EvolDir

April 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

AsilomarUSA InvasionGenetics Aug13-15

REGISTRATION NOW OPEN!

Invasion Genetics: The Baker and Stebbins Legacy A symposium at Asilomar, CA (USA) 13-15 Aug 2014

We are nearing the 50th anniversary of one of the most important books in evolutionary biology: The Genetics of Colonizing Species (1965) edited by Herbert Baker and G. Ledyard Stebbins. This classic volume was based on a symposium at Asilomar, California in 1964 and initiated the study of the genetics and evolution of invasive species. To revisit the historical legacy of the meeting and book, we are pleased to announce a symposium at Asilomar from August 13-15, 2014. The symposium will enjoy support from Wiley-Blackwell Publishers, and associated original papers will appear in a Special Issue of Molecular Ecology in 2015. The symposium proceedings (including the popular question-answer transcripts of the original) will also be published in 2015 as a book to mark the 50th anniversary of the original volume.

Please plan on joining us for this special event! DATES: August 13-15, 2014 LOCATION: Asilomar Conference Grounds (http://www.visitasilomar.com/)

REGISTRATION: Details at http://invasion-genetics.eventbrite.com Contributed posters will be welcomed - title submission will open June 1, 2014.

SPEAKERS/AUTHORS: We have confirmed a broad range of contributors to reflect both the legacy of work on the genetics of colonizing species, and new contributions and perspectives:

Spencer Barrett Tim Blackburn Mark Blows Oliver

Bossdorf Rob Colautti Melania Cristescu Troy Day Katrina Dlugosch Kay Hodgins Pierre Gladieux & Tatiana Giraud Mark Kirkpatrick Russ Lande Jennifer Lau Jonathan Losos John Pannell Stephan Peischl & Laurent Excoffier Loren Rieseberg Johanna Schmitt Rick Shine Neil Tsutsui Mark van Kleunen

ORGANIZERS: Spencer Barrett Rob Colautti Katrina Dlugosch Loren Rieseberg

Katrina M. Dlugosch, PhD University of Arizona

katrina.dlugosch@gmail.com

AustNatlU Biodiversity Apr22-24

CBA Conference announcement: Understanding biodiversity dynamics using diverse data sources

From April 22V24 this year the Centre for Biodiversity Analysis and CSIRO (OCE Cutting Edge Science Symposia) will be hosting a conference and series of workshops at CSIRO Discovery & ANU on Understanding biodiversity dynamics using diverse data sources < http://cba.anu.edu.au/news-events/understanding-biodiversity-dynamics-using-diverse-data-sources >.

In the face of rapid, global environmental change, it is essential that we understand how biodiversity is distributed and its response to environmental change, past and future. This challenge will be met by integrating conventional approaches to biodiversity analyses, spanning environmental, genomic, phylogenetic and trait data in space and time, with cutting-edge informatics, including visualisation, statistical modelling and simulation.

In addition to our invited speakers < http://cba.anu.edu.au/news-events/understanding-biodiversity-dynamics-using-diverse-data-sources/conference-organisation >, we will be encouraging students and early career researchers to present lightning talks and posters < http://cba.anu.edu.au/news-events/understanding-biodiversity-dynamics-using-diverse-data-sources/conference-submissions > on their research and we are offering financial support < http://cba.anu.edu.au/news-events/understanding-biodiversity-dynamics-using-diverse-data-sources/conference-support > for ECRs to attend the meeting. Registration < http://cba.anu.edu.au/news-events/understanding-biodiversity-dynamics-using-diverse-data-sources/conference-registration > is now open.

Please feel free to distribute to anyone who may be interested: http://cba.anu.edu.au/news-events/understanding-biodiversity-dynamics-using-diverse-data-sources Claire Stephens Coordinator | Centre for Biodiversity Analysis

Research School of Biology | Evolution, Ecology & Genetics Gould Building (Bldg 116 Rm 223), Daley Road | The Australian National University | Canberra ACT 0200 T +61 2 612 59492 | E claire.stephens@anu.edu.au | W cba.anu.edu.au < http://hcba.anu.edu.au/ >

Please note: monday - wednesday only

Claire Stephens <claire.stephens@anu.edu.au>

Beijing EvolutionCooperation Apr8-11

Dear colleagues,

>From April 8 to 11, 2014, the National Natural Science Foundation of China (NSFC) < http://www.nsfc.gov.cn/publish/portal1 > and the International Institute for Applied Systems Analysis (IIASA < http://www.iiasa.ac.at/ >) will convene the conference

Evolution of Cooperation

at the Sino-German Center for Research Promotion in Beijing, China. More information on this event is available at www.iiasa.ac.at/cooperation2014 . Thanks to generous funding by NSFC, we still have available a few bursaries covering all local costs, including high-quality hotel accommodation (www.ihg.com/holidayinn/hotels/us/en/beijing/pegsh/hoteldetail), lunches and dinners, as well as local transportation. All scientists receiving a bursary will be invited to give one of ca. 40 conference presentations of 25+5 minutes. Furthermore, we are organizing a free cultural excursion for all speakers on April 12. Should you be interested in participating as a speaker, we will be delighted to hear from you: in this case, please send an email to dieckmann@iiasa.ac.at, attaching your CV and including your proposed presentation title and abstract.

We also have a few places left for junior scientists. For these, working lunches and conference materials will be provided, and no registration fee will be charged. We will greatly welcome the contribution of posters and have set aside a dedicated session for their presentation. If you are interested in participating, please send an email to dieckmann@iiasa.ac.at, and if you like to present a poster, please attach your CV and include your proposed poster title and, if available, abstract.

With best wishes,

Karl Sigmund (karl.sigmund@univie.ac.at) & Ulf Dieckmann (dieckmann@iiasa.ac.at)

Ulf Dieckmann Program Director Evolution and Ecology Program International Institute for Applied Systems Analysis A-2361 Laxenburg Austria

Email dieckmann@iiasa.ac.at Phone +43 2236 807 386 Phone secretary +43 2236 807 231 Fax +43 2236 807 466 or +43 2236 71313 Web http://www.iiasa.ac.at/Research/EEP Online reprints http://www.iiasa.ac.at/~dieckman FishACE Network http://www.iiasa.ac.at/Research/EEP/FishACE FinE Network http://www.iiasa.ac.at/Research/EEP/FinE FroSpects Network http://www.iiasa.ac.at/Research/EEP/FroSpects

dieckmann@iiasa.ac.at

Belgium EMPSEB Sep1-6

Dear Colleagues,

It is our pleasure to announce that registration is now open for the 20th European Meeting of PhD Students in Evolutionary Biology (EMPSEB), to be held in La Roche-en-Ardenne, Belgium, from the 1^st-6^th September, 2014. Deadline for registration is 27^th of March.

Registration cost: euro 350 (Price includes transport to La Roche-en-Ardenne from the airport, accommodation, and meals for the duration of 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 6 days and will involve a variety of activities... plus an optional excursion the last day!

Joining the participants will be a number of senior evolutionary scientists who have been invited to give plenary talks and provide constructive feedback on their research. All the PhD students are required to give a short 15 minute presentation.

Further information can be find on:http://empseb20.com/ You can also follow us on Facebook:https://www.facebook.com/EMPSEB20 & Twitter :https://twitter.com/EMPSEB20 Any enquiries should be directed tosecretary@empseb20.com

We would be very grateful if you could forward this message to anyone you think might be interested.

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

Gwennaël Bataille <gwennael.bataille@uclouvain.be>

Belgium EMPSEB Sep1-6 deadline

Dear colleagues,

Do not forget that the registration deadline for the 20th European Meeting of PhD Students in Evolutionary Biology (EMPSEB 20) is the 27th of March!

More information (including confirmed plenaries and a preliminary schedule) can be find on: http://empseb20.com/ We would be very grateful if you could forward this message to anyone you think might be interested.

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

GwennaÃ≪l Bataille <gwennael.bataille@uclouvain.be>

Cambridge EvolutionaryGenomics Mar18

The Evolutionary Genetics & Genomics Symposium (EGGS) will be taking place in Cambridge (UK) on Tuesday 18th March 2014. The meeting is free to attend and no registration is required.

We have an international line up of speakers that includes three invited speakers:

Dr Virpi Lummaa (University of Sheffield) http://www.shef.ac.uk/aps/staff-and-students/acadstaff/lummaa Dr Richard Durbin (Sanger Institute) http://www.sanger.ac.uk/research/faculty/rdurbin/ Prof Diethard Tautz (Max-Planck-Institut für Evolutionsbiologie) http://www.evolbio.mpg.de/1580376/employee_page?employee_id=12084 The full programme and other details can be found here: http://www.evolutionarygenetics.group.cam.ac.uk/eggs/ The meeting is sponsored by the Genetics Society (http://www.genetics.org.uk/) and is organised by the Cambridge Evolutionary Genetics (CEG) network (http://heliconius.zoo.cam.ac.uk/camevolgen/).

bjl48@hermes.cam.ac.uk

Chicago PlantEvolution Apr19

Chicago Plant Science Symposium 2014April 19 at the Field Museum

The annual Chicago Plant Science Symposium highlights cutting edge research in plant biology, evolution, ecology, and conservation. Our goal is to bring together the plant science community of the greater Chicago area for a day of interesting lectures and discussion. This spring we will host the fourth annual symposium with a one-day event on Saturday*, April 19, 2014* consisting of seven invited speakers. The program will include lunch and a post-conference mixer. Best of all, registration is (as always) free!

The theme this year is *"Symbioses." *We have invited a diverse set of speakers who are investigating many different aspects of symbiosis, involving plants, fungi, algae, and animals (including people). This year's lineup is:

Charles Davis, Harvard University

The big, the bad, and the beautiful: plant parasitism and the origin of the world's largest flowers

Romina Gazis, Clark University

Fungal endophytism and cryptic symbiosis

Peter Kennedy, University of Minnesota

Ecotmycorrhizal specificity and functioning in a global tri-partite symbiosis

Matthew Nelsen, University of Chicago/Field Museum

Exploring the diversity and evolution of lichen associations

Nyree Zerega, Chicago Botanic Garden/Northwestern University

Plants and People: Origins, Diversity, and Conservation of Under-utilized Crops in the genus Artocarpus (Moraceae)

Krissa Skogen, Chicago Botanic Garden/Northwestern University

Pollinators, parasites and floral diversity - assessing the role of mutualism in plant diversity in Onagraceae

Elizabeth Pringle, University of Michigan

Drivers and mechanisms of positive feedback in a plant-ant-hemipteran symbiosis

To register (so we know how much food to order for lunch), please send an email to:

chicagoplantscience@gmail.com

Rick Ree and Pat Herendeen, co-organizers

rree@fieldmuseum.org

CornellU PopulationGenetics July10-12

Dear Colleagues,

Registration for "Principals in Population Genetics: A coalescence of community to celebrate Andy Clark" is now open!

This symposium will be held July 10-12, 2014 at Cornell University in Ithaca, NY. We have an exciting lineup of speakers including

Chip Aquadro Doris Bachtrog Carlos Bustamante Manolis Dermitzakis Marc Feldman John Lis Sarah Tishkoff Mariana Wolfner

The full schedule of speakers, registration information, and travel/accommodation details can be found at www.andyfest.org . We hope to see you in Ithaca in July!

Sincerely,

Nadia Singh and Brian Lazzaro

ndsingh@ncsu.edu

DukeU MimulusEvolution Jun18-20

Hello Mimulus enthusiasts.

The 2014 Mimulus meeting is rapidly approaching. We will begin with an informal gathering on the evening of June 18th and will have *two full days (6/19 and 6/20* up to the Gould lecture at evolution) of lightning talks, updates about Mimulus science and infrastructure, informal science discussion and a lot of fun. The meeting will be on Duke's campus in Durham NC.

Focal topics of discussion will be

– The state of Mimulus genomes and population / species sequencing – Seed collection resources and management – Mimulus taxonomy / naming – Mimulus education and outreach – Mimulus evolution.org site revamp – Mimulus as model system in macro-ecology and macro-evolution – Mimulus evo-devo

Register by adding your name to the google doc (goo.gl/qpfDPD), a title of your lightning talk, and identifying focal topics that most interest you. A tentative schedule is also available as the second sheet on the google doc.

Participant support stipend (up to $600) for educators (i.e., pedagogical collaborators), faculty/postdocs whose primary focus is teaching, and undergraduate attendees may be available. Contact Lila Fishman [lila DOT fishman AT mso DOT umt DOT edu] for more information regarding this support.

address all other questions to mimulus2014@gmail.com with questions see you in durham! the organizers

mimulus2014@gmail.com

Edinburgh QuantGenetics Apr9

The 6th meeting of the Edinburgh Alliance for Complex Trait Genetics (E-ACTG) will take place on the afternoon of Wed April 9th in the Swann Lecture Theatre at the King's Building Campus. Programme below. We welcome any attendees from outwith Edinburgh and the event is free, but we do need to know numbers, so please sign up before April 2nd at:

http://tinyurl.com/E-ACTG6 The programme is:

13.00 Arrival, registration and coffee.

13.30 Lynsey Hall (Department of Psychiatry). Identifying endophenotypes for depression in Generation Scotland .

14.00 Athina Spiliopoulou (IGMM). Genomic prediction of human complex traits.

14.30 Mark Bailey (School of Life Sciences, University of Glasgow) Dissecting candidate gene and gene-environment interaction effects on human quantitative traits - performance, body composition and diabetes risk factors.

