austrian research facilities, and internationally 7. possibly (but not necessarily!) sampling of steppe species in Europe (Alps, Eastern Europe) and central Asia in 2015

Selection criteria A. PhD degree in life sciences B. published research experience in molecular systematics / evolution / biogeography, especially using high-throughput sequencing data C. proficiency in maintenance of Linux systems for bioinformatic purposes, Biopython, mysql, scripting languages (e.g. awk, Perl, R) D. experience in the use of relevant software packages for phylogeographic / phylogenetic analyses E. ability to work as part of a multi-disciplinary team F. ability to work independently G. very good knowledge of English

Salary The annual gross salary is Euro 48,768 for a 40 h/week employment (26 months). This translates into a yearly net income of 31,037 EUR. Extension to 30 months and corresponding reduction of the weekly working hours are possible and welcome. The contract includes health insurance and 5 weeks of holidays annually.

How to apply To apply, please submit by E-mail to <peter.schoenswetter@uibk.ac.at>: a cover letter, systematic point-by-point replies as to your readiness for the responsibilities and how you meet the selection criteria, brief statement of research interests, curriculum vitae, a complete list of publications, and two reference letters.

Applications must be submitted in English until April 30th, 2014.

The University of Innsbruck is striving to increase the percentage of female employees and therefore invites qualified women to apply. In the case of equivalent qualifications, women will be given preference. An offer of employment is contingent on a satisfactory pre-employment background check.

The research institution and its environment Detailed information about the Evolutionary Systematics group can be found at http://www.uibk.ac.at/botany/units_research_groups/evolutionary_systematics.html.en .

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UKansas Bioinformatics

Postdoctoral researcher position available in computational global change ecology. Dr Daniel Reuman is recruiting into his lab in the University of Kansas Department of Ecology and Evolutionary Biology and the Kansas Biological Survey. Research will focus on software aspects of two large projects: 1) Ramifications of metapopulation synchrony through the complex North Sea and North Atlantic metacommunities in the face of climate change; and 2) Revealing the mechanisms linking the structure, functioning, and dynamics of whole ecological communities using likelihood. The researcher will be expected to contribute to software development for both projects, collaborating with teams of biologists, statisticians, and modellers and pursuing independent research questions. The position could be suitable for scientists from diverse training backgrounds. See http://employment.ku.edu/staff/313BR for details or to apply. Contact reuman@ku.edu with questions.

Daniel C. Reuman Senior Lecturer, Department of Life Sciences Imperial College London http://www3.imperial.ac.uk/people/d.reuman Visiting Assistant Professor, Laboratory of Populations, Rockefeller University Grand Challenges in Ecosystems and the Environment initiative, member

Director, MSc in Quantitative Biology http://www3.imperial.ac.uk/lifesciences/postgraduate/courselist/quantitative-biology
Director, MRes in Biodiversity Informatics and Genomics http://www3.imperial.ac.uk/pgprospectus/facultiesanddepartments/lifesciences/postgraduatecourses/biodiversityinformaticsgenomics
+44 (0)20 7594 2401

"Reuman, Dan" <d.reuman@imperial.ac.uk>

UKansas ComputationalBiol

Postdoctoral researcher position available in computational global change ecology. Dr Daniel Reuman is recruiting into his lab in the University of Kansas Department of Ecology and Evolutionary Biology and the Kansas Biological Survey. Research will focus on software aspects of two large projects: 1) Ramifications of metapopulation synchrony through the complex North Sea and North Atlantic metacommunities in the face of climate change; and 2) Revealing the mechanisms linking the structure, functioning, and dynamics of whole ecological communities using likelihood. The researcher will be expected to contribute to software development for both projects, collaborating with teams of biologists, statisticians, and modellers and pursuing independent research questions. The position could be suitable for scientists from diverse training backgrounds. See http://employment.ku.edu/staff/313BR for details or to apply. Contact reuman@ku.edu with questions.

d.reuman@imperial.ac.uk

ULille France Arabiodopsis SelfIncompatibility

Post-doctoral position on the origin of functional novelty at the self-incompatibility locus in Arabidopsis

We are looking for a post-doctoral associate to work on allelic diversification at the self-incompatibility locus in the outcrossing Arabidopsis species /A. halleri/. While the genes encoding self-incompatibility are typically highly multiallelic, the emergence of new allelic specificities has remained a mystery. This is in particular due to the functional constraint caused by the fact that these genes encode a molecular lock-and-key mechanism, whereby both the lock and the key must both be hit by novel cognate mutations in order for the system to remain functional. To address this issue, the project will use a ≪ resurrection ≫ approach to reconstruct ancestral protein sequences and express them in /A. thaliana/ using tools of genetic transformation to test whether contemporary specificities have retained identical recognition phenotypes as compared to their ancestor.

The ideal candidate should have either previous experience with genetic transformation in /A. thaliana/ and a keen interest in evolutionary biology or a strong background in evolutionary biology with demonstrated abilities in either molecular biology or the management of large experimental designs in plants. A high level of autonomy is required. Initial duration of the post-doc in one year with possible extension for an additional 6 months. Salary is competitive and commensurate with experience. The position is available now and the starting date should be no later than July 1^st .

Applicants should send a letter describing their qualifications, a research statement, a curriculum vitae, and names, addresses, email addresses and telephone numbers of three references through emails vincent.castric@univ-lille1.fr and Xavier.Vekemans@univ-lille1.fr

Contact :

Vincent CASTRIC & Xavier VEKEMANS

UMR CNRS 8198 Laboratoire de Genetique et Evolution des Populations Vegetales

Université Lille 1 - Sciences et Technologies

59655 Villeneuve d'Ascq

FRANCE

Vincent CASTRIC CR1 CNRS, HDR.

UMR CNRS 8198 Laboratoire de Genetique et Evolution des Populations Vegetales Université Lille 1 - Sciences et Technologies Batiment SN2, bureau 108 59655 Villeneuve d'Ascq - FRANCE Tel: +33 3 2033 5923 - Fax: +33 3 2043 6979 http://gepv.univ-lille1.fr/ Vincent CASTRIC <Vincent.Castric@univ-lille1.fr>

UMassachusetts Boston Phylogenetics

Postdoctoral research associate in phylogenetic comparative methods

A postdoctoral position is available in the Revell lab (http://faculty.umb.edu/liam.revell/) at the University of Massachusetts Boston in theoretical phylogenetics and/or computational phylogeny methods. Applicants should have a Ph.D. and extensive training and experience in one or more of the following areas: phylogeny method development or application in software; theoretical evolutionary quantitative genetics; and/or evolutionary computational biology. The ideal candidate will also have broad training in evolutionary biology, strong writing skills, and prior teaching or mentoring experience.

The postdoc hired from this search will play a key role in a recently funded NSF project to develop and apply new methods for evolutionary analysis in the context of phylogenetic trees. Major goals of this project include developing new visualization methods for phylogenetic comparative biology, improving the integration of phylogeny inference and comparative analysis, and bridging micro- and macroevolution in phylogenetic comparative biology. Consequently, the best candidate for this position will have skills and experience in multiple areas. The project also has substantial training goals, including the development of a new series of phylogenetic analysis mini-courses in Latin America, and a young developers' workshop at UMass Boston's Nantucket Field Station. The successful candidate will also be expected to participate in some of these programs.

The position is available for one year with the possibility of renewal. Start date is flexible. Please email Liam Revell (liam.revell@umb.edu) with any questions about this position.

A complete application for this position will include: (1) a brief cover letter; (2) a curriculum vitae; (3) a maximum two-page statement of your research experience & interest; and (4) names & contact information for three references. Applications can be submitted online via UMass Boston's Interview Exchange system via the following URL: http://www.phytools.org/postdoc.search/. The position is open until filled, but applications should be sent by May 29, 2014 for full consideration.

UMass Boston provides equal employment opportunities (EEO) to all employees and applicants for employment.