15.00 Tea.

15.30 Stuart Ritchie (CCACE). Alcohol consumption and lifetime change in cognitive ability: A gene-by-environment interaction study.

16.00 Chris Pooley (The Roslin Institute). Estimation of major gene effects on susceptibility, infectivity and recovery rates from epidemic data.

16.30 Lutz Bunger (SRUC). Long-term selected mouse lines - A unique resource for complex trait dissection.

17.00 David Hume (The Roslin Institute). Promoting the Genome.

17.40 Discussion and drinks!

Josephine Pemberton

Prof. J.M. Pemberton Institute of Evolutionary Biology University of Edinburgh West Mains Road EH9 3JT

Tel: 0131 650 5505 Fax: 0131 650 6564 Web: http://wildevolution.biology.ed.ac.uk/ J.Pemberton@ed.ac.uk

Guelph OE3C2014 May8-10 LateRegistration

Dear Colleagues,

Late registration for the Ontario Ecology, Ethology, and Evolution Colloquium will be open until 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 Wolbachia Jun5-11

We kindly remind you that early registration for the 8th International Wolbachia Conference, held from 6 to 11 June 2014 in Innsbruck, Austria, will close on 28 March 2014, i.e., in 14 days. Afterwards, no submission of poster or oral presentations will be possible, and 15% late registration charge will be added to the conference fees.

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

Dr. Wolfgang Arthofer

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

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

LakeTahoe PlantConvergentEvolution Jul15-18

34th New Phytologist Symposium. Systems biology and ecology of CAM plants Lake Tahoe, California, USA, 15-18 July 2014 http://www.newphytologist.org/symposiums/view/5 Travel grants are available for students and early career post-docs. Application deadline 11th APRIL 2013.

Poster abstract submissions are open. Submission deadline 9th MAY 2013

Places are limited so please register early.

SCOPE Crassulacean acid metabolism (CAM) is a striking example of convergent evolution found in about 7% of higher plants that significantly enhances plant water-use efficiency by facilitating the nocturnal uptake of CO, coupled with daytime stomatal closure. The increased frequency of drought over the past century, as well as substantial current variation and predicted future increases in its global occurrence, has intensified interest in understanding how CAM plants are so well adapted to survive in water-limited environments. High-throughput sequencing of transcriptome, genome and proteome has been initiated internationally for several CAM species and the large-volume datasets generated from these projects look set to provide a step-change in our understanding of the mechanistic basis and evolutionary origins of CAM biochemistry. Effective utilization of these resources requires collaboration among molecular geneticists, physiologists, ecologists and taxonomists to generate hypotheses that expand the potential of the CAM system for developing more water-use efficient crops, and for informing the improvement of economically and ecologically relevant CAM species for bioenergy production and the maintenance of ecosystem services.

The following major topical themes will be covered:

- Ecology: CAM species are key components of threatened biomes that include tropical montane cloud forests and xerophytic succulent scrub. - Evolution: Date-calibrated phylogenies generate specific hypotheses about the evolutionary origins of CAM and the palaeoecological context in which particular lineages arose. - Ecophysiology and metabolism: How is the diel supply and demand for carbon coordinated with stomatal conductance to optimize carbon gain and water-use efficiency? - Genomics: What are the molecular triggers that underpin the C -CAM transition? How does transcriptional/posttranscriptional regulation achieve the manifestation of CAM on a background of C biochemistry? - Exploiting CAM for sustainable productivity: What are the prospects for engineering CAM into C crops? Can species such as be exploited for biofuel production on nonagricultural or under-utilized semi- arid lands?

FORMAT We aim to promote basic research in CAM by integrating functional genomics with biochemistry, physiology, development, ecology, and evolutionary studies to gain new insights into the regulatory mechanisms and evolutionary origins of the pathway. We will highlight the potential of CAM research for tackling bioenergy and environmental challenges pertaining to water security and resource limitation and the maintenance of productivity and ecosystems services in a changing world. In addition to this, specific talks will look at new research areas and address the big questions for future research. The symposium will take place over four days at the Granlibakken Resort and Conference Center, on the north shore of Lake Tahoe, Tahoe City, CA, USA. There will be dedicated time for discussions, posters, selected poster talks, a field trip and a conference dinner.

ORGANISING COMMITTEE (Chair) Professor Xiaohan Yang Oak Ridge National Laboratory, USA Dr Anne Borland University of Newcastle, UK Professor John C. Cushman University of Nevada, Reno, USA Dr James Hartwell University of Liverpool, UK Professor Joseph Holtum James Cook University, Australia Professor Stan D. Wullschleger Oak Ridge National Laboratory, USA

SPEAKERS Anne Borland Newcastle University, UK Susie Boxall University of Liverpool, UK Thomas Brutnell Donald Danforth Plant Science Center, USA Johan Ceusters Katholieke Universiteit Leuven, Belgium John Cushman University of Nevada, Reno, USA Sarah Davis Ohio University, USA Erick de la Barrera Centro de Investigaciones en Ecosistemas, Mexico Erika Edwards Brown University, USA Luciano Freschi University Sao Paulo, Brazil Howard Griffiths University of Cambridge, UK

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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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Lancaster BSPB ProtistEvolution Apr23-25

Early Bird Registration Deadline - 14th March 2014

The BSPB Spring Meeting 2014 will take place at Lancaster University, UK which is set in 360 acres of beautiful parkland and lies approximately three miles south of the City of Lancaster. The campus is easily accessible via road and rail, and is within 70 miles of Manchester's International Airport. The meeting opens on the Wednesday evening with a Plenary Lecture on the use of protists to investigate eukaryotic origins, given by Martin Embley. Two symposia then follow.

The first celebrates the distinguished career of Bland Finlay who, after 35 years of protistan research, has recently retired from his academic post at Queen Mary University of London. Speakers paying tribute to Bland's contribution to protistan biodiversity, biogeography and ecology include Genoveva Estaban, Tom Fenchel, Stephen Maberly, Bill Martin and David Wilkinson.

The second symposium examines the evolution and ecology of flagellate protists within the guts of insects, with invited contributions from Rod Dillon (Sand fly), Petros Ligoxygakis (Drosophila), Eamonn Mallon (Bumblebee) and Renate Radek (Termites). The meeting also welcomes contributed papers on any aspect of protistology and is particularly keen to encourage student contributions. Students presenting at the meeting will be eligible for the Humphrey Smith Student Prizes for best oral and poster presentations.

Further information about the meeting can be found using the links below but important dates for your diary are:

- Friday 14th March 2014: Deadline for early bird registration rates

- Wednesday 26th March 2014: Deadline for securing campus accommodation

- Wednesday 9th April 2014: Registration for the meeting closes

martcarr74@gmail.com

Lausanne ESEB Aug10-15 CallForProposals

ESEB 2015 Lausanne: CALL FOR SUBMISSION OF SYMPOSIUM PROPOSALS

The 15th Congress of the European Society for Evolutionary Biology will take place in Lausanne (Switzerland), August 10-15, 2015.

Submissions for symposium proposals are now invited. These will be processed through our website, currently at: http://www3.unil.ch/wpmu/-eseb2015/ 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/ You will be asked to provide:

1. The names and e-mail addresses of one organizer (for all communication) and one co-organizer (as a replacement). Both must be committed to attend the whole meeting. 2. The proposed symposium title. 3. A summary of max 200 words explaining why you think this makes a good subject for the ESEB Congress. 4. The names of one or two invited speakers (please check beforehand whether these people are available). Organizers cannot invite themselves to their own symposium.

The deadline for submission is June 30, 2014. Proposals will be evaluated by the Scientific Committee, and the selected list communicated in September 2014. Symposia proposals on overlapping subjects may be requested to fuse.

A call for talk and poster submissions will be sent out in November 2014, with a deadline of January 15, 2015. At this time, symposium organizers must be prepared to screen submissions for their symposium (for which an on-line evaluation system will be available).

Symposia typically start with one or two invited speakers (40 min each, including discussion) and are followed by submitted talks (15 min plus 5 for discussion). The time window allotted to each symposium will be decided by the Scientific Committee, depending on the number and quality of submissions. Some symposia might be cancelled at this stage if they do not arouse sufficient interest.

We do not provide financial support for organizing a symposium, but ESEB will pay the registration fee for invited speakers.

Check our webpage for updates: www.unil.ch/eseb2015; or www3.unil.ch/wpmu/eseb2015/symposium-information.

We look forward to your contributions.

The ESEB2015 organizing committee

John Pannell <John.Pannell@unil.ch>

Lisbon FishSexDetermination Sep23-24

*First Announcement***

*International Conference on***

“Sex Determination and Differentiation in Fishes – Genes, Environment and Behaviour”

Dear colleagues,

You are now invited to attend the International CONFERENCE on“SEX DETERMINATION AND DIFFERENTIATION in fishes – GENES, ENVIRONMENT AND BEHAVIOUR”.

It will take place September 23^th –24^th , 2014 at Fundação da Faculdade de Ciências, Lisboa.

This***conference***aims to promote knowledge exchange and debate on the latest findings regarding processes of sex differentiation and mechanisms of primary sex determination in fishes*.****Genetic*/epigenetic, environmental and behavioural factors will be discussed as well as the diversity of evolutionary scenarios described in fishes.

This international meeting will feature three outstanding speakers in the field: /Manfred Schartl/, University of Würzburg, Germany; /Francesc Piferrer/, Institut de Ciencies del Mar, CSIC, Barcelona, Spain; and /Rui Oliveira/, ISPA, Portugal. Poster sessions and oral presentations are also on the schedule.

We would greatly appreciate your collaboration in promoting this conference by distributing this Announcement to your colleagues, lab personnel and associates that could benefit from participating in this conference.

The second announcement with all details on registration and abstract submission will soon be available at the conference's webpage.

As co-chairs, we look forward to your presence at this world-class scientific conference.

Thank you!

Maria João Collares-Pereira & Maria Manuela Coelho

cspereira@fc.ul.pt

Carla Pereira Evolutionary Genetics Group, CBA-FCUL

Carla Pereira <cspereira@fc.ul.pt>

Montreal GenomesBiomes May25-29 DeadlineExt

The deadline to submit a POSTER presentation to Genomes to Biomes has been extended to April 4. Registration remains open until May 18.

http://genomesbiomes.ca/home.html Join the nearly 900 participants from 14 countries who have registered to date!

La date limite pour soumettre une présentation par AFFICHES a Genomes aux Biomes été prolongé jusqu'au 4 avril. Inscription reste ouverte jusqu'au 18 mai.

http://genomesbiomes.ca/HomeFrancais.html Rejoignez les près de 900 participants de 14 pays qui se sont inscrits à ce jour!

Chris Cameron (local organizing commitee)

Sciences biologiques, Université de Montréal https://www.webdepot.umontreal.ca/Usagers/cameroc/MonDepotPublic/Cameron/index.htm http://en.wikipedia.org/wiki/Universit%C3%A9_de_Montr%C3%A9al Cameron Christopher <c.cameron@umontreal.ca>

Newcastle EcologicalGenetics Mar14

Dear all,

The deadline for booking the Ecological Genetics Group meeting is getting near: 14th March!

The conference was going to be held at Longhirst Hall: however, they have gone into liquidation on Friday. I found this out Monday morning. I am pleased to say I have found an alternative venue: Copthorne Hotel in Newcastle. http://www.millenniumhotels.co.uk/copthornenewcastle/ It is City centre, Quayside, lovely location. A few minutes' walk from Newcastle Central station with excellent train, metro and bus connections. There is ample (free) parking. Rates for conference are still the same: £275 for full package, £225 for shared twin room and discount for PhD students and Genetics Soc members.

I will email with those who have already booked to ensure they are aware of the situation. I will also update the website soon and include a preliminary programme.

Please book as soon as possible and before the 14th March: use the existing booking system and even though the booking system will mention Longhirst Hall, this will be Copthorne Hotel.

Best wishes, Kirsten

Dr Kirsten Wolff Reader in Evolutionary Genetics Newcastle University, School of Biology Devonshire Building 5th floor Newcastle NE1 7RU, UK Phone: 0191 208 5626/4852 Fax: 0191 208 5229 email: kirsten.wolff@ncl.ac.uk www.staff.ncl.ac.uk/kirsten.wolff/ http://conferences.ncl.ac.uk/ecologicalgeneticsgroup2014/ kirsten.wolff@newcastle.ac.uk

PortTownsend Washington EvoWIBO Apr25-27 deadline

The registration deadline for Evo-WIBO 2014 is fast approaching (March 23rd). Space is limited and we've already had a significant number of registrants. If you're planning on coming to the conference please register soon to ensure your spot (http://blogs.uoregon.edu/evowibo/).

Hope to see you in Port Townsend!

– Bill

wcresko@uoregon.edu

PuertoRico SMBE2014 Jun8-12 AbstDeadlineMar18

Dear Colleagues:

We are still accepting abstracts for poster presentations for SMBE 2014 in San Juan Puerto Rico. The deadline is March 18th 2014. You can submit your abstract and register at http://smbe.org/annual/2014/ The venue for the 2014 meeting will be the Caribe Hilton Hotel, San Juan. The meeting will feature 39 concurrent symposia on the variety of topics in Molecular Biology and Evolution, and feature a number of prominent speakers, including Dr. Eric Green, Director of the National Human Genome Research Institute (NHGRI), Dr. Sara Tishkoff, David and Lyn Silfen University Professor, Genetics & Biology, University of Pennsylvania, and the Society Founder, Dr. Masatoshi Nei. President Dr. Brandon Gaut will present the Nei Plenary Lecture, named after Dr. Masatoshi Nei.

A pool side welcome party will take place on Sunday 8th June in The Caribe Hilton, we look forward to seeing you all there and welcoming you to Puerto Rico.

The official program will begin on Monday the 9th of June and will consist of 4 parallel sessions which will run throughout the 4 days. It will include some exciting keynote addresses and lectures.

The SMBE funds a number of awards each year and these include among others the Walter M. Fitch Award Competition as well as an Undergraduate Mentoring Program Award. Details of all the awards can be found here on the SMBE 2014 website.

We hope you will support our award nominees by taking the time to view their presentations and posters during the meeting. We will also have dedicated posters sessions each evening and we are working to ensure that both you and the poster presenters are given ample time throughout the meeting to explore this body of work.

The final evening, Thursday 12th of June, will be the main SMBE social evening. This will be a ticketed event ($100.00) and will take place in the 'Old Casino', the Antiguo Casino in the San Juan Old Town. Tickets for this event will be limited, but it's sure to be a great carnival atmosphere so book your tickets early.

The abstract system is now closed for submissions for oral presentations but will remain open for poster presentations only and the deadline for poster submissions is March 18th.

Online Registration is now open and you will be able to book your accommodation and social events through this system. We are really looking forward to #SMBE14.

See you there!

Make sure to keep up to date with all the meeting developments through our Facebook and twitter accounts by using the hashtag #smbe14 and be sure to tell your friends and colleagues.

Thank you very Much

Taras K Oleksyk President of Local Organizing Committee SMBE 2014 Puerto Rico

Taras Oleksyk <oleksyk@gmail.com>

Raleigh Evolution Jun20-24 ChildcareTravelAwards

Sign up for childcare, travel awards and other opportunities at Evolution 2014 < http://evolution2014.org/ >, to be held June 20-24 in Raleigh, NC

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

Raleigh Evolution Jun20-24 MSIFaculty

Evolution 2014 MSI Faculty Travel Award - DEADLINE APPROACHING!

Are you a faculty member at a minority-serving institution (MSI)? Apply now for a travel award to attend Evolution 2014 from June 20-24 in Raleigh, NC (www.evolution2014.org).

The National Evolutionary Synthesis Center (NESCent - www.nescent.org), with support from the Society for the Study of Evolution, is pleased to announce travel awards for faculty from Minority Serving Institutions to attend Evolution 2014, as part of our continuing outreach efforts focusing on groups that are underrepresented in evolutionary science.

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

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

To apply, please visit www.nescent.org/-Evo2014facultyapp Application Deadline: March 31st, 2014 (Awards will be announced by April 4th, 2014)

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

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

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

Raleigh Evolution Jun20-24 RegistrationOpen

www.evolutionsociety.org SOCIETY FOR THE STUDY OF EVOLUTION

Dear SSE Colleagues:

You can now register for Evolution 2014 - just visit www.evolution2014.org. This year SSE will meet in Raleigh, North Carolina on June 20-24. This is the premier opportunity to share scientific research on evolution. You will find information about the conference on this website, answers to commonly asked questions in the FAQs, and explanatory text in the registration pages. Here are some helpful tips:

* Registration costs depend on whether you are a student or a postdoc, and whether you are a member of one of the three societies. (It works out that the discounted membership rate for registration far offsets the membership fees for any of the three societies)

* As with last year’s conference, we will have a Super-Social event with food and drink at the North Carolina Museum of Natural Sciences on the last night of the conference (Tuesday, 24 June). This event is included in the cost of your registration.

* You can return to the registration site after you have registered to submit your presentation. Just click on the “Author Center” in the menu once you have logged in.

* This year, you will see that we are collecting abstracts for all presentations except lightning talks. We are doing this for two reasons - first, it will provide more information to attendees about your presentation, and second, it will allow us to group presentations into appropriate sessions.

* Once all talks have been confirmed, there will be a link for you to upload your presentation. This will happen in early May.

You can get the latest updates on the meeting by following @Evol2014 (https://twitter.com/Evol2014) on

Twitter. And if you want to start a conversation about the conference, be sure to use #Evol2014 (https://twitter.com/search?q=%23Evol2014&src=hash) .

SSE Business Office PO Box 299 | St. Louis Missouri, 63166 314-577-9566 www.evolutionsociety.org

** friend on Facebook (http://www.facebook.com/groups/21306713056/?fref=ts) ** forward to a friend (http://us2.forward-to-friend1.com/forward?u=7b5241ec2a609d26192947333&id=0cc97060aa&e=5d55ef0512)

Society for the Study of Evolution <hcacanindin@evolutionsociety.org>

Raleigh Evolution Jun20-24 Undergraduates

Undergraduate Diversity at Evolution 2014 - DEADLINE APPROACHING!

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 Evolution Jun20-24 UpcomingDeadlines

Dear colleagues,

A quick note about upcoming deadlines for the Evolution 2014 Conference at Raleigh, North Carolina, from 20-24 June 2014:

* 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 sign-up ends < http://evolution2014.org/wpgforms/student-volunteers-2/ > * 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/ >

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 NorthCarolina Evolution2014 Jun20-24

Registration for Evolution 2014 is now open!

Just visit www.evolution2014.org to register.

You will find information about the conference on this website, answers to commonly asked questions in the FAQs, and explanatory text in the registration pages. Here are some helpful tips: * Registration costs depend on whether you are a student or a postdoc, and whether you are a member of one of the three societies. (It works out that the discounted membership rate for registration far offsets the membership fees for any of the three societies). * As with last year's conference, we will have a Super-Social event with food and drink at the North Carolina Museum of Natural Sciences on the last night of the conference (Tuesday, 24 June). This event is included in the cost of your registration. * You can return to the registration site after you have registered to submit your presentation. Just click on the "Author Center" in the menu once you have logged in. * This year, you will see that we are collecting abstracts for all presentations except lightning talks. We are doing this for two reasons - first, it will provide more information to attendees about your presentation, and second, it will allow us to group presentations into appropriate sessions. * Once all talks have been confirmed, there will be a link for you to upload your presentation. This will happen in early May.

You can get the latest updates by following @Evol2014 on Twitter. And if you want to start a conversation about the conference, be sure to use #Evol2014.

If you have any questions, bugs or error reports, please send an email to organizer@nescent.org.

We look forward to seeing you in 4 months!

Allen Rodrigo Chair, Evolution 2014 Organizing Committee

a.rodrigo@nescent.org

Salvador Brazil PlantEvolution Oct19-24

The Latin American Association of Botany and the Brazilian Botanical Society invites the botanical community to attend the XI Latin American Congress of Botany. The event will be held in Salvador, Bahia, Brazil from October 19-24. Registrations and additional information is available at http://-www.65cnbot.com.br/EN Sincerely,

Ana Maria Giulietti Harley, President of the Association for Latin American Botany, <anagiulietti@hotmail.com>

Tania dos Santos Silva, President of the XI Latin American Congress, <tanialantana@gmail.com>

Alina Freire-Fierro, Member of the Superior Council, <agf36@drexel.edu>

Email: alina.ff@gmail.com

Alina Freire-Fierro, M.S. Collection Manager of Botany, PH Herbarium Academy of Natural Sciences of Drexel University 1900 Benjamin Franklin Parkway Philadelphia, PA 19103, USA

www.ansp.org www.botanica-alb.org www.neotropicos.net Alina Freire-Fierro <alina.ff@gmail.com>

SanJoseStateU LifeDiscovery Oct3-4

Life Discovery is a collaborate initiative among the Ecological Society of America, the Botanical Society of America, the Society for the Study of Evolution and the Society for Economic Botany.

FINAL CALL FOR PRESENTATION PROPOSALS DUE MARCH 15, 2014

2nd Life Discovery-Doing Science Education Conference October 3-4, 2014 San José State University, San José CA

www.esa.org/ldc Students Indifferent to Biology? Do you have ideas to bring the excitement of discovery and the wonder of a rapidly changing biology to your students? Then join us in Realizing Vision and Change, Preparing for Next Generation Biology! Share your lesson ideas and resources and receive helpful peer feedback at the education share fair roundtables. Instructors, researchers, curriculum developers, technology experts and department leaders are all vitally needed in this project and welcome!

We invite proposals for the Education Share Fair

Roundtables (45 mins) to share ideas that are suitable, scalable, and adaptable to secondary and post-secondary levels of education in addressing the objectives of both the K12 Next Generation Science Standards (NGSS) and the Vision and Change for Undergraduate Biology Education (V&C).

What is the Education Share Fair Roundtable format? Each presentation will be at a roundtable with up to seven other participants. Discussions can cover issues related but not restricted to core concepts, teaching methodology, misconceptions, assessment or educational extensions. This session is designed for educators to share lesson ideas and resources (images, datasets, charts, case studies, videos etc.) at any stage of development to receive peer feedback. Success stories and preliminary ideas are both welcome. All presenters with fully developed teaching ideas are strongly encouraged to publish in the LifeDiscoveryEd Digital Library as a record of conference proceedings.

Sponsor and Exhibit opportunities are now available

Questions? Contact ldc@esa.org (mailto:ldc@esa.org)

** forward to a friend

Society for the Study of Evolution <hcacanindin@evolutionsociety.org>

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

Tentative schedule:

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

Including: Wilhelmine 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

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 Earlybird registration through May 15 Students $150 (student awards available) General $200

Poster abstracts due April 15 Contributed paper abstracts due April 1

Please visit the AGA website to register and book housing:

http://www.theaga.org/sample-page/aga2014/ Because all sessions are plenary, most contributed presentations will be in the form of posters. However, I have saved a few speaker slots for contributed talks. If you are interested in being considered for a contributed talk, by 1 April please send a 400-word abstract of the proposed talk, along with a one-paragraph explanation of how it would complement the theme of the meeting, to: robinw3@uw.edu, and put “AGA Contributed Paper” in the subject line. You will be notified by 15 April whether your talk is accepted; those not selected have the option to present a poster instead.

Robin Waples, AGA President

agajoh@oregonstate.edu

Serbia GeneticsSociety Sep28-Oct2

Dear colleagues,

On behalf of the Serbian Genetics Society, it is our pleasure to invite you to participate in the V Congress of the Serbian Genetics Society. The congress will take place from 28th September to 2nd October 2014 at Hotel Djerdap, Kladovo, Serbia. This congress allows you to meet people working at all levels of biological organization and organism groups, as well as all methods currently in use in population and evolutionary genetics, mutagenesis, molecular genetics, medical genetic, breeding V including genetic analysis in field and laboratory studies. From eminent speakers coming from all over Europe we expect to hear about the new frontiers and latest breaking results in genetics.

You can find more information at web page: http://www.dgsgenetika.org.rs/v-congress.php Information on the Web will be updated timely. Meanwhile, please contact the Congress Organizers for further information.

We would also appreciate if you could forward this e-mail to your colleagues and within your research groups and institutions.

Best regards, Zorana Kurbalija Novicic, PhD On the behalf of Organizing Committee Department for Genetics of Population and Ecogenotoxicology Institute for Biological Research, University of Belgrade, Serbia kurbalija@ibiss.bg.ac.rs

Zorana Kurbalija <kurbalija@ibiss.bg.ac.rs>

Trento Italy Drosophila suzukii May28-29

*Biology and Evolution of Drosophila suzukii *

Fondazione Edmund Mach, Casalino (Vigalzano) Pergine Val Sugana, Trento, Italy. 28-29 May 2014

A meeting aimed at gathering researchers currently working or interested in the Biology of D. suzukii. The goal is to share latest findings in the field, help organizing future research, and establishing collaborations. Expected themes include, but are not restricted to:

Population, phylogeny, evolution

Genetics, molecular and developmental biology

Neurobiology, Ethology, chemical ecology

Wolbachia and other endosymbionts

Genomics of D. suzukii and of sister species

The meeting: Expected participants are not only those working in the agriculture/pest management field, but also those using D. suzukii as new model organisms in biological studies. Meeting will consist of a series of short talks with plenty of time for discussion, and likely small round tables on particular topics. We will try to allocate a slot to all those interested in giving a talk; if we will receive too many submission we will select talks in order to cover as much themes as possible and give a good representation of the labs/researchers active on D. suzukii. English is the official language. The meeting is a (free) satellite of the Workshop of Integrated Soft Fruit Production which will be held during the three previous days at the same location; this workshop needs registration with fees and will host another D. suzukii symposia focused on agricultural applied matters: http://eventi.fmach.it/Iobc/General-Info . *Location:* The meeting will be held in the village of Pergine Val Sugana, a few miles from Trento. https://maps.google.com/?ll=46.069062,11.201935&spn=0.076341,0.144711&t=h&z=13 .It will be held on Thursday 28 March, from 09:30 to 19:30 with the very likely possibility of enlarging it to the Friday 29 depending on abstracts received.

Registration: The meeting is free of charge, with coffee breaks and wine & cheese offered by the organization. But registration is compulsory before 7th of April with an email to omar.rota@fmach.it. If you want to give a talk please add a short abstract to your email. For details on accommodation and travel info: http://eventi.fmach.it/Iobc/Accomodation-Info .

Organisers: Omar Rota-Stabelli and Gianfranco Anfora, Fondazione Edmund Mach.