– Liam J. Revell, Assistant Professor of Biology University of Massachusetts Boston web: http://faculty.umb.edu/liam.revell/ email: liam.revell@umb.edu blog: http://blog.phytools.org Liam.Revell@umb.edu

UMichigan TreeSnail EvolGenomics

UMichigan.Tree.Snail.Evolutionary.Genomics

Postdoctoral opening in the evolutionary genomics of endangered tree snails

Position is available beginning October 2014 to work at the University of Michigan (Ann Arbor) with Diarmaid Ó Foighil and Taehwan Lee.

We are looking for a highly motivated postdoc with a background in comparative evolutionary genomics to participate in an ongoing research project. It concerns Tahitian tree snail species (Partulidae) that differentially survived a recent mass extinction event and involves working with museum, captive and remnant wild specimens. A background in invertebrate biology is preferred. Demonstrated expertise in next-generation sequencing, bioinformatics and comparative/population genomics is required.

The position will be initially funded for one year, with the possibility of renewal for up to two additional years contingent on funding and satisfactory performance. Salary and benefits are competitive. Ann Arbor is a classic American college town. It routinely makes the national "best of" lists (www.annarborusa.org/live-here/facts-rankings) and the University of Michigan's Department of Ecology & Evolutionary Biology is an excellent academic environment with a dynamic and interactive research program (http://www.lsa.umich.edu/eeb/).

The position is available October 1st 2014, but the start is flexible to some degree. Applicants should have earned their Ph.D. by September 2014 and should send (to the email address below) a cover letter with a statement of background and research interests, a *Curriculum Vitae* and the names and contact details of three references. Review of applications will begin May 1st, 2014; however, the position will remain open until filled.

Diarmaid Ó Foighil, University of Michigan Museum of Zoology and Department of Ecology & Evolutionary Biology, 1109 Geddes Avenue, Ann Arbor, MI 48109-1079.

diarmaid@umich.edu

Phone: 734 647 2193

www.lsa.umich.edu/UMICH/eeb/Home/People/O'Foighil-CV-2014.pdf The University of Michigan is an equal opportunity/affirmative action employer.

Diarmaid O'Foighil <diarmaid@umich.edu>

UMinnesota FungalGenomics

Postdoctoral Position - Fungal Genomics and Metabolomics University of Minnesota, St. Paul, MN

Position description:

A postdoctoral position focused on comparative genomics, metabolomics, and regulatory mechanisms of secondary metabolites in fungi is available in the Bushley lab. This project will focus on population genomics of fungi (Fusarium, Tolypocladium spp.) to investigate regulation and evolution of secondary metabolite genes, clusters, and metabolites. The project will adopt an interdisciplinary approach that integrates next-generation genome sequencing and assembly, comparative genomics, and RNA-Seq experiments with analyses of chemical products. Genome resequencing will examine the roles of structural variation, transposition, selection, genome methylation, and other evolutionary processes in driving the diversification of secondary metabolite genes and clusters. Strain specific differences in metabolite expression will be investigated under a variety of different media conditions and data will be integrated to develop and analyze metabolic and regulatory networks involved in controlling secondary metabolism.

Minimum requirements: A Ph.D. in molecular biology and genetics, mycology, genomics, chemistry, biochemistry, or related fields. The ideal candidate will have existing skills in two or more of the following: experience in sequencing and analysis of next-generation sequence data, bioinformatics and comparative genomics, molecular biology, mass spectrometry, nmr, and a willingness to learn new techniques. The initial appointments is for 1 year, with an opportunity for renewal for a second year. The position is available beginning in June 2014. Start date is flexible. Salary range $38,000 - $43,000 depending on experience, plus health benefits.

To apply: Any questions regarding the position should be directed to kbushley@umn.edu. Informal inquiries are welcome. Applicants must apply through the University of Minnesota Office of Human Resources website (employment.umn.edu/applicants/Central?quickFind9828) and include a CV, a cover letter detailing research interests and experience, and contact information for three references. Screening of applicants will begin May 15 until a suitable candidate is found.

Kathryn Bushley Assistant Professor University of Minnesota Department of Plant Biology 822 BioSci Bldg 1445 Gortner Avenue St. Paul, MN 55108

phone: 612-625-8213

Kathryn Bushley <kbushley@umn.edu>

UNebraska InsectAdaptation

A postdoctoral position is available in the Department of Entomology, University of Nebraska Lincoln. Nick Miller is looking for a motivated postdoc to work on the emerging adaptation of Diabrotica virgifera virgifera (western corn rootworm) to transgenic Bt maize. Responsibilities will include insect rearing for lab selection experiments and crosses, producing libraries for Illumina sequencing and analyzing data for population genomics and QTL mapping studies.

Required qualifications: A PhD in biology, genetics, entomology or a related discipline.

Desired qualifications: * Experience working with insects. * Experience with standard molecular techniques * Experience working with large data sets in a Linux/UNIX environment * Demonstrated ability to develop publishable manuscripts in a timely manner * Although not essential, some programming skills would be advantageous

The start date for the successful applicant will be around September ’ October 2014 but interested individuals are encouraged to apply immediately. For further information, please contact:

Nick Miller

Department of Entomology University of Nebraska-Lincoln Lincoln NE 68583 USA

nick.miller@unl.edu

UNotreDame MalariaMosquito PopulationGenomics

POSTDOC: Population Genomics of Malaria Mosquitoes

A Postdoctoral position (1 year with possible extensions up to 5 years) is available immediately in the evolutionary genomics group of Nora Besansky (www3.nd.edu/~nbesansk/).

We are seeking highly qualified and enthusiastic applicants with a quantitative background in theoretical/statistical population genetics and evolutionary biology, experience in genomic data analysis, and at least some knowledge of primary short read analysis.

Our ongoing research centers on the evolutionary, ecological and population genomics of Anopheles mosquitoes that transmit malaria. In particular, we study those species responsible for the majority of malaria cases and deaths on the African continent, An. gambiae and An. funestus. These two Afrotropical species each belong to cryptic species complexes bearing their names, and both nominal taxa display considerable genetic heterogeneity and population structure suggesting further genetic subdivision and potential speciation. We study their population genomics at different spatial scales, from local to regional and continental. We are particularly interested in how spatially varying selection (e.g., along environmental gradients of aridity: Cheng et al 2012, Genetics 190:1417), ongoing ecological speciation (e.g., Cassone et al 2014, Mol Ecol 10.1111/mec.12733; Guelbeogo et al 2014, Malar J 13:65), and genetic introgression (e.g., Besansky et al. 2003, PNAS 100:10818) impact patterns of genomic and transcriptomic variation. Specific projects ongoing in the laboratory include the functional genomics of chromosomal inversions–which we are approaching through systems genetics and genome-wide association studies, the genetic basis of saltwater tolerance in the An. gambiae complex, Y chromosome structure and evolution in the An. gambiae complex, and the ecological genomics of incipient species of An. gambiae and An. funestus. The availability of annotated reference genome assemblies for both species (Neafsey et al 2013, G3 3:1191), and their relatively small genome size (~250 Mb) allows us to use whole genome sequencing of pools or barcoded individual mosquitoes from natural populations to approach these questions. Our work on these large data sets is facilitated by extensive collaboration with computer scientists both on and off campus (S. Emrich, ND; A. Phillippy & S. Koren, Battelle National Biodefense Institute), and with a statistical geneticist (M. Hahn, Indiana University, Bloomington). In addition to the NIH-funded projects based in the Besansky lab, we are actively engaged in large international consortia, one of which is modeled on the Human HapMap project and has sequenced over 1000 individual An. gambiae genomes sampled across Africa (MalariaGen; www.malariagen.net/projects/vector). Furthermore, opportunities for collaboration and exchange are available with partners in Europe and Africa [F. Simard, C. Costantini: IRD, Montpellier; D. Ayala: IRD/Gabon; M.C. Fontaine: Univ. of Groningen, Netherlands (beginning Fall 2014)]. The successful candidate will help develop and lead a project in at least one of the areas of ongoing research in the laboratory, and would be expected to contribute collaboratively to others.