Rimmie <rupinderkaur@fmach.it>

Tucson DeepGenomics Apr3-5 DiscountRegExtended

DISCOUNTED REGISTRATION HAS BEEN EXTENDED TO MARCH 26 – REGISTER TODAY!

We are pleased to announce the National Science Foundation's Integrative Graduate Education and Research Traineeship (NSF-IGERT) Symposium on Deep Genomics on April 3-5, 2014 in Tucson, Arizona.

Symposium website: www.genomics.arizona.edu/meeting.html The University of Arizona IGERT Program in Comparative Genomics is sponsoring an international meeting on Deep Genomics. The symposium's theme this year encompasses broad scale comparative inferences in the three areas of our training program, including comparative and evolutionary genomics of divergent species, genomics of development, traits, and related interaction networks originating early in evolutionary history, and computational challenges associated with genomics at a broad phylogenetic scale. The meeting will take place at the Marriott University Park Hotel adjacent to the University of Arizona campus in Tucson on Thursday-Saturday, April 3-5, 2014. The format of the meeting will allow considerable time for informal discussion and interaction among participants. Participation by graduate students and postdoctoral fellows is strongly encouraged, and discounted rates for registration will be available.

REGISTRATION Early registration deadline (extended): March 26, 2014 Faculty: $150, Students and Postdocs: $75

KEYNOTE SPEAKER Kenneth Wolfe - University College Dublin, Ireland

CONFIRMED SPEAKERS Robert Beiko - Dalhousie University, Canada William Cresko - University of Oregon Miklos Csuros - Universite de Montreal, Canada Patrick Degnan - University of Illinois Dannie Durand - Carnegie Mellon University Veronica Hinman - Carnegie Mellon University Erin Kelleher - University of Houston Junhyong Kim - University of Pennsylvania Laura Landweber - Princeton University Li-Jun Ma - University of Massachusetts Michael Nodine - Gregor Mendel Institute, Austria Robert Reed - Cornell University Shin-Han Shiu - Michigan State University Joseph Thornton - University of Chicago Travish Wheeler - HHMI Janelia Farm

POSTER SESSION The symposium will feature a poster session. Please refer to the website for more information: www.genomics.arizona.edu/meeting.html Please contact Dr. Michael Sanderson, sanderm@email.arizona.edu, with all scientific queries.

Please contact Mrs. Pennie Liebig, genomics@email.arizona.edu, with all registration or administrative queries.

We hope to see you in April!

genomics@email.arizona.edu

Tucson Arizona DeepGenomics Apr3-5 EarlyDeadlineMar14

DEADLINE FOR EARLY REGISTRATION IS NEXT WEEK!

We are pleased to announce the National Science Foundation's Integrative Graduate Education and Research Traineeship (NSF-IGERT) Symposium on Deep Genomics on April 3-5, 2014 in Tucson, Arizona.

Symposium website: http://www.genomics.arizona.edu/meeting.html The University of Arizona IGERT Program in Comparative Genomics is sponsoring an international meeting on Deep Genomics. The symposium's theme this year encompasses broad scale comparative inferences in the three areas of our training program, including comparative and evolutionary genomics of divergent species, genomics of development, traits, and related interaction networks originating early in evolutionary history, and computational challenges associated with genomics at a broad phylogenetic scale. The meeting will take place at the Marriott University Park Hotel adjacent to the University of Arizona campus in Tucson on Thursday-Saturday, April 3-5, 2014. The format of the meeting will allow considerable time for informal discussion and interaction among participants. Participation by graduate students and postdoctoral fellows is strongly encouraged, and discounted rates for registration will be available.

REGISTRATION Early registration deadline: March 14, 2014 Faculty: $150, Students and Postdocs: $75

Late registration deadline: March 26, 2014 Faculty: $175, Students and Postdocs: $90

KEYNOTE SPEAKER Kenneth Wolfe - University College Dublin, Ireland

CONFIRMED SPEAKERS Robert Beiko - Dalhousie University, Canada William Cresko - University of Oregon Miklos Csuros - Universite de Montreal, Canada Patrick Degnan - University of Illinois Dannie Durand - Carnegie Mellon University Veronica Hinman - Carnegie Mellon University Erin Kelleher - University of Houston Junhyong Kim - University of Pennsylvania Laura Landweber - Princeton University Li-Jun Ma - University of Massachusetts Michael Nodine - Gregor Mendel Institute, Austria Robert Reed - Cornell University Shin-Han Shiu - Michigan State University Joseph Thornton - University of Chicago Travish Wheeler - HHMI Janelia Farm

POSTER SESSION The symposium will feature a poster session. Please refer to the website for more information: www.genomics.arizona.edu/meeting.html Please contact Dr. Michael Sanderson, sanderm@email.arizona.edu, with all scientific queries. Please contact Mrs. Pennie Liebig, genomics@email.arizona.edu, with all registration or administrative queries.

We hope to see you in April!

genomics@email.arizona.edu

Turku Finland ButterflyEvol Aug11-14

Dear all, We are pleased to announce that abstract submission is now open for the 7th International Conference on the Biology of Butterflies to be held in Turku, Finland on August 11 to 14, 2014. You can find the link to the abstract submission page here: http://nymphalidae.utu.fi/icbb2014/abstract.html . The deadline for abstract submission is May 1, 2014. The registration pages will soon be opened as well. Submitted oral presentations will be reviewed by the scientific committee as well as organizers of afternoon sessions. For the moment, there are no limits on the number of submitted posters. Details about the afternoon sessions can be found here: http://nymphalidae.utu.fi/icbb2014/symposia.html . We look forward to your abstracts and above all to seeing you here in Turku in August!

On behalf of the organizing committee, Niklas Wahlberg

– Niklas Wahlberg Professor Laboratory of Genetics Department of Biology University of Turku 20014 Turku FINLAND

Phone: +358 2 333 5569 Fax: +358 2 333 6680 Skype: niklas_w2

Nymphalidae Systematics Group: http://nymphalidae.utu.fi

Turku Finland ButterflyEvol Aug11-14 AcceptingAbstracts

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 on the 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. E. Hornett (USA/UK), Dr. T. Huigens (Netherlands) and Dr. M. Gibbs (UK).

We are now accepting abstracts for talk or poster presentation for the [3]Butterflies as hosts[2] symposium. ### Deadline for abstract submission is the 1st May 2014 ###

Talk info: 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 Deadline for abstract submission is the 1st May 2014. To submit an abstract for a talk/poster please email the symposium convener Anne Duplouy at anne.duplouy@helsinki.fi with Butterfly conference 2014 as the email's subject. Email 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 info can be found here: http://nymphalidae.utu.fi/icbb2014/registration.html

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 <anne.duplouy@helsinki.fi> Anne Duplouy <anne.duplouy@helsinki.fi>

Turku Finland ButterflyEvolution Aug11-14

Dear all,

Registration is now open for the 7th International Conference on the Biology of Butterflies to be held in Turku, Finland, August 11 to August 14. Details can be found here: http://nymphalidae.utu.fi/icbb2014/registration.html . Abstract submission is also open http://nymphalidae.utu.fi/icbb2014/abstract.html . We already have an excellent line up of invited talks and are looking forward to receiving many more excellent submitted talks on all aspects of butterfly biology! This is truly a multidisciplinary conference where the overarching theme is the taxon being studied. Presentations will range from how genes interact to why there are so many species, and everything in between.

We look forward to seeing you in Turku, Finland this summer!

Best regards, Niklas Wahlberg

– Niklas Wahlberg Professor Laboratory of Genetics Department of Biology University of Turku 20014 Turku FINLAND

Phone: +358 2 333 5569 Fax: +358 2 333 6680 Skype: niklas_w2

Nymphalidae Systematics Group: http://nymphalidae.utu.fi Niklas Wahlberg <niklas.wahlberg@utu.fi>

UIllinois UC ArthropodGenomics Jun12-14

ARTHROPOD GENOMICS 2014

Registration is now open for the 8th Annual Arthropod Genomics Symposium.

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.

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/ ags@igb.illinois.edu

UToronto Mississauga InvasivePlantEvol Aug6-8

Terrestrial Invasive Plant Species II: Registration is now open

Registration and abstract submission are now open for the second Terrestrial Invasive Plant Species (TIPS II) meeting; please visit the conference website (https://secure.utm.utoronto.ca/tips2/) for details. This meeting will be held at the University of Toronto Mississauga on 6-8 August 2014. We are inviting presentations on the ecology, evolution, impacts, and management of plants invading terrestrial systems in Ontario, Canada and surrounding areas.

The meeting will focus on plant invaders in an ecological context, with sessions highlighting their interactions with their physicochemical surroundings and with other biota (competitors, herbivores, microbes, biocontrol agents). Goals include: 1) disseminating up-to-date science on the ecology of invasive plants, 2) creating a milieu for sharing best practices among conservation agencies, park managers and others and 3) providing a forum for practitioners and scientists to meet and discuss priorities, emerging threats, and funding opportunities.

We expect about 250 participants, including university students, researchers, resource managers, and government representatives. An initial day will be devoted to registration, a reception, and pre-conference field trips, followed by two full days of presentations, including 20-minute contributed oral presentations, research posters, and networking sessions. Presentations will be organized thematically; we anticipate sessions devoted to management, biocontrol, impacts, ecological interactions, and related topics. Major support has been provided by the Invasive Species Centre and the University of Toronto.

Early bird registration ends on May 31; regular pre-conference registration ends on July 20. Abstracts should be submitted by June 20. Please visit https://secure.utm.utoronto.ca/tips2/ for updates and more information. We hope to see you in Mississauga this summer!

TIPS II Organizing Committee:

Peter Kotanen, Biology, University of Toronto Mississauga

Sandy Smith, Faculty of Forestry, University of Toronto

Ben Gilbert, Ecology and Evolutionary Biology, University of Toronto

Roberta Fulthorpe, Physical and Environmental Science, University of Toronto Scarborough

Peter M. Kotanen Associate Professor Department of Ecology & Evolutionary Biology University of Toronto at Mississauga 3359 Mississauga Road Mississauga, ON, L5L 1C6 CANADA tel: 905-828-5365; fax: 905-828-3792 skype: peter.kotanen e-mail: peter.kotanen@utoronto.ca http://www.utm.utoronto.ca/ ~ w3pkota/ Peter Kotanen <peter.kotanen@utoronto.ca>

GradStudentPositions

HamburgU 2PhD EcologicalGenomics

I would like to bring to your attention to two PhD positions in evolutionary biology available at the Department of Biology at the University of Hamburg.

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Universität Hamburg invites applications for two

Research Associates commencing on June 1st 2014 (earliest starting date).

The positions are part time (19.5 hours per week) and are remunerated at the 13 TV-L salary level. The short-term, three-year contract terminates on May 31st 2017.* The short-term nature of this contract is based upon §2 of the Academic Short-term Contract Act (WissZeitVG). The University aims to increase the number of women in research and teaching and explicitly encourages women to apply. Equally qualified female applicants will receive preference in accordance with Hamburg's Higher Education Act (HmbHG).

Tasks: Duties primarily include research and a moderate amount of teaching. The success-ful candidate will also have the opportunity to pursue further academic qualifications, in particular a doctoral dissertation, in accordance with §28 (1) sentence 3 of Hamburg's Higher Education Act (HmbHG).

Position 1

Area(s) of responsibility: The groups focus on global biodiversity and evolutionary genomics of freshwater zooplankton (Daphnia), using next-generation sequencing data. Bioinformatics tools are used to detect local adaptation patterns in natural populations and experimental cultures will allow assessing the phenotype/genotype correlation. The candidate will be planning these experiments and analyse the data in collaboration with another graduate student (focusing on the bioinformatics part). Furthermore, the candidate will use molecular techniques (quantitative real-time PCR on RNA and genomic DNA) to confirm the outcome of the in silico analysis. The candidate is encouraged to develop specific projects of her or his own choice as long as they include mining this data and are conducted in collaboration with other members of the group.

Requirements: A university degree in a relevant field: Biology The candidates should: - be familiar with molecular methods and have a strong background in evolutionary biology / molecular ecology. In addition, knowledge of population genetics will be advantageous. - be creative, critical and have conceptual thinking skills. - have good communication and writing abilities in English. - be able to work both independently and as part of a multidisciplinary team.

Position 2

Area(s) of responsibility: The groups focus on global biodiversity and evolutionary genomics of freshwater zooplankton (Daphnia), using next-generation sequencing data. Bioinformatics tools are used to detect local adaptation patterns in natural populations and experimental cultures will allow assessing the phenotype/genotype correlation. The candidate will be analysing the NextGen data and plan/conduct follow-up studies on candidate genes, in collaboration with another graduate student (focusing on the experimental part). The Next Gen data analysis includes (but is not limited to) differential expression analysis, SNP calling and eQTL analysis. The candidate is encouraged to develop specific projects of her or his own choice as long as they include mining this data and are conducted in collaboration with other members of the group.

Requirements: A university degree in a relevant field: Biology, Bioinformatics The candidates should: - be familiar with bioinformatics methods and have a strong background in evolutionary biology / molecular ecology. In addition, knowledge of population genetics will be advantageous. - be familiar with at least one of these scripting languages: python, perl, C++, R - be creative, critical and have conceptual thinking skills. - have good communication and writing abilities in English. - be able to work both independently and as part of a multidisciplinary team.

The working language of the group is English, willingness to learn German is necessary to allow a better integration/communication in the institute and in daily life. Severely disabled applicants will receive preference over equally qualified non-disabled applicants. Applications should include a letter of application with mention of the preferred position, a detailed curriculum vitae, an abstract of your master thesis, and copies of degree certificate(s), as well as the names of two scientific referees. These documents should be submitted as a single pdf-file in the given order. The deadline for applications is April 30th 2014. Please send applications to Mathilde Cordellier, cordellier@bio.lmu.de

For further information, please contact Semra Ünsal on 040-428 38 3858 or cordellier@bio.lmu.de. Alternatively, please consult our website http://evol.bio.lmu.de/people/group_parsch/cordellier_m/index.html . * In accordance with §§27, 28 of Hamburg's Higher Education Act (HmbHG).

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HeinrichHeineU Germany ModelingPhotosynthesisEvol

PhD studentship in the Cluster of Excellence CEPLAS / Heinrich Heine University Düsseldorf, Germany

“In silico exploration of evolutionary paths towards C4 metabolism” The Cluster of Excellence CEPLAS invites applications for a 3 year Ph.D. position (50 %, EG 13 TV-L) at the Heinrich Heine University Düsseldorf (Bioinformatics) within the CEPLAS Graduate School.

CEPLAS - Cluster of Excellence on Plant Sciences - is a joint effort of Heinrich Heine University, University of Cologne, Max Planck Institute for Plant Breeding Research, and Research Centre Jülich. Researchers of these institutions are pursuing innovative strategies for sustainable plant production.

The CEPLAS Graduate School offers a comprehensive, interdisciplinary Ph.D. training programme in the fields of molecular plant sciences, plant genetics, and quantitative biology that is jointly organised by all four partnering CEPLAS institutions in the Cologne/Düsseldorf area of Germany. The position is to be filled at the earliest opportunity.

Future Ph.D. students will join courses in transferable and scientific skills, practical courses in state-of-the-art laboratory methods, regular seminars and retreats.

We are looking for a highly qualified individual with a strong interest in mathematical modeling of biological systems. You should hold a Master degree or equivalent in a biological science (with a proven interest in mathematics or computer science) or in a quantitative science such as physics (with a proven interest in biology).

This project aims to further develop a mathematical model of C4 photosynthesis evolution (Heckmann et al., Cell 153:1579). The eventual goal is to guide experiments that combine genetic manipulations with artificial selection to increase the yield of C3 crops such as rice.

For detailed information about CEPLAS please visit www.ceplas.eu. For more information on the project or to apply, please contact Martin Lercher (lercher@cs.uni-duesseldorf.de).

Martin Lercher Professor of Bioinformatics Heinrich Heine University Düsseldorf, Germany

lercher@cs.uni-duesseldorf.de Tel. +49 211 81-10546 Mobile +49 151 22964073 http://www.cs.hhu.de/en/research-groups/bioinformatics Martin Lercher <lercher@cs.uni-duesseldorf.de>

IowaStateU InsectEvolution

Graduate Assistantship at Iowa State University

A graduate assistantship for a Ph.D. candidate is available in the research group of Aaron Gassmann in the Department of Entomology at Iowa State University (http://www.ent.iastate.edu/dept/faculty/gassmann/). Current research within this group focuses on insect resistance management, integrated pest management, agroecology, and interactions between agricultural pest insects and crops producing insecticidal toxins derived from Bacillus thuringiensis (Bt). Possible research topics addressed through this assistantship could include: fitness trade-offs that accompany Bt resistance; genetic analysis of Bt resistance traits; tritrophic interactions among insects, plants and entomopathogens; landscape level analysis of the occurrence of Bt resistance in western corn rootworm; and interactions of western corn rootworm with RNAi corn. Interested individuals should send a cover letter describing their research interests and career goals, the names and contact information of three references, and curriculum vitae to Aaron Gassmann (aaronjg@iastate.edu).

Iowa State University is an Affirmative Action/Equal Opportunity Employer.

aaronjg@iastate.edu

JohannesGutenbergU CapeEricaNGS

Evolutionary diversification in Cape Erica 'next generation' sequencing

We are looking for a motivated candidate with MSc-level background in evolutionary biology, bioinformatics or closely related fields for a three year DFG funded project based at the Johannes Gutenberg-Universität in Mainz, Germany. The candidate will need excellent lab skills including experience with 'next generation' DNA sequencing technologies and the related bioinformatics techniques. Good spoken and written English is essential.

The Cape Floristic Region (CFR) of South Africa is a botanical hotspot and its most species rich clade, the genus Erica, is a key taxon for understanding the causes of evolutionary diversification. The object of this project is to test a number of factors proposed as drivers of the high plant diversity of the CFR, using a group of closely related Erica species. The candidate will obtain NGS data targeted to represent numerous, meaningfully resolved independent gene trees and analyse the data with coalescence-based species tree inference methods. The results will be used to test various evolutionary hypotheses as well as to re-assess species boundaries in the group. Differing aspects of the biology of the system will be addressed in collaboration with specialists in South Africa and internationally.

Application (CV including referees, covering letter; by email to pirie@uni-mainz.de) deadline is 31st March 2014. For further information contact Michael Pirie: pirie@uni-mainz.de

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Dr. Michael D. Pirie Institut für Spezielle Botanik und Botanischer Garten Johannes Gutenberg-Universität Anselm-Franz-von-Bentzelweg 9a 55099 Mainz Germany

http://www.spezbot.fb10.uni-mainz.de/eng/135.php
pirie@uni-mainz.de

MNHN Paris MolluscSystematics

Open PhD Position

Muséum National d'Histoire Naturelle, Paris, France

Area of research: Palaeontology and Molecular systematics of Cenozoic and Recent molluscs, Gastropoda

PhD Title: Timing of diversification of the Bursidae (Gastropoda: Tonnoidea)

Supervisors: Dr. Didier MERLE, Dr. Michel LAURIN & Dr. Nicolas PUILLANDRE E-mails: dmerle@mnhn.fr, laurin@mnhn.fr, puillandre@mnhn.fr

Host laboratory: CR2P CNRS-MNHN-UPMC, Muséum National d'Histoire Naturelle, Paris, France. Associated Research units: 1Â) CR2P, CNRS-MNHN-UPMC, Centre de recherche sur la Paléobiodiversité et les Paléoenvironnements - Equipes 1 ≪ Paléoécosystèmes : analyse, compréhension, évolution ≫ and 2 ≪ Diversification des Métazoaires ≫ 2Â) ISyEB Institute CNRS MNHN UPMC EPHE (Institut de Systématique, Evolution, Biodiversité), UMR 7205, Equipe 3E ≪ Exploration, Espèce, Evolution ≫

State of the art: Time-calibrated phylogenetic trees are increasingly used in biology, in particular to highlight evolutionary radiations or biological crises, to establish a correlation between speciation and extinction rates and environmental changes or to compare diversification rates between clades. Also, modern comparative methods for establishing correlations between characters generally require trees with estimated branch lengths. For a long time, the dating of the tree of the life was based solely on the fossil record. During the last decades, the fast progress in molecular phylogenetics allowed inference of divergence times, but paleontological data have been under-exploited for this purpose, with few (mostly minimal) paleontological are constraints used in each study.. Both communities (paleontologists and molecularists) gain to work together on this theme, because fossils are not available for each node of the tree and because molecular phylogenetics still relies mostly on fossils to calibrate their trees. The Bursidae (Mollusca: Gastropoda) represents an ideal model for an interdisciplinary study combining molecular phylogenetic trees and paleontological morphological and stratigraphic data. It contains around one hundred currently recognized extant and extinct species resulting from a Cenozoic radiation. So far, it was little studied: a sole molecular phylogeny of the Bursidae was published by our team (Castelin et al. 2012) and no phylogeny dealing with the fossil record is available.

Objectives: The goal of this project is to date the diversification of Bursidae, which is currently poorly constrained and based on a subsample of the known diversity. To achieve this objective, molecular (for extant taxa) and morphological (on extant and extinct taxa) data will be independently analyzed before being used in a combined, total evidence analysis. Our new method will use the resulting trees and detailed stratigraphic data to supply more reliable estimated geological ages for taxa than those supplied by the classical paleontological approaches. This implies a clearly multidisciplinary approach, including a step (the incorporation of all taxa into a “total evidence” phylogeny) that has never, to our knowledge, been undertaken in molluscs.

Methodology: Molecular phylogenetics: knowing the limitations linked to the molecular approaches based on a few genes, the objective will be to apply an approach using NTS (New Technologies of Sequencing) to identify multiple markers. Paleontological phylogenies: the phylogenetic analysis will use cladistics and methods of formalization of the characters (ontogenetic and topological correspondence and criterion of conjunction) to propose hypotheses of primary homologies. It will rely mainly on the treatment of the numerous sculptural characters of the bursid shell. The PhD student will use a total evidence approach to establish a robust phylogeny of the Bursidae with a dense taxonomic sampling. Both sets of data (molecular and morphological) can be combined according to various methods to date the tree of life. The classical approach consists in specifying the age of certain nodes based on simple paleontological constraints (typically mostly minimal ages). A second approach (total evidence dating) consists in incorporating extinct taxa directly into the analysis, to incorporate the uncertainty on their systematic position and estimate the length of the branches. Finally, the third strategy consists in using birth and death models and trees incorporating stratigraphic data (about extinct taxa) to estimate the age of clades. This method, which we are currently developing to exploit phylogenies with a fossil record, will be used in the project to obtain paleontological age priors that will be used to produce a molecular timetree.

Material: 17 species of Bursidae are already sequenced for several genes, and their DNA is available. The collections of the MNHN from

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MNHN Paris6U EvolutionaryMetagenomics

Hello,

Please find below the description of a graduate position on 'Network analyses of the impact of a quick dietary shift in the gut microbiome of the lizard species, Podarcis sicula'

This PhD proposal aims at determining what it takes (in terms of microbiome changes) to become an herbivorous lizard in less than 35 years.

Most lizards are insectivorous. Yet, several species and populations of lacertid lizards have evolved toward an omnivorous or even herbivorous diet. Our model system, Podarcis sicula, a lizard species has shown rapid evolution of feeding and digestive tract morphology in manipulated populations. In 1970, five breeding pairs of the insectivorous P. sicula were transferred from the islet of Pod KopiÅte to the islet of Pod Mraru, Croatia. 36 years later (representing about 30 P. sicula generations), the transplanted P. sicula on Pod Mraru had become mostly herbivorous. This dietary shift resulted in changes in head size and bite force among the populations on the two islands, and most striking changes in the lizards guts, since the herbivorous Pod Mraru lizards had developed an elaborate hindgut chamber with cecal valves, which had not been seen in any other population of P. sicula. These valves facilitate plant digestion by the gut microbial community of the lizard hosts. With the advances of next generation sequencing, this system offers a unique opportunity to investigate the impact of this dietary change at the level of the microbiome using metagenomic and metranscriptomic data. We will take advantage of the inclusive powerful comparative framework offered by sequence similarity networks, and exploit concepts of graph theory, to analyze the functioning and the evolution of genetic diversity of the lizard gut microbiomes in such massive datasets. In short, we will address the following questions through a comparison of the gut microbiomes of insular herbivorous lizards and of their insectivorous relatives:

1) Does the taxonomy of the microbiome correlates with the diet? 2) What changes in gene content and functions did the dietary shift produce? In particular, what gene families were acquired/lost during this transition? 3) What role did the gut mobilome play in these functional changes? 4) Overall, were the changes mostly functional (and through lateral gene transfer) or taxonomical (through a deep change of the microbial populations)

To tackle these issues, the candidate's main goal will be to use and develop novel exploratory methods, based on sequence similarity graphs to describe and compare the taxonomical and functional diversity of metagenomes and metatranscriptomes of gut microbiomes of lizards, and to assess the possible impact of lateral gene transfer within this microbial community in this remarkable adaptive shift.

He/ she will work within a consortium of friendly herpetologists (Anthony Herrel), computer scientists (Philippe Lopez) and evolutionary microbiologists (Eric Bapteste), and be hosted in the University Pierre and Marie Curie and in the National Museum of Natural History, in Paris.

Ideally, the candidate should have some background in bio-informatics (to use and improve our labs existing tools) and a strong interest for evolutionary biology. He/she will benefit from a Labex BCDiv grant (1757 euro/month for 3 years.) and will be enrolled in the doctoral program at the Muséum National d'Histoire Naturelle in Paris with a start date of September 1st 2014.

Potential candidates should send a CV, two letters of recommendation, a pdf copy of their master's thesis, and a letter of motivation in English to Eric Bapteste (eric.bapteste@snv.jussieu.fr) and Anthony Herrel (anthony.herrel@mnhn.fr). The applications will be closed June 20, 2014. The three top-ranked candidates will be invited for an interview.

Eric Bapteste <epbapteste@gmail.com>

MPI Tuebingen EvolutionaryGeneticsRecombination

Recombination Hotspots and Adaptive Evolution

A PhD position in evolutionary genetics and genomics is available in the Jones Lab at the Max Planck Institute in Tuebingen, Germany. This is one four positions funded by a prestigious 2M EURO European Research Council funded grant investigating the evolution of recombination in adaptation in stickleback fish, an evolutionary model organism.