REQUIREMENTS: (1) A PhD in genetics/genomics, evolutionary biology, bioinformatics, or a related discipline; (2) a strong background in statistics and population genetics; (3) proficiency in the Linux/Unix computing environment and familiarity with R and at least one other programming language (e.g. Python or Perl); (4) experience with the analysis of high throughput biological data sets; and (5) good communication skills and proficiency in English, both speaking and writing.

PREFERENCES: If the Ph.D. was conferred in the biological sciences, we are looking for subsequent qualification and/or experience in bioinformatics; if the Ph.D. was conferred in statistics, computer science, or mathematics, we are looking for subsequent qualification and/or experience in the biological sciences. In addition to meeting all the requirements, the ideal candidate will be a highly motivated individual with demonstrated expertise in population genomics or human genetics and evolutionary biology, strong statistical skills, experience with next generation sequence and analysis of whole genome sequence data, a good understanding of molecular biology, and an excellent record of scientific publication. Fluency in French is a plus.

HOW TO APPLY: Applicants should submit a single PDF file (to nbesansk [at] nd.edu) containing (1) a cover letter briefly summarizing past research accomplishments and future goals; (2) a CV; (3) two recent publications; and (4) the names and contact information for three references. Screening of applicants will begin immediately and continue until the position is

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UOslo PaleoData

Be at the cutting edge: 3 year postdoc at the Centre for Ecological and Evolutionary Synthesis, University of Oslo modeling paleo data using capture-recapture, occupancy and comparative approaches. http://uio.easycruit.com/vacancy/1168135/96871?iso=no Lee Hsiang Liow (Ph.D) Centre for Ecological and Evolutionary Synthesis (CEES)

Department of Biosciences University of Oslo, Norway folk.uio.no/leehl

Lee Hsiang Liow <l.h.liow@ibv.uio.no>

URhodeIsland DiatomTranscriptomics

Postdoctoral Research Associate Position: Examining Microbial Interactions in Marine Plankton

The Rynearson lab at the University of Rhode Island, Graduate School of Oceanography invites applications for a Postdoctoral Research Associate. The research project, funded by the Gordon and Betty Moore Foundation, will examine microscale interactions between marine diatoms and bacteria and is a collaboration with Professor D. Hunt, Duke University.

Responsibilities and Duties: The postdoctoral associate will be primarily responsible for analysis of the gene expression component of the project and will be working with high-throughput transcriptomic data and physiological data to tease apart diatom-bacteria interactions. Responsibilities include dissemination of results in publications and presentations, contributions to the functioning of the lab, and assistance with graduate and undergraduate student mentoring. The successful applicant will have the opportunity to design follow-on controlled laboratory experiments and with future proposal preparation.

Qualifications: Candidates are required to have a Ph.D. degree by August 2014 in Computer Sciences, Oceanography, 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 either the analysis of high throughput sequencing data including programming knowledge or with experimental marine microbiology.

Appointment: The position is for 12 months initially, commencing July or August 2014 and renewable for an additional 12 months 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 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.

Closing date: For full consideration, applications should be received by May 5, 2014.Further information: Rynearson lab: http://www.gso.uri.edu/users/rynearson URI Graduate School of Oceanography: http://www.gso.uri.edu/ Hunt Lab: http://oceanography.ml.duke.edu/hunt/ Tatiana Rynearson <rynearson@mail.uri.edu>

USFS Oregon EvolutionaryGenetics

POST-DOCTORAL RESEARCH GENETICIST/ECOLOGIST

A postdoctoral research position is available at the USDA Forest Service Pacific Northwest Research Station in Corvallis, Oregon. The candidate will conduct ecological genetics research to explore population variation in adaptive traits of native grasses and forbs of the western United States. The primary goal of the research is to model responses in adaptation and adaptive traits as a function of the environments of planting sites and seed sources. The employee will use the knowledge gained to evaluate alternatives for guiding population movement for restoration of native plant communities including considerations of climate change. The position is a two-year, full-time term position, with the possibility for extension of an additional two years dependent upon funding and performance. Shorter appointments may be possible (e.g., sabbaticals for university faculty). Salary is approximately $61,867 per year (GS-11) depending on qualifications. The employee will be eligible for health and life insurance, annual (vacation) and sick leave, and will be covered by the Federal Employees Retirement System.

Qualifications: US citizen with PhD in ecology, botany, forestry, genetics or related field prior to beginning employment; demonstrated knowledge of statistical analysis and associated software (including SAS and R) for nonlinear mixed-effects models and multivariate analysis; demonstrated skills in communicating science through publications and public speaking; knowledge of GIS is desirable. The position is full-time for 13 to 48 months and will be filled at the GS-11 level.

To apply: Send curriculum vitae and cover letter indicating interests and qualifications along with a copy of your college transcripts (unofficial copies are fine). Include a list of your publications (including a pdf or link to one or more featured publications) and at least three professional references with information on how to contact them (email and phone number). Indicate when you would be available in your cover letter and please state that you are a US citizen. Applications will be accepted until close of business by April 30, 2014, but it is in the applicant's best interest to turn in their application as soon as possible. Send the information to Dr. Brad St.Clair at bstclair@fs.fed.us.

Please pass this advertisement on to interested parties.

Brad St.Clair Research Geneticist US Forest Service, Pacific Northwest Research Station 3200 SW Jefferson Way, Corvallis, Oregon 97331-4401 ph: (541) 750-7294, fax: (541) 750-7329 email: bstclair@fs.fed.us

bstclair@fs.fed.us

USP Brazil EvolutionModularity

Fellowship opportunity

- *No:* 602 - *Title:* Post doctoral fellowship in Evolutionary Biology - *Field of knowledge:* Genetics - * FAPESP process:* 11/14295-7 < http://www.bv.fapesp.br/pt/auxilios/46489/modularidade-e-suas-consequencias-evolutivas/ > (página do projeto na Biblioteca Virtual FAPESP) - *Project title:* Modularity and its evolutionary consequences - *Working area:* Evolutionary Biology - *Principal investigator:* Gabriel Marroig - *Unit/Instituition:* Instituto de Biociências/USP - *Partner Instituition:* - *Partner Representative:* - *Deadline for submissions:* 22/05/2014 - *Publishing date:* 17/04/2014 - * Summary:*

The Instituto de Biociências, located at the Universidade de São Paulo (USP) seeks candidates to fill a postdoctoral scholarship from FAPESP - *www.fapesp.br/en/5427*

The research area includes: The study of modularity (genetic and phenotypic) in bats and their evolutionary consequences for morphological diversification in the group.

The candidate should preferably have a database on morphometric data already collected in a representative group of bats with enough diversity and phylogenetic scope to allow analysis of modularity and the evolution of characters mean based on a comparative framework.

The candidate should also have a solid foundation in statistics, quantitative genetics, evolutionary biology and have notions of comparative analysis and programming.

This position will be under the supervision of Associate Prof. Gabriel Marroig. The candidate must be interested in working in collaboration with other researchers and postgraduate students within the research group.

The applicant must submit by May 22, 2014, for *gmarroig@usp.br* address, a text explaining their research experience and interest in the area as well as an updated resume containing names and contact information of three teachers who can provide references professionals about the candidate.

The candidate will be selected by the analysis of the documentation and the position is open immediately to implement the fellowship.

Gabriel Marroig <gmarroig@gmail.com>

UZurich Biodiversity

The Altermatt lab at the Institute of Evolutionary Biology and Environmental Studies (IEE) of University of Zurich and the Department of Aquatic Ecology of Eawag, Switzerland, has a vacancy for:

A Postdoc Position in Metacommunity-/Metaecosystem Ecology

Project title: Bridging biodiversity and ecosystem functioning in dendritic networks: a meta-ecosystem perspective

Understanding the causes and consequences of biodiversity is among the most challenging goals in ecology. Recent results indicate a generally positive effect of diversity on ecosystem processes. Up to now, almost all work on biodiversity-ecosystem functioning has been conducted in a non-spatial, one-patch perspective. Natural ecosystems, however, are spatially explicit, and there is substantial flow of material and organisms among patches and ecosystems. This project aims at applying the concept of meta-ecosystems to empirical data in spatially explicit dendritic networks.

In a project linked to two complementing PhD theses, the Postdoc Fellow will use a laboratory protist microcosm system to experimentally test interacting effects of habitat network structure and ecosystem functioning. As a group, we will extend these findings to mesocosm experiments and large-scale field studies with amphipods to study ecosystem functioning in Swiss river networks. The Postdoc will synthesize the findings, and link or expand existing theoretical work. In the whole project, diversity and ecosystem functioning will be studied in spatially explicit dendritic networks in a highly consistent framework. Ultimately, we want to get a comprehensive understanding of biodiversity and ecosystem functioning in riverine systems.

Competitive applicants will have previous experience in ecology, biodiversity and spatial dynamics and be interested in participating in this extensive new research project. They will be highly motivated, enthusiastic and independent scientists. Candidates should have a good conceptual understanding of ecological theory, excellent experimental skills and/or a strong background in quantitative modeling. Excellent communicational and writing skills in English, experiences with publishing scientific articles, good work ethics, and creative thinking are desired. A PhD in Ecology or related subject is necessary for admission. The working language in the Altermatt lab is English.

The Altermatt lab has a shared base at University of Zurich and at Eawag. It offers a stimulating and international research environment, excellent research facilities and a lively and social working place. Zurich hosts many other research groups in ecology and biodiversity research, and is among the world's leading cities in terms of science, culture and quality of life. The positions will be for a period of two years, and could start in the second half of 2014. The project is financed by the Swiss National Science Foundation (SNSF Research Professorship to Florian Altermatt from August 2014 onwards).

For further information, consult

http://homepages.eawag.ch/ ˜ altermfl/Home.html http://www.ieu.uzh.ch/index.html www.eawag.ch or directly contact Dr. Florian Altermatt: Tel: +41 58 765 55 92, E-mail: florian.altermatt@eawag.ch

Applications must be submitted by 10th May 2014 and should include a motivation letter with a description of pertinent experience, a complete CV (incl. publication list), the names (with e-mail addresses) of three academic references, and copies of certificates of academic qualifications. The application should be submitted as one single pdf-file.

We look forward to receiving your application through the online application form at:

http://internet1.refline.ch/673277/0266/++publications++/3/index.html Any other way of applying will not be considered.

florian.altermatt@eawag.ch

VanderbiltU EvolutionOfHumanBirth

PostDoctoral Position at Vanderbilt University - Evolution of Human Birth A postdoctoral position is available in the Rokas lab at Vanderbilt University in Nashville, Tennessee to study the evolutionary genomics of human pregnancy. The ideal candidate will have a strong background in evolutionary genomics, familiarity with scripting languages, a strong publication track record, and a commitment to teamwork.

The candidate will join a team of researchers working on developing the computational and conceptual tools necessary for generating a comprehensive evolutionary synthesis of human birth. Through the generation of database tools that will build bridges between evolutionary biologists, geneticists, molecular and developmental biologists, physiologists, obstetricians, and social anthropologists, and by exploiting the power of within and between species genomic comparisons, our research project aims to elucidate the evolution of human birth and pregnancy.

The project is funded by the March of Dimes and is in close collaboration with the Abbot lab (http://vanderbilt.edu/abbotlab/Home.html) and is one of the five major research themes that comprise the March of Dimes Ohio Collaborative (http://prematurityresearch.org/ohiocollaborative/).

For more information on the Rokas lab: http://as.vanderbilt.edu/rokaslab/ For more information on Nashville: http://www.vanderbilt.edu/nashville/ and http://www.nytimes.com/2013/01/09/us/nashville-takes-its-turn-in-the-spotlight.html Interested applicants are encouraged to send a CV, an one-page statement of past research accomplishments, and contact information for three references to Antonis Rokas at antonis.rokas@vanderbilt.edu

The position is available effective immediately. Best, Antonis

Antonis Rokas Associate Professor of Biological Sciences and Biomedical Informatics Cornelius Vanderbilt Chair in Biological Sciences Department of Biological Sciences Vanderbilt University VU Station B 351634, Nashville, TN 37235 Email: antonis.rokas@Vanderbilt.Edu Tel: +1-615-936-3892 Fax: +1-615-343-6707 http://as.vanderbilt.edu/rokaslab/ antonis.rokas@Vanderbilt.Edu

WashingtonU StLouis GenomicImprinting

Evolution of genomic imprinting postdoctoral fellowships at Washington University in St. Louis. Social insects provide an outstanding opportunity to test novel predictions of the kinship theory of genomic imprinting in social insects (Queller 2003 BMC Evolutionary Biology 3:15). This project involve testing for such imprinting using genomic techniques. Experience with RNA-seq methods and analysis is desirable.

David Queller and Joan Strassmann lead a friendly and interactive team of highly motivated, creative, and smart investigators. We are seeking energetic postdocs with strong backgrounds in areas such as evolutionary biology, social behavior, mutualism, microbial evolution, genomics, and molecular biology. Check out our website, (http://strassmannandquellerlab.wordpress.com/) for more information on our lab, or Strassmann's blog (http://sociobiology.wordpress.com). To apply, please email Patrick Clark (pclark@wustl.edu), specifying "imprinting postdoc" in the subject line. Please attach a single file including CV, statement of research interests, and the names, phone numbers, and email addresses of three references. Women and underrepresented minorities are particularly encouraged to apply. Funding is from the John Templeton Foundation. We will begin reviewing applications by 15 May 2014 and will continue to accept them until the positions are filled. Postdocs may start immediately but date is negotiable.

queller@biology2.wustl.edu

WashingtonU StLouis MicrobialSociality

Microbial sociality postdocs in the Queller-Strassmann lab at Washington University in St. Louis. One or more postdoctoral positions for 2-3 years are available for work on either of two projects involving evolutionary aspects of microbial sociality.

1. Experimental evolution of cooperation in microbes, especially in population structures relevant to "higher" organisms (Queller et al. 2013 Biology Letters 9:20130636; Kuzdzal-Fick et al. 2011. Science 334: 1548-1551)

2. The farming and defensive symbioses of Dictyostelium discoideum amoebas and bacteria (Brock et al. 2011 Nature 469:393-396; Brock et al 2013 Nature Communications 4:2385; Stallforth et al. 2013PNAS 110:14528-14533)

David Queller and Joan Strassmann lead a friendly and interactive team of highly motivated, creative, and smart investigators. We are seeking energetic postdocs with strong backgrounds in areas such as evolutionary biology, social behavior, mutualism, microbial evolution, genomics, and molecular biology. Check out our website, (http://strassmannandquellerlab.wordpress.com/) for more information on our lab, or Strassmann's blog (http://sociobiology.wordpress.com). To apply, please email Patrick Clark (pclark@wustl.edu), specifying either "experimental evolution postdoc" or "farming postdoc" in the subject line. Please attach a single file including CV, statement of research interests, and the names, phone numbers, and email addresses of three references. Women and underrepresented minorities are particularly encouraged to apply. Funding is from the John Templeton Foundation. We will begin reviewing applications by 15 May 2014 and will continue to accept them until the positions are filled. Postdocs may start immediately but date is negotiable.

queller@biology2.wustl.edu

YaleU MicrobialEvolution

Yale Postdoctoral Position in Microbial Evolutionary Ecology

A two- to three-year postdoctoral position is available immediately in the laboratory of Paul Turner in the Department of Ecology and Evolutionary Biology at Yale University. We are seeking a highly motivated and creative individual to participate in ongoing experimental projects relating to eco-evolutionary theory. These projects concern (i) role of environmental heterogeneity on adaptability of bacteriophages, (ii) role of niche construction in the evolutionary ecology of virus- cancer cell interactions, and (iii) effects of host density on virulence evolution in killer viruses of yeast. The successful candidate will engage in these projects in the first year, while increasingly developing and leading projects of their own design as the position continues. The experiments can utilize high-throughput, automated measures of evolving microorganisms via liquid-handling robotics. Experience with these technologies is preferred, but all strong candidates will be considered.