We study the molecular mechanisms underlying adaptive evolution and speciation. The goal of this particular project is to use cutting-edge techniques to characterize, quantify, map and manipulate meiotic recombination hotspots at unprecedented resolution across the genome, among individuals, and between species. We will map the genetic basis of recombination modifiers and study the effects of recombination variation on individual fitness in the lab and field. This groundbreaking research will elucidate how a fundamental biological process shapes the genomic basis of adaptive divergence in natural populations.

Your role: You will provide a comprehensive view of genetic factors underlying variation in recombination and its role in adaptive evolution. Your research will comprise both computational (dry) and experimental (wet) components. For computational work you will be responsible for genetically mapping variation in recombination hotspots in F2 families using whole genome sequence data, and searching for genomic features associated with recombination hot- and coldspots. In the wetlab you will work on functionally dissecting hotspot modifiers, and study the fitness consequences of recombination between adaptive loci in lab and natural populations.

Requirements: You will have a Masters or equivalent degree in the area of genetics, bioinformatics, molecular biology and/or evolution. We are looking for person with training in molecular biology techniques such as cloning, library preparation, fluorescent in situ hybridisation, and computational genomic methods including experience with unix and coding in C, python, perl, or R. The successful candidate will demonstrate a passion to study genetics and the molecular mechanisms of evolution.

Our Team: You will work in a multidisciplinary team that uses population genomics, genetics, molecular, developmental, and evolutionary biology to study the molecular mechanisms underlying adaptation and speciation in the threespine stickleback fish. Our research group is funded by the European Research Council (ERC) and the Max Planck Society and is located on the Max Planck campus in Tuebingen, Germany. Our campus hosts world-class research groups, including 7 other ERC-funded teams, and operates state-of-the-art sequencing and other core facilities. English is the working language. All seminars and communications are in English.

Our Offer: The position is for three years. Salary and benefits are according to the German public service pay scale (TVöD Bund).

The Max Planck Society seeks to increase the number of women in areas, where they are underrepresented, and therefore explicitly encourages women to apply. Disabled applicants with equal qualifications will be given preferential treatment.

To Apply: Consideration of applications will begin on April 15th 2014, and will remain open until filled. Please send your application with 1. a statement of research interests and why you have applied for this position, 2. your CV, and 3. three reference letters to Dr Felicity Jones at fcjones@tuebingen.mpg.de or the postal address below. Incomplete applications will not be considered.

Dr. Felicity Jones Friedrich Miescher Laboratory of the Max Planck Society Spemannstrasse 39 72076 Tuebingen Germany

jones.floss@gmail.com

MPI Tuebingen GenomeBioinformatics

Positions in genome bioinformatics

Two positions at the PhD/Master student and postdoc level are available for developing new algorithms and strategies for analysis of second- and third-generation sequencing data, and for using these data to study a wide array of biological questions, with an emphasis on genome assemblies, annotation and genome comparisons. Initial appointments for PhD students and postdocs will normally be for three years. The positions are available immediately.

Candidates will have demonstrated experience in sequence and genome analyses, with at least some knowledge of primary short read analysis and genome/transcriptome annotation. Proven skills in at least one major programming or scripting language (PERL/PYTHON, Java, C/C++) and Linux/Unix computing environment (Bourne/Bash shell scripting) are a must. Good understanding of molecular biology, experience with assemblies and familiarity with biostatistics including knowledge of R are a plus.

The lab comprises a mix of computational scientists, biologists with strong bioinformatics skills and molecular biologists. It provides unique opportunities, as the lab is not only very well funded, but bioinformaticians are also involved in designing genomic analyses from day one, and often propose their own project ideas. Our work in this and other areas routinely results in high-profile publications, making it an extraordinary place for talented and ambitious students and postdocs.

The lab has been an early adopter of next generation sequencing technologies and has used these for diverse applications, from studying de novo mutations and epimutations to being the first to fine-map and identify a causal mutation using bulk segregant sequencing (Schneeberger et al., Nature Methods 2009; Ossowski et al., Science 2010; Becker et al., Nature 2011). A major effort is in understanding within- and between-species sequence variation, using both resequencing and de novo assembly strategies (Cao et al., Nature Genetics 2011; Hu et al., Nature Genetics 2011; Slotte et al., Nature Genetics 2013). A flagship project is the 1001 Genomes project for Arabidopsis thaliana (http://1001genomes.org). In this area, we have already gathered experience with PacBio data and will have early access to nanopore sequencing.

We are working closely with other groups that are primarily informatically oriented. These include Daniel Huson (Univ. Tuebingen), Bernhard Schölkopf (Max Planck Institute for Intelligent Systems, Tuebingen) and Karsten Borgwardt (currently Max Planck, soon ETH Zurich/Basel). Additional information on the group, the institute, and Tuebingen can be found on our website (http://weigelworld.org).

For Master and PhD students, we expect that you can provide at least two letters of reference and that you describe in detail your practical programming experience.

For postdocs, we expect that you have published (or are close to publishing) at least one first-author paper in a major international journal. Please send a letter that outlines which projects you are particularly interested in.

For both graduates students and postdocs, we hope to see a cover letter that details how your experience and interest would fit with the projects outlined above.

Please send applications, with a statement of purpose, names of references, and the subject line <bioinformatics posting> to Detlef Weigel: weigel@tue.mpg.de

rebecca.schwab@tuebingen.mpg.de

MaxPlanck 10 EvolutionaryBiology

The *International**Max Planck Research School**for Evolutionary Biology*

is offering *up to**10 PhD fellowships*.

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

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

*To obtain further information about our PhD program and application details please visit our website at http://imprs.evolbio.mpg.de. *

Well-motivated and highly-qualified students from all countries are welcome to apply. A Master of Science degree or a Diploma as well as a strong interest in Evolutionary Biology and flexibility in the research project are prerequisites for entering the program. We are looking forward to your online application for a PhD fellowship in the beautiful landscape of Northern Germany.

The deadline for applications is April 20, 2014.

The selection week will be held from June 23 - 27 and

the program itself starts on September 22, 2014.

Contact: Dr. Kerstin Mehnert,

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

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

The coordinator

Kerstin Mehnert

The steering committee

Diethard Tautz, Hinrich Schulenburg, Manfred Milinski and Thorsten Reusch

– Dr. Kerstin Mehnert Scientific Coordinator IMPRS, Press and Public Relations, International Office

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Kerstin Mehnert <mehnert@evolbio.mpg.de>

MonashU LifeHistoryEvolutionaryEcol

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

Deadline: 15 April 2014

TEXT: Top-up PhD scholarship “Telomere dynamics in free-living fairy-wrens”

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 field-work and/or birds a bonus. Note that the application process is quite competitive, international students without at least one first author publication in an international journal (in the topic or of ecology or evolution) are not usually successful. 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 two referees before 15 April 2014 to meet the Monash application deadline of 31 May.

Further details:https://sites.google.com/site/petersresearchgroup/ Dr. Anne Peters Senior Lecturer / ARC Future Fellow School of Biological Sciences, 18-G22 Monash University Melbourne, VIC 3168 Australia

anne.peters@monash.edu

https://sites.google.com/site/petersresearchgroup/ http://www.biolsci.monash.edu.au/staff/peters/index.html http://scholar.google.com/citations?user=jpoOPNEAAAAJ

Anne Peters <anne.peters@monash.edu>

Montpellier Tunicate EvoDevo

Hello,

A 3-year PhD fellowship is available from October 1st 2014 in Montpellier (France) to study the molecular mechanisms underlying morphological stasis during evolution.

The question: Evolutionary biology studies mostly focus on the mechanisms driving innovation and adaptation. Morphological features can however remain stable over surprisingly long periods of time, and in spite of extensive genome sequence alterations. Very little is known about the determinants of this morphological robustness to genomic changes, which may involve a careful balance between external selection and internal developmental constraints. It is also not known how morphological stasis can be broken to give rise to new life forms. We are studying this phenomenon in chordates using two groups of tunicates as models. Ascidian embryos have shown exceptional morphological stability since the Cambrian, over 500 million years ago, despite extreme genome sequence divergence. By contrast, the embryos of thaliaceans, a pelagic group, which causes sessile ascidians to be paraphyletic, have undergone a radical morphological change from their ascidian-like ancestors, associated to an ecological transition from sessility to pelagy.

*The project: *The aim of the PhD project will be to identify molecular mechanisms underlying ascidian morphological stasis and thaliacean divergence. Morphological evolution is thought to be mostly driven by coding or non-coding changes in the transcriptional gene regulatory networks underlying embryonic development. To shed light on the evolution of such networks, you will use extensive genomic and transcriptomic ascidian and thaliacean datasets to explore the evolutionary forces that shape regulatory proteins and the /cis/-regulatory sequences driving their expression.The project will mostly involve advanced computational and statistical analyses of existing, unpublished, sequencing data. You will be involved in the precise definition of the project.

Qualifications: An MSc degree in a relevant field is mandatory. Ideal candidates will be strongly driven for a research career with thorough education and strong interest in evolutionary biology, population genetics and genomics, and potentially developmental biology. Programming skills are expected. Some experience in genomics would be a plus but is not mandatory. Proficiency in English or French is needed.

Conditions: The PhD training comprises three years of full time research. The successful candidate will be jointly affiliated to the complementary research teams of Emmanuel Douzery (Institute for Evolutionary Biology of Montpellier, ISEM) and Patrick Lemaire (Center for Research in Macromolecular biochemistry, CRBM, Montpellier). The student will be mostly based at ISEM.

Application: The application should include 1) a one-page description of your education, research interests and motivation for PhD studies, 2) a CV with grades or ranks, 3) Contact information (name, address, email address, and phone number) for at least two referees. The application can be written in English or French and should be sent by e-mail to Emmanuel Douzery (emmanuel.douzery@univ-montp2.fr) and Patrick Lemaire (patrick.lemaire@crbm.cnrs.fr). Applications are open from March 1st 2014 and will remain open until the position is filled.

Suggested readings: Lemaire P. Evolutionary crossroads in developmental biology: the tunicates, /Development/, 138(11):2143-52.(2011) Tsagkogeorga, G., Turon, X., Galtier, N., Douzery, E. & Delsuc, F. Accelerated evolutionary rate of housekeeping genes in tunicates. /Journal of molecular evolution/ *71*, 153–67 (2010). Sella, G., Petrov, D., Przeworski, M. & Andolfatto, P. Pervasive natural selection in the /Drosophila/ genome?///PLoS genetics/ *5*, e1000495 (2009). Garfield, D., Haygood, R., Nielsen, W. & Wray, G. Population genetics of cis-regulatory sequences that operate during embryonic development in the sea urchin /Strongylocentrotus//purpuratus/. /Evolution & Development/ *14*, 152–67 (2012).

Patrick Lemaire CRBM 1919 Route de Mende F-34293 MONTPELLIER Cédex 5 France http://www.crbm.cnrs.fr/index.php/en/patrick-lemaire-uk email: patrick.lemaire@crbm.cnrs.fr

Frédéric DELSUC (Chargé de Recherche CNRS) Case Courier 64 Institut des Sciences de l'Evolution – UMR5554-CNRS-IRD Université Montpellier 2 Place Eugène Bataillon 34095 Montpellier Cedex 05 France Tel: (+33) 4 67 14 39 64 FAX: (+33) 4 67 14 36 10 Email: Frederic.Delsuc@univ-montp2.fr Webpage: http://fdelsuc.perso.neuf.fr Frederic.Delsuc@univ-montp2.fr

Oslo 2 EvodevoModeling

I would like to bring to your attention two PhD positions in evolutionary developmental biology are available at the Department of Biology at the University of Oslo. One of these will be focused on mathematical or statistical modeling of the GP map, and the other on the developmental basis of speciation and reproductive isolation.

The deadline is 20 April.

The announcement (pasted below) and further information can be found at the following link:

http://uio.easycruit.com/vacancy/1149295/-96323?iso=no If you are interested in the modeling position feel free to contact me at "thomas.hansen@bio.uio.no". For interest in the speciation position contact Paul Grini (p.e.grini@ibv.uio.no).

Sincerely,

Thomas F. Hansen

Two positions as PhD Research fellow in Evolutionary Developmental Biology is available at the Department of Biosciences. The fellowship will be for a period of up to 4 years, with 25 % compulsory work (e.g. teaching responsibilities at Department of Biosciences) if the Department finds the candidate suited. Otherwise, the fellowship will be for a period of up to 3 years, with no compulsory work. Starting date no later than 01.10.2014.

Job/ project description: The two positions are part of an initiative to strengthen research in evolutionary developmental biology (Evodevo) at the University of Oslo. The position will be associated with the Centre for Epigenetics, Development and Evolution (CEDE, www.mn.uio.no/ibv/evogene/cede/) , which is a prioritized research area at the Department of Biosciences. The main objectives of the PhD projects is to 1) develop mathematical or statistical models of the genotype-phenotype map in the context of evolutionary developmental biology, and 2) to understand the developmental basis of hybridization barriers in eukaryote systems and diversification processes at the species level.