This postdoctoral position is in association with the Yale Institute for Biospheric Studies program in Eco-Evolutionary Dynamics, which is co-directed by David Vasseur, David Post, and Paul Turner. Through this program, the candidate will participate in regular working groups combining international leaders in experimental and theoretical approaches to eco-evolutionary dynamics. More information on the Department of Ecology and Evolutionary Biology is available at www.yale.edu/eeb. For information about postdoctoral appointments at Yale, see http://www.yale.edu/postdocs/. Applications should be emailed to Paul Turner (paul.turner@yale.edu) and include a CV, short statement of research interests, and contact information for three references. Applications will be considered beginning on May 1, 2014.

Paul E. Turner Chair of Ecology and Evolutionary Biology Yale University New Haven, CT 06520 (203) 432-5918 http://www.yale.edu/turner/ paul.turner@yale.edu

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ZEM UZurich EvolutionaryMedicine

Post-doctoral research associate. 70-100%. Starting date: from July 2014.

The Zentrum für Evolutionäre Medizin (ZEM) is an interdisciplinary centre specialising in the study of evolutionary medicine. We combine four main research areas (biomolecular, morphology, imaging and basic research) to investigate the evolution of diseases (including infectious and joint diseases) by the use of historical, archaeological and/or mummified remains.

The Molecular Group is based in the purpose built state-of-the-art ancient DNA laboratory, and comprises of one full time post-doc, two PhD students and a technician. We are seeking another postdoctoral associate.

The successful applicant will be highly motivated and skilled in all aspects of ancient DNA research and dedicated to furthering their career in academia (e.g. undertake habilitation) . S/he will be willing to assist in ongoing projects of the ZEM, be able to manage their own medically relevant research project as well as assist with student training, teaching and supervision.

Candidates must possess a PhD in ancient genetics or associated discipline with a minimum 3 years experience in ancient DNA. They must have high throughput sequencing experience, good communication (written and oral) skills and be abile to work in a team and individually. Bioinformatics experience and teaching / supervising experience are an advantage.

The position is open to individuals who wish to maintain existing associations, and may require international travel for sample identification and/or collection.

To apply please send a single .pdf file containing: Full CV, list of publications, past and present funding, two references, and a letter of motivation to irina.rau@uzh.ch by the 15th May 2014.

Abigail Bouwman <abigail.bouwman@uzh.ch>

WorkshopsCourses

Arolla Switzerland SocialEvolution Jul13-15

WORKSHOP

SOCIAL EVOLUTION: MERITS AND LIMITATIONS OF INCLUSIVE FITNESS THEORY

WHEN: 13-15 July 2014 WHERE: Arolla (Swiss Alps)

DESCRIPTION: Inclusive fitness theory is generally assumed to sufficiently explain the evolution of social behaviour. However, empirical evidence is accumulating that other evolutionary concepts need to be involved to explain cooperation and social structure in a wide range of taxa. This includes the archetypical examples of altruism, like the reproductive division of labour in eusocial hymenoptera and the cooperative breeding groups observed in many vertebrates. Recent evidence from insects and vertebrates reveals that high levels of relatedness can even reduce rather than further cooperation and altruism.

The aim of this workshop is to combine pertinent evolutionary theoreticians and empiricists to discuss complementary evolutionary mechanisms to inclusive fitness theory. This is a topic of great interest to students and biologists in general, because there is a growing awareness that explanations based on inclusive fitness, which have dominated the theoretical and empirical literature for the past half century, cannot account for many examples of apparently altruistic behaviour observed in nature.

INFO & REGISTARTION: http://biologie.cuso.ch/index.php?id=1128&clear_cache=1&tx_displaycontroller[table]=members&tx_displaycontroller[showUid]=1898

SPEAKERS: Prof. Rufus Johnstone, University of Cambridge (UK) Prof. Laurent Lehmann, University of Lausanne (CH) Dr Christina Riehl, Harvard University (US) Prof. Hanna Kokko, Australian National University (AU) Dr Erol Akcay, University of Pennsylvania (US) Dr Elli Leadbeater, University of London (UK)

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Caroline Betto-Colliard Department of Ecology and Evolution Biophore Building University of Lausanne CH-1015 Lausanne Switzerland

tel: + 41 21 692 4218 fax: + 41 21 692 4265 Office: 3206

http://www.unil.ch/dee/page55421.html Caroline Betto-Colliard <caroline.betto-colliard@unil.ch>

Cambridge WTAC GeneticAnalysisDiseases Jul23-29

Application Deadline Approaching, 11 April 2014

Human Genome Analysis, Genetic Analysis of Multifactorial Diseases Venue: Wellcome Trust Genome Campus, Hinxton, Cambridge, UK When: 23 - 29 July 2014

Course organiser: Daniel Weeks (University of Pittsburgh, USA) Course instructors: Heather Cordell (Institute of Genetic Medicine, Newcastle University, UK) Janet Sinsheimer (University of California, Los Angeles, USA) Eric Sobel (University of California, Los Angeles, USA) Joe Terwilliger (Columbia University, New York, USA) Simon Heath (Centre Nacional d'Anàlisi Genòmica (CNAG), Barcelona, Spain)

Guest speakers: Cornelia van Duijn (Erasmus University Medical Center, The Netherlands) Dajiang Liu (Penn State College of Medicine, USA) Dorret Boomsma (VU University Amsterdam, The Netherlands) Eris Moses (The University of Western Australia) Philippe Froguel (Imperial College London, UK)

Summary: This advanced course covers statistical methods currently used to map disease susceptibility genes, with an emphasis on (but not limited to) methods that can analyse family data or a combination of families and individuals. Discussions of the latest statistical methodology are complemented by practical hands-on computer exercises using state-of-the-art software. The statistical basics behind each method will be carefully explained so that participants with a non-statistical background can understand.

We will discuss fundamental issues needed to increase success in gene mapping studies including: optimal study design, power to detect linkage and association, determining the most appropriate statistical methods and software, interpretation of statistical results and trouble shooting. We will also cover the basic principles of statistical inference, hypothesis testing, population and quantitative genetics and Mendelian inheritance. Our interactive and intensive educational program will enable one to better carry out sophisticated statistical analyses of genetic data, and will also improve one's interpretation and understanding of the results. All the software used is freely available, so that skills learned can be easily applied after the course.

Teaching will take the form of lectures by invited speakers, informal tutorials, hands-on computer sessions, and analysis of disease family data sets. There will also be an opportunity to discuss participants' own data sets.

Registration fee and bursaries: Registration (including accommodation and all meals) £890. Limited bursaries are available covering up to 50% of the registration fee.

Full details: http://www.wellcome.ac.uk/Education-resources/Courses-and-conferences/Advanced-Courses-and-Scientific-Conferences/Advanced-Courses/WTX026851.htm JanetS@mednet.ucla.edu

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Finland InfectiousDiseases Aug17-24

LAST REMINDER (application deadline 15 April) Summer school: Dynamics of Infectious Diseases (17-24 August 2014, Finland)

Dear Colleagues,

We are pleased to invite students and young researchers to the 2014 edition of The Helsinki Summer School on Mathematical Ecology and Evolution, an EMS-ESMTB School in Applied Mathematics, which will focus on the dynamics of infectious diseases. The school will be held between 17 and 24 August 2014 in Turku, Finland. The core program consists of five series of lectures,

Odo Diekmann: Population dynamics of infectious diseases Frank Ball: Stochastic models of epidemics Thomas House: Networks and epidemics Michel Langlais: Spatial dynamics of infectious diseases Troy Day: Evolution of hosts and pathogens

All young researchers working in mathematical epidemiology, ecology or evolution can apply from all countries, especially from Europe and the Mediterranean. The school is aimed at graduate students of mathematics, but we also welcome students of biology with sufficient background in mathematics, as well as advanced undergraduates and postdocs.

The deadline for applications is 15 April 2014. There is no registration fee. For more details and application, see http://mathstat.helsinki.fi/research/-biomath/summerschool2014/ . Eva Kisdi, Mats Gyllenberg and Elina Numminen

kisdi@mappi.helsinki.fi

Ireland PhylogeneticSummerCourse Aug31-Sep5

Dear EvolDir readers,

We are pleased to announce a week-long, intensive phylogenetics course covering all aspects of modern molecular phylogenetics and phylogenomics.

This course starts with the basics of phylogenetic reconstruction and deals with all the major methods and all kinds of data from genes to genomes. Therefore, it is particularly suited to researchers that have a keen interest in phylogenetic reconstruction but have little or no practical experience or theoretical background (ideally suited to new Masters/PhD students/post-docs, but also investigators moving into this area of research). We welcome organismal phylogeneticists or genome scientists who are trying to make sense of the evolutionary history of any kind of gene or genome.

You can find out more about this course here:

http://bioinf.nuim.ie/phylogenetics-summer-course-2014/ Please pass this message on to anybody you feel might be interested.

Kindest regards,

James.

James McInerney PhD DSc, Molecular Evolution & Bioinformatics Unit, Department of Biology, National University of Ireland Maynooth, Co. Kildare, Ireland. website — http://bioinf.nuim.ie/james-mcinerney/ mcinerney.james@gmail.com

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Jaca Spain MarginalPopulationsAdaptation Jul7-11

The 2014 Training School of Cost Action FP1202 MaP-FGR will be organized in Jaca (Spain) on 7-11 July 2014, kindly hosted by University of Saragoza.

The topic of this 2014 TS will be "Adaptation and evolution of Marginal-Peripheral populations of forest trees at the leading, altitudinal and rear edges of species distribution".

The TS will focus on: Introduction of "population", "marginal-peripheral (MaP) population" concepts; Ecological aspects of forest species distributions; Forest population genetics and the key role of MaP populations; Conservation and adaptation of MaP populations (including adaptation, resilience and phenotypic plasticity in MaP populations); MaP at leading edges, Map at rear edges and MaP at altitudinal edges; Scientific methods on adaptive traits and strategies related to the conservation in situ and ex situ of MaP populations and related forest genetic resources; Management of MaP reproductive materials and related legislation (based on information available in National Reports prepared by European/Mediterranean partners in the context of the first State of the World Forest Genetic Resources). Presentation of most recent study cases on adaptation and evolution of MaP FGR at the edges of species distribution ; Presentation of the trainees own researches on MaP population and FGR.

Financial support is available for trainees from COST countries, approved Near Neighbour Institutions (NNC) and approved European RTD Organisations.

The call for applications and the related Vademecum are available on the webpage of the Cost Action MaP-FGR at http://map-fgr.entecra.it/?p05 . Deadline for application is 16th May 2014.

bruno.fady@avignon.inra.fr

MathVillage Turkey QuantEvolutionaryBiol Sep14-21 Deadline

****NOTE that the early application deadline is next week: April 22nd.

*Workshop / Summer school “Quantitative Evolutionary Biology – understanding evolution with models and genomes.”

*Time and Place September 14-21, 2014, Mathematics Village, Sirince, near Izmir (western Turkey).

*Keynote lecturers Aida Andres (MPI for Evolutionary Anthropology, Leipzig) Nick Barton (IST-Austria, Klosterneuburg) Thomas Lenormand (CEFE/CNRS, Montpellier) Pleuni Pennings (Stanford University, California)

*Description The workshop is mainly targeted towards advanced graduate students and early post-docs studying evolutionary theory, evolutionary genetics or evolutionary genomics. However, we also accept a limited number of more experienced researchers in these fields that can share their knowledge with the students and that are open to collaboration with the scientists in the workshop. The main body of the workshop will consist of keynote lectures (see above), and group projects developed by students under the supervision of young scientists. There will also be various short lectures and seminars during the workshop.

*For more information, visit http://qevolution2014.wordpress.com/ *Application deadlines Early: April 22, 2014 (recommended as the number of attendees and fellowships are limited) Late: June 15, 2014

*Other Participating Scientists Melis Akman (UC, Davis), Tugce Bilgin (UZH, Zurich), Emily Jane McTavish (University of Kansas), Tiago Paixao (IST Austria), Lilia Perfeito (Gulbenkian Inst, Oeiras)

*Organizers Mehmet Somel (METU, Ankara), Hannes Svardal (GMI, Vienna), Murat Tugrul (IST Austria)

*Co-sponsor: ESEB Global Training Initiative & NESCent

Murat Turul

PhD Student @ Barton Group Evolutionary Genetics, IST-Austria

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Murat Tugrul

muratugrul@gmail.com

MDIBL Maine EnvironmentalGenomics Aug2-9

Next-Generation Summer Course in Environmental Genomics at the Mount Desert Island Biological Lab

A technical course to guide research into how environmental conditions affect gene responses and the fitness of organisms

Date: August 2 to August 9, 2014. Number of participants: Restricted to 25.

http://www.mdibl.org/courses/-Environmental_Genomics/399/ The faculty at MDIBL is pleased to again offer a training course in Environmental Genomics, aiming to better understand technologies and approaches used to discover how gene function is influenced by environmental conditions while accounting for variation that exists within and among natural populations. This course is built on the paradigm that the research field will most effectively grow by properly designing large-scale experiments enabled by drastically increased sample-throughput and lower sequencing costs. Most importantly, the bioinformatics challenges of manipulating and analysing population-level genomics data must be addressed.

This course is designed to train the next-generation of environmental scientists, which have included in past years: university professors, postdoctoral researchers, doctoral students and government scientists, representing institutions from North America and Europe. Most responded in the departure survey that the course curriculum, choice of technologies, and effectiveness provided sufficient training to either begin or enlarge an environmental genomics project in their own laboratories. All reported that they would recommend this course to a colleague.

This course trains researchers to design studies, and to collect and analyse DNA re-sequencing and RNA-Seq gene expression data. Daphnia is used for training because of its growing use as a model system for environmental genomics and for improving environmental health protection, yet the skills learned during the course will be applicable to all study systems with maturing genomics resources. Much time is devoted to guiding the current and future projects of attendees.

Ultimately, participants will be better positioned to incorporate these technologies into their own research laboratories, while better understanding how functional genomics and automation can be applied to ecology, evolution and environmental toxicology.

Course Faculty include: * John Colbourne (University of Birmingham & MDIBL) * Joseph Shaw (Indiana University & MDIBL) * Benjamin King (MDIBL) * Andrew Whitehead (University of California Davis) * Gary Churchill (Jackson Laboratory) * Trudy Mackay (North Carolina State University) * Thomas Hampton (Dartmouth College) * Luisa Orsini (University of Birmingham) * John Novembre (University of Chicago) * Michael Herman (Kansas State University) * Wes Warren (The Genome Institute, Washington University)

plus many more. Mount Desert Island Biological Laboratory Old Bar Harbor Rd., Salisbury Cove, ME 04672 MDIBL - http://www.mdibl.org j.k.colbourne@bham.ac.uk

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MTRL Florida MethodsGenomicAnalysis Jun15-Jul5

Dear colleagues -

After receiving overwhelming interest we are excited to announce that we will be teaching three workshops on Methods in Ecological and Evolutionary Genomics at the Mote Tropical Research Laboratory, Florida Keys.

Metabarcoding of Symbiont Communities June 15 - June 20

Whole-genome genotyping with 2bRAD June 20 - June 27

Global gene expression profiling with tag-based RNA-Seq June 27 - July 5

To learn more about the specifics of each workshop, please go to our website: http://www.bio.utexas.edu/research/matz_lab/matzlab/MEGA2014.html Prerequisites The workshops aim at researchers at or above graduate-level actively working in the field of evolution and/or ecology. Practical molecular biology experience, however limited, will be helpful. People with earlier experience with metabarcoding, RNA-seq and RAD are welcome: we use the latest wet-lab methods and analysis protocols developed in the Matz lab, which would be very useful even for an experienced practitioner. The students will need to bring your own laptop with installed R and (for PC users) SSH terminal application.