Position 1 PhD Research Fellow in (Theoretical) evolutionary developmental biology A core concept of evodevo is the genotype-phenotype (GP) map, which connects genetic variation to phenotypic variation and to potential for evolutionary change. The aim of the project is to develop or investigate models of the GP map that can be related to specific biological study systems or specific evolutionary questions investigated by the group. There is considerable flexibility as to the exact topics, and the interests of the candidate will be important in defining the study objects. The project should include mathematical or statistical modeling aimed at understanding how properties of the GP map determines variational phenomena such as integration, modularity, canalization, plasticity, robustness, pleiotropy and epistasis. These properties can then be linked to evolutionary topics such as evolvability, constraints and reproductive isolation. These models can be abstract or linked to specific biological systems. The latter may take the form of "causally-cohesive models" in which lower-level physiological or developmental parameters are given an articulated and ideally empirically-based connection to the genotype, and higher-level phenotypes are emerging from a mathematical model of the physiology. The modeling can focus on gene regulation, cell-cell communication, epigenetics or physiological and developmental mechanisms. The successful candidate will receive training in mathematical and statistical modeling and in the field of evolutionary developmental biology and epigenetics. The supervisor of the theoretical aspects will be professor Thomas F. Hansen. In addition the candidate will work with one or more members of the group in relation to specific questions or study systems. For a complete list of members in the group see www.mn.uio.no/ibv/evogene/cede .Candidate study systems include epigenetics, development and gene-regulation networks in Arabidopsis (Reidunn Aalen, Melinka Butenko, Paul E. Grini), bryozoan polymorphism and colony development (Lee Hsiang Liow), evolution of multicellularity (Kamran Shalchian-Tabrizi), consequences of hybridization or the evodevo of bill-shape variation (Glenn-Peter SÃtre).

Position 2 PhD Research Fellow in evolutionary developmental biology An ultimate effect of phenotypic change is speciation, which represents the branching of "the three of life". We would like to understand the mechanistic basis (genetic and epigenetic) as well as the phenotypic consequence leading to post-zygotic barriers, and subsequently possible speciation, across eukaryote lineages. Hence, genetic and epigenetic approaches are combined with ecological and evolutionary thinking to understand diversification processes of life. We have established the genus Arabidopsis and Passer sparrows as model systems for addressing the underlying processes of phenotypic

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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

RyersonU PlantEvolution

The Campbell Plant Evolutionary Ecology Lab (< http://www.ryerson.ca/plantevolecollab/ >*) has research opportunities for a doctoral student to participate in its research program. The program seeks to identify (using ecoinformatic databases and phylogenetic tools) plant species suitable to remove indoor air pollutants. A fellowship of $18,000 annually for three years will be available through our Molecular Science Graduate Program (http://www.ryerson.ca/graduate/programs/molecular_science/).

Under my close supervision and with the help of undergraduate research assistants, the student will create two databases of plants known to clean air and North American plant traits that may indicate a species could clean air. The PhD student and I will then derive a predictive tree-based classification model and validate it.

The student will have administrative responsibilities, which include:

1. Writing scientific papers, progress reports, and posters. 2. Maintaining the project's database; as well as supervising and verifying contributions from undergraduate research assistants.

Qualifications: Hold a MSc in bioinformatics, botany, biostatistics or related field. Have research experience in plant ecology. Have knowledge of ecological modelling and contemporary multivariate statistical methods. Ryerson University is an english-speaking university and communication in english is necessary to succeed here.

Documents to provide by email: Applicants for this position should email me a short cover letter indicating their motivation, accompanied by a current CV and the names and contact information of three references. I will begin to review the applications on 15 April 2014:

Lesley Campbell Department of Chemistry & Biology, 350 Victoria St. Ryerson University, Toronto (ON) M5B 2K3, Canada

Email: *L**esley.G.Campbell@Ryerson.ca*

Lesley Campbell <lesley.g.campbell@ryerson.ca>

SUNY StonyBrook AppliedEvolution

The masters program in Applied Ecology is intended to address the need for professionals in environmental sciences all levels of government, environmental departments of large industrial companies, environmentalconsulting firms, and non-governmental conservation organizations. The Applied Evolution concentration will also prepare students for work in these sectors, specifically for technical positions that require genetic, evolutionary and population based analytical skills. Career paths in biotechnology, forensics and biomedicine will also be available to graduates of this program. The ecological and evolutionary concentrations are useful for further specialized degree programs or careers in education. Please see http://life.bio.sunysb.edu/ee/masters.htm Liliana M. Davalos

Assistant Professor Consortium for Inter-Disciplinary Environmental Research (CIDER), and Ecology and Evolution, SUNY Stony Brook

Office phone: 631 632 1554

http://life.bio.sunysb.edu/ee/davaloslab/The_Lab.html Associate Editor, Molecular Phylogenetics and Evolution http://www.sciencedirect.com/science/journal/10557903 Associate Editor, Quarterly Review of Biology http://www.press.uchicago.edu/ucp/journals/journal/qrb.html lmdavalos@gmail.com

SaintMarysU WhaleReproductiveSuccess

Genetics, cancer, and reproductive success in the St. Lawrence beluga

I am looking for a M.Sc. student to start in September 2014 at Saint Mary's University in Halifax, Nova Scotia. The research project will involve looking at genes involved in cancer susceptibility and reproductive success in the St. Lawrence beluga whale population (Delphinapterus leucas).

Applicants should be highly motivated, independent, and have an excellent academic record. Students already with scholarships will be prioritized, but having funding is not a requirement.

Interested applicants should submit a CV and brief letter (< 1 page) explaining their interest in pursuing a M.Sc. in general, and in this project in particular, to Tim Frasier (timothy.frasier@smu.ca).

Timothy R. Frasier Associate Professor Department of Biology & Forensic Sciences Program Saint Mary's University Halifax, Nova Scotia

Timothy.Frasier@smu.ca

SalfordU UK EvolutionaryBiol

The School of Environment & Life Science at Salford University, Manchester, calls for outstanding PhD applicants in several areas of Biology and Environmental Science, many of which are specifically relevant to evolutionary biology - see list here: http://www.salford.ac.uk/study/postgraduate/fees-and-funding/funded-phd-studentship/pathway-to-excellence-studentships/schools-and-colleges/school-of-environment-and-life-sciences The PhD projects are fully funded for three years and will be awarded to the best candidates, on a competitive basis. Please note that fees are covered in full only for UK and EU citizens. Non-EU citizens are not necessarily excluded, but in case of success they would need to match the non-EU fee shortfall.

Specific queries can be addressed to the listed prospective supervisors. See the academics' contacts here: http://www.salford.ac.uk/environment-life-sciences/academics Thank you.

Professor Stefano Mariani Chair in Conservation Genetics | School of Environment & Life Sciences Room 316, Peel Building, University of Salford, Salford M5 4WT, UK t: +44 (0)161-295-6913 | m: +44 (0)7712-689-871 s.mariani@salford.ac.uk| http://hub.salford.ac.uk/bicome/2013/01/22/stefano-mariani/ http://www.salford.ac.uk/environment-life-sciences/els-academics/stefano-mariani The new Stock Identification Methods book is out: http://www.sciencedirect.com/science/book/9780123970039 Mariani Stefano <S.Mariani@salford.ac.uk>

SanFranciscoStateU MolecularEvolution

Molecular Evolution and Bioinformatics, San Francisco

The lab of Scott Roy at San Francisco State University is seeking masters students in molecular evolution. We focus on using bioinformatics and theoretical tools to study the evolution and function of genome and gene structure, with a special focus on introns, splicing and alternative splicing in nuclear genomes. Current projects probe trans-splicing, minor spliceosomal introns, miRNAs, alternative promoters, balancing selection, alternative splicing in microbial eukaryotes, intron length evolution, dual targeting of proteins, and the role of splicing in post-transcriptional regulation. Other topics of interest include the origins of eukaryotes, intrinsically disordered proteins, behavioral ecology, the evolution of self incompatibility in plants, and all kinds of other stuff that does not currently come to mind.

Our nascent website is at http://biology.sfsu.edu/people/scott-roy, and our publications can be found by pubmed'ing "roy sw."

If interested, please send an email with a bit about your interests and background to scottwroy@gmail.com.

Scott W. Roy Assistant Professor San Francisco State University San Francisco, CA

Scott Roy <scottwroy@gmail.com>

StellenboschU AvianEvolution

The role of birds in shaping networks of interactions between plants, arthropods and fungi in South Africa.

What will the World be like without birds? We know that birds pollinate many plant species, they disperse the seeds of an even greater number, in addition they are predators that prey on innumerable insects every day. Nevertheless, the world without birds is difficult to imagine because so many factors interact in complex ways to shape the natural world around us. To answer the question of the ecological significance of birds we are conducting a bird exclusion experiment on an unprecedented scale. “The World without Birds” consists of six walk-in cages, each of which excludes birds from a 20 X 20 m area of natural Fynbos vegetation in the spectacular Jonkershoek Valley in the Cape Fold Mountains of Africa. The experimental setup, which is already in place, offers the opportunity to test a range of ecological theories with direct implications for conservation. Two important avenues of research remain open: How important are birds as predators; and as vectors of mites and fungi that live inside Protea inflorescences? An overarching aim is to gain a general understanding of how networks of ecological interactions form, and respond to species loss. Both projects have a strong theoretical basis, while at the same time requiring detailed natural history observations.

The Botany and Zoology Department at Stellenbosch University has a vibrant Plant-Animal Interactions study group consisting of several researchers and students. These projects are supervised by Prof. Anton Pauw, Dr. Francois Roets and Prof. Cang Hui, who specialize in evolutionary ecology, entomology and mathematical ecologyrespectively. The values of the bursaries are R 50 000 p.a. for MSc and R 70 000 p.a. for Ph.D. South African students will be given precedence for funding, but students from other countries can apply for our departmental Foreign Students' Bursary and will find the University registration fees to be modest. For primary consideration, applicants should apply by 28 April 2014. Informal inquiries, prior to formal application, are welcomed. To apply, please email: 1) a one-page letter explaining why you are interested in this project, why you are qualified for it and when you can begin; 2) your university transcripts; 3) your curriculum vitae; 4) the names and email addresses of three referees. The successful applicant will be informed by mid May.

Assoc. Prof. Anton Pauw Department of Botany and Zoology Stellenbosch University Private Bag 1X Matieland 7602 South Africa Tel +27 21 808 3314 Cell +27 83 682 4177 Fax +27 21 808 2405 apauw@sun.ac.za

apauw@sun.ac.za

UAdelaide ClimateAdaptation AncientDNA

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

Project 1: Epigenetic modifications in adaptation to climate change

Project 2: Phylogenomic analysis of the impacts of climate change, population fragmentation and localised extinctions

Two PhD positions are available at the Australian Centre for Ancient DNA, School of Earth & Environmental Sciences, at the University of Adelaide (http://www.adelaide.edu.au/acad).

These positions are open to both international and domestic students with a strong academic achievement in either of the following areas: evolutionary biology, bioinformatics, or molecular biology. 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/).

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/ . The projects are described below. There is the potential for fieldwork, and training in ancient DNA, bioinformatics, genomics, and population genetics. Interested applicants are encouraged to send a resume and a cover letter to Dr Bastien Llamas (bastien.llamas@adelaide.edu.au) or Dr Julien Soubrier (julien.soubrier@adelaide.edu.au).

1) The role of epigenetic modifications in bovid adaptation to environmental change (Australian Research Council grant LP130100646). Supervision: Dr Bastien Llamas and Prof Alan Cooper This project will use a novel experimental system to explore the potentially crucial role of epigenetics in long-term evolution and how animal populations adapt to rapid climate change. Bones of ancient bison and cattle preserved in Alaskan/Siberian permafrost or European caves will be analysed for epigenetic markers using advanced Next Generation Sequencing approaches, and the patterns contrasted over a 30,000-year record of major climatic and environmental shifts. This project has strong potential to reveal key loci for climate adaptation in vertebrates, and to examine the interaction of climate changes and genomic responses. Most previous genetic research has been blind to epigenetic modifications, and this study promises to be a major advance in addressing

this issue, with considerable implications for conservation genetics and the cattle industry.

2) Using phylogenomics to record the impacts of climate change, extinction and population fragmentation (Australian Research Council grant DP140104233). Supervision: Dr Julien Soubrier and Prof Alan Cooper This project will use ancient DNA from permafrost-preserved Steppe bison bones and bovid exome capture systems to build a detailed record of the genomic impacts of rapid climate and environmental change at the end of the Pleistocene (30-11 kyr). The project will analyse how ancestral genetic diversity is distributed amongst surviving populations following major bottlenecks or localised extinctions, and the role of different nuclear loci under selection and drift. It will track genomic changes through time to create a powerful temporal dataset of genomic adaptation and evolution, and will generate critical data for the wider study of evolutionary processes such as extinctions, speciation and conservation biology and management.

bastienllamas@gmail.com

UAlaska Fairbanks SalmonEvolution

M.S. GRADUATE RESEARCH ASSISTANT OPPORTUNITY, UNIVERSITY OF ALASKA FAIRBANKS

This project will explore ecological and evolutionary responses by sockeye salmon to climate change in the Kvichak River watershed of southwest Alaska

Applications are sought for a M.S. position under the co-supervision of Drs. Jeff Falke (https://www.sfos.uaf.edu/directory/faculty/falke/) and Peter Westley (https://www.sfos.uaf.edu/directory/faculty/westley/) in the Alaska Cooperative Fish and Wildlife Research Unit & School of Fisheries and Ocean Sciences at the University of Alaska Fairbanks (UAF).

Responsibilities – The successful applicant will conduct analyses of historical long-term temperature and spawn timing data, spend time and work at remote field camps, and oversee a laboratory experiment to assess responses of incubating salmon embryos to varying temperature regimes. The student will work closely with graduate students and faculty at UAF as well as the University of Washington's Alaska Salmon Program (http://fish.washington.edu/research/alaska/), local native communities, state, and federal agencies interested in the project. As such, good communication and social skills are vital.