To enroll By April 30, 2014, send an email with "MEGA 2014" in the subject line to all the instructors (Mikhail Matz <matz@utexas.edu>, Sarah Davies < daviessw@gmail.com>, Rachel Wright <rachelwright8@gmail.com>), indicating your interest, and a short description of your research focus (or simply references to your relevant publications). Please specify how likely you are to participate, assuming that you will have to pay the workshop's fee by May 15 (more details on making payments will be provided here later). Each part of the workshop is limited to 12 participants, first come first serve (assuming the prerequisites are met).

Please do not hesitate to contact us should you have any questions. Best regards,

Mikhail V. Matz: matz@utexas.edu Sarah W. Davies: daviessw@gmail.com Rachel M. Wright: rachelwright8@gmail.com

Sarah W. Davies M.Sc. Graduate Student University of Texas at Austin

daviessw@gmail.com

MTRL Florida MethodsGenomicAnalysis Jun15-Jul5 2

We are very excited to offer the Methods in Ecological Genomics Workshops this summer in the Florida Keys. Unfortunately, for some reason we don't seem to be receiving nearly as many applications in response to the official workshop announcement (http://www.bio.utexas.edu/research/matz_lab/matzlab/MEGA2014.html) as the community interest expressed in our earlier surveys have suggested. If you plan on attending any of our workshops but are waiting on financial approval, please still email us to avoid the cancelation of these workshops.

To express interest please send an email with "MEGA 2014" in the subject line to all the instructors (Mikhail Matz <matz@utexas.edu>, Sarah Davies < daviessw@gmail.com>, Rachel Wright <rachelwright8@gmail.com>) with just a few words about yourself:

1. Are you a graduate student, postdoc, or faculty?
2. Where?
3. What is you research area?

Hope to see you in Florida!

Sarah W. Davies, Ph.D.

University of Texas at Austin

daviessw@gmail.com

MTRL Florida MethodsGenomicAnalysis Jun15-Jul5 Deadline

Hello colleagues,

We just wanted to remind you that the deadline for signing up for our Methods in Ecological Genomic Analysis (MEGA) workshops is fast approaching!

http://www.bio.utexas.edu/research/matz_lab/matzlab/MEGA2014.html Metabarcoding of Symbiont Communities June15 - June 20

Whole-genome genotyping with 2bRAD -very few spots left! June 20 - June 27

Global gene expression profiling with tag-based RNA-Seq - very few spots left! June 27 - July 5

By April 30, 2014, please send an email with 'MEGA 2014' in the subject line to all the instructors (Mikhail Matz <matz@utexas.edu>, Sarah Davies <daviessw@gmail.com>, Rachel Wright <rachelwright8@gmail.com>), indicating your interest, and a short description of your research focus (or simply references to your relevant publications). Please specify how likely you are to participate, assuming that you will have to pay the workshop's fee by May 15. Each part of the workshop is limited to 12 participants, first come first serve (assuming the prerequisites are met).

As always please email if you have any questions! We hope to see you in Florida this summer! Cheers Misha, Rachel and Sarah

Sarah W. Davies Ph.D. University of Texas at Austin

daviessw@gmail.com

Online GMOD Training May19-23

http://gmod.org/wiki/GMOD_Online_Training_2014 The Generic Model Organism Database (GMOD; http://gmod.org) project is offering an online training course for those interested in learning how to use and deploy GMOD's free, open-source bioinformatics software. The GMOD project provides interoperable tools for visualising, storing, and disseminating genetic and genomic data.

The course will be held from 19th-23rd May 2014, with online tuition and interaction with tutors occurring between (approximately) 9am and 5pm US Eastern time.

Components covered in the online training include:

-Chado database schema -Galaxy analysis pipeline -GBrowse genome browser -JBrowse genome browser -MAKER genome annotation pipeline -Tripal website generator and database interface -WebApollo manual gene annotation software

By the end of the course, participants will have hands-on experience of setting up and using core components needed for a modern genomics project.

More information and application form: http://gmod.org/wiki/GMOD_Online_Training_2014 Please feel free to email help@gmod.org if you have any questions.

– Amelia Ireland GMOD Community Support Generic Model Organism Database project http://gmod.org || @gmodproject

amelia.ireland@gmod.org

Oxford BiolSeqAnalysis Jul16-19

BIOLOGICAL SEQUENCE ANALYSIS AND PROBABILISTIC MODELS Workshop

* 16-19 July, 2014 * Venue: Merton College, Oxford * Registration and Abstract deadline: 19 May * Registration includes lodging and meals * Website for more information: alturl.com/sz33u

The fields of genetics and evolutionary biology are currently developing at a huge pace. As a result our underlying theoretical understanding, our models of genetics and evolution, as well as their associated inferential methods are all undergoing rapid development, underlining the interest for a meeting dedicated to this topic.

The focus of the meeting will be methods and inference in population genetics, phylogenetics and functional genomics. This meeting brings together leaders from several areas of biological sequence analysis, with an emphasis on advancing the underlying theoretical models that many problems share. Topics will include evolution of pathogens; disease epidemiology; the population genetics of cancer; and phylogenetic and population genetic models for studying sequence evolution.

The conference will be held in Merton College, Oxford, UK, one of the city's oldest colleges. The registration fee of Â£385 includes on-site housing and meals.

For more information and signing up, go to the following website: alturl.com/sz33u

We will be able to host up to ~90 participants. All participants are expected to contribute actively by presenting a talk or a poster. Additional speakers will be selected based on submitted abstracts. To promote scientific collaboration, we will distribute an abstract book that will include contact information for all attendees.

Organisers: Adam Siepel Anders Krogh Gerton Lunter Gil McVean Molly Przeworski Richard Durbin Thomas Mailund

Confirmed speakers: Aleksandra Walczak Alexei Drummond Amy Williams Asger Hobolth Barbara Engelhardt Carolin Kosiol Dan Gusfield Daniel Wegmann David Balding Heng Li Ida Moltke Ines Hellmann Joe Pickrell Jonathan Marchini Kay Prüfer Kelley Harris Lior Pachter Peter Ralph Sharon Browning Simon Myers Yun Song Zam Iqbal Benedict Paten Jouni Sirén

Guy Sella Philipp Messer Johannes Soeding

Adam Charles Siepel <acs4@cornell.edu>

Roscoff France MarineGenomics May25-Jun7

SUMMER COURSE ON MARINE GENOMICS AT THE MARINE BIOLOGICAL STATION OF ROSCOFF (F)

Second announcement

>From May 25th - June 7th, 2014 the 10th Summer Course on Marine Evolutionary & Ecological Genomics will take place at the Station Biologique de Roscoff, Roscoff, France.

Aims: The two week course, which consists of lectures, tutorials and computer labs, aims to highlight the crucial role of marine genomics for the understanding of the marine environment and for an efficient use of its resources. It takes place at the Biological Station, a vibrant research community of 273 scientists and support personnel, located in the old town and fishing port of Roscoff, Brittany, France. Advanced PhD students and junior postdocs are encouraged to apply.

The course includes lectures, tutorials and computer based exercises on the following topics. * Genomics - next generation sequencing, database searching, basic skills in data handling and bioinformatics * Population genomics - diversity, structure, connectivity and gene flow, assignment, effective population size, population dynamics, adaptive variation * Environmental genomics - environment - genome interactions, ecogenomics, metagenomics and metagenetics * Functional genomics - genome structure, molecular evolution at the functional level, genomic architecture, functional networks * Comparative genomics - whole genome comparisons, concatenated phylogenies, genome organization, annotating genomic information, co-evolution

The course covers all aspects of life in the ocean.

Target group PhD students (at least in their second year) and junior postdocs with a solid knowledge in phylogenetics and/or population genetics. 18 participants will be selected on the following criteria: 1. Relevance of the course for their PhD or post-doc project 2. Background and experience 3. We aim at training people with different research backgrounds; not more than one person per institute will be considered. We implement a gender policy.

The selected persons will be notified by mid April and will have to confirm attendance within 7 days. There is a waiting list in case of non-confirmations and cancellations.

Teaching staff : Jonas Collén, SB-Roscoff, FR Simon Creer, U Bangor, UK Yves Desdevises, UPMC, Banuyls, FR Jakob Hemmer-Hansen, DTU-Aqua, DK Erica Leder, U Turku, Fi Frédéric Partensky, SB-Roscoff, FR Daniel Vaulot, SB-Roscoff, FR Filip Volckaert, KULeuven, BE Mathias Wegner, GEOMAR, Kiel and AWI-Sylt, GE

Organizing committee Jonas Collén, SB-Roscoff, FR Damien Guiffant, SB-Roscoff, FR Matthias Obst, Univ. Gothenburg, SW Jeanine Olsen, Univ Groningen, NL Filip Volckaert, KU Leuven, BE

For information and application please check http://meeg2014.sciencesconf.org . The application deadline is April 8 2014.

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

SWRS Arizona LepidopteraEvolution Aug14-23

Announcing the sixth annual Lep course, 14- 23 August, 2014.

Held at the South West Research Station (SWRS) in the Chirichahua Mountains in SE Arizona (a 2 1/2 hour drive from Tucson), the focus of the Lep course is to train graduate students, post-docs, faculty, and serious citizen-scientists in the classification and identification of adult lepidoptera and their larvae. Topics to be covered include an extensive introduction into adult and larval morphology with a focus on taxonomically-important traits, extensive field work on both adults and larvae, collecting and curatoral techniques, genitalic dissection and preparation, larval classification, use (and abuse) of DNA bar coding, and general issues in lepidoptera systematics, ecology, and evolution.

THE LOCATION: With its extensive series of Sky-Island mountain ranges, SE Arizona has the highest lepidoptera diversity in the US. With low desert scrub, oak and mixed oak-pine woodland, lush riparian, juniper, Douglas fir, and mountain meadow habitats all within a 40 minute drive from the station, the SWRS is an ideal location from which to sample this diversity (of both habitats and species).

Partial list of Invited instructors (subject to change): John Brown (Smithsonian), Rich Brown (Mississippi Entomological Museum), Marc Epstein (CDFA), Chris Grinter (Denver Museum of Nature & Science), Bruce Walsh (University of Arizona), Dave Wagner (University of Connecticut) and Ray Nagle (University of Arizona).

Fees: Tuition for the course is $1070 for students and $1170 for non-students to be paid by all participants on being informed of their acceptance. Tuition covers overhead costs of the workshop and room and board at the SWRS. Deadline for applications is 14 June 2014.

For more information, see http://research.amnh.org/swrs/education/lepidoptera-course or www.lepcourse.org or contact Bruce Walsh at jbwalsh@u.arizona.edu You can also see photos and comments from students in previous courses at their facebook site, “2011 Lep Course, SWRS SEAZ”.

jbwalsh@email.arizona.edu

UFribourg Switzerland GenomicsSpeciationContinuum Sep4-5

Dear colleagues,

I am pleased to inform you that registration for our 2014 'Fribourg Ecology & Evolution days' workshop is now open. The event will take place on 4-5 September 2014 at University of Fribourg, Switzerland. The theme of this year's workshop is 'GENOMICS OF THE SPECIATION CONTINUUM'.

Invited Speakers: NICOLAS BIERNE, CNRS Montpellier (FR) ALEX BUERKLE, University of Wyoming (USA) MIKKEL SCHIERUP, Aarhus University (DK) OLE SEEHAUSEN, EAWAG (CH) TANJA SLOTTE, Uppsala University (SE) JOHN WIENS, University of Arizona (USA)

Organizers: CHRISTIAN LEXER, University of Fribourg (CH) DANIEL WEGMANN, University of Fribourg (CH) HEINZ MUELLER-SCHAERER, University of Fribourg (CH) ALEX WIDMER, Swiss Federal Institute of Technology (ETH), Zurich (CH)

Our yearly Fribourg Ecology & Evolution workshops gather lively small crowds of PhD students and researchers around our invited speakers. Previous editions of this workshop series have triggered stimulating discussions on topics of mutual interest in an informal setting, and we look forward to continuing this tradition with this year's event. For more information about the workshop and venue, please visit:

http://www.unifr.ch/biol/ecology/CUSO/EEday2014/index.html Abstract submission is now open and closes 1 July. Registration is now open and closes 1 August.

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UlosAndesBogota Phylogenetics Jul8-11

This is just a reminder that applications for our Universidad de los Andes, Bogotá course on phylogenetic comparative methods in R are due in one week on Thursday May 1, 2014. The course is free to attend, and we expect that the majority of admitted students coming from outside Bogotá will be offered support for travel & accommodation. More information can be found in the original English & Spanish advertisements, below:

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Intensive short course on phylogenetic comparative methods in R (Spanish description below)

We are pleased to announce a new graduate-level intensive short course on the use of R for phylogenetic comparative analysis. The course will be four days in length and will take place at the Universidad de los Andes, Bogotá, Colombia from the 8th to the 11th of July, 2014. This course is partially funded by the National Science Foundation, with additional support from the University of Massachusetts Boston and the Universidad de los Andes. There are a number of full stipends available to cover the cost of travel, room and board for qualified students and post-docs. Applicants are welcome from any country; however we expect that most admitted students will come from Colombia and the Andean region. Accepted students from further afield may be offered only partial funding for their travel expenses. Topics covered will include: an introduction to the R programming language, tree manipulation, independent contrasts and phylogenetic generalized least squares, ancestral state reconstruction, models of character evolution, diversification analysis, and community phylogenetic analysis. Course instructors will include Dr. Liam Revell (University of Massachusetts Boston), Dr. Luke Harmon (University of Idaho), and Dr. Andrew J. Crawford (Universidad de los Andes).

Instruction in the course will be primarily in English; however some of the instructors and TAs of the course are competent or fluent in Spanish and English. Discussion, exercises, and activities will be conducted in both languages.

To apply for the course, please submit your CV along with a short (maximum 1 page) description of your research interests, background, and reasons for taking the course. Admission is competitive, and preference will go towards students with background in phylogenetics and a compelling motivation for taking the course. Applications should be submitted by email to bogota.phylogenetics.course@gmail.com by May 1st, 2014. Applications may be written in English or Spanish; however all students must have a basic working knowledge of scientific English. Questions can be directed to liam.revell@umb.edu.

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Curso posgrado de métodos comparativos filogenéticos en R

Nos complace anunciar un nuevo curso corto e intensivo a nivel de posgrado sobre el uso de R en investigaciones científicas que usan métodos comparativos filogenéticos. El curso tendrá una duración de cuatro días y se llevará a cabo en la Universidad de los Andes (Bogotá, Colombia) entre el 8 y el 11 de julio de 2014. Este curso está parcialmente financiado por la National Science Foundation de los Estados Unidos, con el apoyo adicional de la Universidad de Massachusetts Boston y la Universidad de los Andes. Hay varios estipendios completos disponibles para cubrir los costos de tiquetes y alojamiento para estudiantes e investigadores postdoctorales calificados. Estudiantes de cualquier país serán aceptados; sin embargo anticipamos que la mayoría de los estudiantes aceptados serán de Colombia y otros países andinos. Estudiantes provenientes de países más alejados tendrán la posibilidad de recibir solo apoyo parcial para costear los gastos del viaje. Los temas que serán discutidos en el curso incluyen: una introducción al idioma de programación de R, manipulación de los árboles filogenéticos, mínimos cuadrados generalizados en un contexto filogenético, reconstrucciones de los estados ancestrales, modelos de evolución, análisis de la diversificación en el contexto de una filogenia, y análisis filogenéticos de comunidades ecológicas. Los instructores del curso serán: Dr. Liam Revell (University of Massachusetts Boston), Dr. Luke Harmon (University of Idaho), y Dr. Andrew J. Crawford (Universidad de los Andes).

El curso será dictado principalmente en inglés; sin embargo algunos de los instructores y TA del curso hablan fluido el español. Las discusiones, los ejercicios, y las actividades del curso se harán en español e inglés.

Para aplicar al curso, deben enviar una copia de su CV con una corta (1 página) descripción de sus intereses científicos, experiencia, y razones por las cuales quieren tomar el curso. El proceso de admisión será competido, y se preferirán estudiantes con conocimientos en filogenética

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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

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.