Qualifications – B.S. in fisheries, ecology, or closely related field. Experience conducting fieldwork in remote locations and use of small boats is preferred. The ideal candidate will have interests in quantitative ecology, evolution, experimental design, and experience using statistical packages such as Program R. Applicants will be assessed based on a combination of their stated interest in the position, prior experiences, and track record of academic performance (GPA and GRE scores). We expect the successful applicant will have a GPA of > 3.2 and GRE scores > 60th percentiles in 2/3 of the categories of the General Exam.

Salary – $31,000 per year, plus tuition waiver and student health benefits for two years. The incumbent will be expected to serve as a teaching assistant for one semester.

Closing date – Open until filled. Expected start date is Fall 2014.

To Apply – Send the following via email to both Dr. Falke (Jeffrey.Falke@alaska.edu) and Dr. Westley (pwestley@alaska.edu): 1) cover letter describing your personal interests, experiences, and goals, 2) current resume or CV, 3) copies of unofficial transcripts, 4) copy of GRE scores from the General Exam, and 5) contact information for three references.

westleypeter@gmail.com

UBern PlantBiodiversity

PhD student position in plant community ecology in the Biodiversity Exploratory Project at the University of Bern

The position at the Department of Plant Ecology at the Institute of Plant Sciences of the University of Bern, Switzerland (www.botany.unibe.ch), is available from 1 May 2014. We are looking for a highly motivated PhD student to work on plant diversity and community ecology in the context of the Biodiversity Exploratory Project (www.biodiversity-exploratories.de).

In this project we study the relationship between plant diversity, land-use in forests and grassland and ecosystem processes in three regions in Germany. Furthermore, in collaboration with Prof. Norbert Hölzel at the University of Münster and other groups within the consortium, we will establish a combined disturbance and seed addition experiment to test questions on community assembly processes and community stability. Finally, we will use trait-based approaches to understand the relationship between plant diversity and ecosystem processes, including the stability of ecosystem functions.

Candidates with strong backgrounds in plant community ecology, experimental ecology, and the statistical analysis of ecological data are especially welcome.

We offer a stimulating and pleasant working environment in beautiful Bern combined with the experimental facilities and stimulating research collaboration in the Biodiversity Exploratory consortium.

For more information please contact Professor Markus Fischer or Dr. Daniel Prati at markus.fischer@ips.unibe.ch or daniel.prati@ips.unibe.ch.

Please send your complete application (letter of motivation, CV, contact details of at least two references) as one single pdf to markus.fischer@ips.unibe.ch. The position remains open until the appropriate candidate is found.

markus.fischer@ips.unibe.ch

UBern PlantEvol

PhD student position in plant population biology in the biodiversity-ecosystem function context at the University of Bern The position at the Department of Plant Ecology at the Institute of Plant Sciences of the University of Bern (www.botany.unibe.ch) is available from 1 May 2014. We are looking for a highly motivated PhD student to work on plant population biology in the context of a large-scale biodiversity experiment, the Jena grassland experiment (www.the-jena-experiment.de). In collaboration with PD Dr. Christiane Roscher at UFZ Halle and Prof. Dr. Hans de Kroon at the University of Nijmegen we study plant population biology of several species as a function of increasing plant diversity. Moreover, for a subset of species, we analyse the role of genetic differentiation for plant performance as a function of increasing plant diversity. Candidates with strong backgrounds in plant population biology, experimental ecology, and the statistical analysis of ecological data are especially welcome. We offer a stimulating and pleasant working environment in beautiful Bern combined with the experimental facilities and stimulating research collaboration in the Jena experiment consortium. For more information please contact Professor Markus Fischer at markus.fischer@ips.unibe.ch Please send your complete application (letter of motivation, CV, contact details of at least two references) as one single pdf to markus.fischer@ips.unibe.ch to arrive on 31 March 2014 the latest.

markus.fischer@ips.unibe.ch

UCollege London Biodiversity

This Mres in Biodiversity, Evolution & Conservation offers a programme organized jointly by University College London, the Natural History Museum and the Institute of Zoology of the Zoological Society of London. It will train the next generation of people who wish to pursue careers in the related fields of biodiversity, evolution and conservation, be that through academic research, environmental policy and management, applied conservation, public health, or scientific journalism.

Our programme focuses in particular on the analytical approaches and cutting edge quantitative tools used in ecology, evolutionary biology, genetics, bioinformatics, systematics, palaeobiology, conservation, and environmental biology. The taught courses will be delivered by a dedicated team of lecturers from all three participating institutions, offering the complementary perspectives of lab, field and collections-based research approaches.

The taught courses will prepare each student for two 18-week research projects they will undertake at the three institutions, providing them with first hand experience of working in the different intellectual environments of some of the UKs leading academic and research institutions.

For more detailed information and on how to apply please visit our website at https://www.ucl.ac.uk/-biosciences/masters/MResbec Those who wish to apply for scholarship funding (particularly overseas students) need to apply by 31 March 2014. The deadline for applications is Friday 1 August 2014.

Regards, Ronald

Dr Ronald A. Jenner Department of Life Sciences The Natural History Museum Cromwell Road London SW7 5BD United Kingdom

Tel. +44 207 942 6885 (office) / 5774 (lab) Fax. +44 207 942 5054 http://www.nhm.ac.uk/research-curation/life-sciences/aquatic-invertebrates/research/comparative-venomics/index.html MRes Biodiversity, evolution and conservation: http://www.nhm.ac.uk/research-curation/training/mres-biodiversity-evolution-conservation/index.html
Ronald Jenner <r.jenner@nhm.ac.uk>

UFlorida SpatialEcologyBehavior

Ph.D. student position in behavioral ecology, spatial ecology, and evolution at the University of Florida starting Fall 2014.

Applicants must have a M.S. in ecology, evolutionary biology, behavior, or a related field. If you are interested in the position, please email Dr. Rob Fletcher at robert.fletcher@ufl.edu before April 5th. With your email, please include your resume, unofficial transcrips, GRE scores, and a cover letter. The successful applicant will be awarded a fellowship through the UF Entomology program that includes four years of guaranteed funding at $22,000/year plus tuition and benefits.

This position would be co-advised by Christine Miller (Entomology & Nematology Department; http://millerlab.net) and Rob Fletcher (Wildlife Ecology and Conservation Department; http://plaza.ufl.edu/robert.fletcher/) at the University of Florida, with field research at the Ordway-Swisher Biological Station, near Melrose, FL. Work will focus on animal behavior, population dynamics, and spatial networks using the unique research system of a cactus-feeding insect, the cactus bug (Chelinidea vittiger), and its Opuntia host plants. We have an ongoing field experiments funded through the National Science Foundation to test for the resiliency of population networks of cactus bugs to environmental change (habitat loss). The student would work in the context of these broad experiments to understand how behavior (foraging, habitat selection, dispersal, or mating strategies) drive ecological and evolutionary processes under rapid environmental change.

Cactus bugs are excellent species to investigate these questions because they have short generation times, individuals can be easily tracked through mark-recapture techniques, and their habitat can be readily manipulated in the field. This system is truly unique for experimentally addressing questions regarding animal dispersal (e.g., Fletcher et al. in press; Ecology), population dynamics (Fletcher et al. 2013, Nature Communications), landscape ecology (Fletcher et al. 2011, PNAS), foraging behaviors (Miller et al. 2012, Animal Behavior), and reproduction (Miller et al. 2013, PLoS One). This position could include field and modeling components to address questions of fundamental importance that lie at the interface of ecology, animal behavior, and environmental change.

Information about Gainesville, Florida:

Situated in the rolling countryside of north central Florida, Gainesville is much more than a stereotypical college town. Home of the University of Florida, seat of Alachua County's government and the region's commercial hub, it is progressive, environmentally conscious and culturally diverse. The presence of many students and faculty from abroad among its 99,000-plus population adds a strong cross-cultural flavor to its historic small-town Southern roots. Its natural environment, temperate climate and civic amenities make Gainesville a beautiful, pleasant and interesting place in which to learn and to live. Gainesville has been ranked as one of the best cities to live in the United States.

UFlorida TropicalEvolutionBehavior

Ph.D. student position in tropical evolutionary biology and behavior at the University of Florida starting Fall 2014.

This position will be based at the University of Florida, but field research will be conducted at the Smithsonian Tropical Research Institute in Panama. The successful applicant will have latitude to work on a variety of questions related to sexual selection, phenotypic plasticity, social behaviors, and/or parental investment in the fascinating research system of the tropical heliconia bug and its heliconia host plants (Miller 2008 Behavioral Ecology; Miller & Emlen 2010 Evolutionary Ecology). Videos of male competitions in a closely-related species can be viewed at https://www.facebook.com/media/set/ ?set=vb.141409729252695&type=2. The Smithsonian Tropical Research Institute provides a terrific experience for motivated graduate students, see http://www.stri.si.edu/ . Applicants must have completed or will soon complete a M.S. in ecology, evolutionary biology, behavior, or a related field. If you are interested in the position please email Dr. Christine W. Miller (http://www.millerlab.net; cwmiller@ufl.edu) by

April 5th. With your email, please include your resume, unofficial transcrips, GRE scores, and a cover letter. The successful applicant will be awarded a fellowship through the UF Entomology program that includes four years of guaranteed funding at $22,000/year plus tuition and benefits. The University of Florida has a strong community of behavioral ecologists and evolutionary biologists (http://evolution.group.ufl.edu/), and Gainesville is a great place to live.

UGlasgow CropAdaptation

PhD Studentship, University of Glasgow

Food security in the omics era: the role of polyploidy, hybridisation and mating system on the ability of crops to adapt to changing environments

An acknowledged threat to food security is the ability of crops and livestock to respond to increased environmental variability resulting from climate change. In plants, crops are often selected to be able to self-propagate but this comes at a cost to genetic variation, which could reduce potential for adaptation to changing environments. Hybridising different strains can increase genetic variation and combine desirable traits from different species but this is often accompanied by doubling of the genome (polyploidisation) to increase stability of the hybrid combination. Theoretically, this should increase flexibility to adapt to changing conditions. However, the relative effects of such breeding strategies on adaptability and the consequences for yield of economically important traits remain largely untested. Importantly, plants adapting to changing environments need to be able to continue to attract beneficial symbionts (pollinators and soil microbes that enable them to process nutrients) and to combat potentially new threats (pathogens and herbivores) but it is not known how the combination of mating system, ploidy and hybridisation affect such interactions. An exciting technological development is characterisation of microbial communities using deep sequencing approaches. The vast amounts of data generated and the difficulty of resolving species based on short sequences means that improved methods need to be developed for characterising microbial diversity and interpreting what this means for interacting organisms.

Using a common garden approach, combined with generation and analysis of deep sequencing data, and development of advanced statistical approaches to characterising biodiversity, the purpose of this multidisciplinary project is to use economically important Brassica napus (oilseed rape, which is used for both biofuel and edible oil production and is a polyploid hybrid that reproduces by self-fertilising) as a model to investigate:1) the relative ability of plants with different traits to adapt to new environments; 2) the role of the microbial community in plant adaptation;3) the consequences of the interaction between plant fitness and microbial community diversity for oil seed yield.

Project team:

Dr Barbara Mable (Principal investigator), Institute of Biodiversity, Animal Health & Comparative Medicine Dr Christina Cobbold (Co-investigator), School of Mathematics and Statistics Dr Bill Mullen (Co-investigator), Institute of Cardiovascular and Medical Sciences Dr Chris Quince (Co-investigator), School of Engineering Mr. Stephen Herrington (Project Partner), Curator, Glasgow Botanic Gardens

Application Process: Please contact the Principal investigator (Barbara.mable@glasgow.ac.uk) directly to enquire about applying for this scholarship. In the first instance, please send your CV and a written personal statement (no more than 300 words) of why you are interested in applying for this PhD position.

Eligibility: There are no citizenship or residency restrictions but applicants should have an equivalent of a UK 2:1 (B average) in a relevant undergraduate degree and/or have passed a Master's degree with at least a Merit (B average). This project requires strong quantitative skills but prior experience with advanced statistics or bioinformatics is not required. An interest in working with plants will be a strong factor in shortlisting applicants but prior experience is not essential.

UGlasgow CropAdaptation 2

PhD Studentship, University of Glasgow

Food security in the omics era: the role of polyploidy, hybridisation and mating system on the ability of crops to adapt to changing environments

An acknowledged threat to food security is the ability of crops and livestock to respond to increased environmental variability resulting from climate change. In plants, crops are often selected to be able to self-propagate but this comes at a cost to genetic variation, which could reduce potential for adaptation to changing environments. Hybridising different strains can increase genetic variation and combine desirable traits from different species but this is often accompanied by doubling of the genome (polyploidisation) to increase stability of the hybrid combination. Theoretically, this should increase flexibility to adapt to changing conditions. However, the relative effects of such breeding strategies on adaptability and the consequences for yield of economically important traits remain largely untested. Importantly, plants adapting to changing environments need to be able to continue to attract beneficial symbionts (pollinators and soil microbes that enable them to process nutrients) and to combat potentially new threats (pathogens and herbivores) but it is not known how the combination of mating system, ploidy and hybridisation affect such interactions. An exciting technological development is characterisation of microbial communities using deep sequencing approaches. The vast amounts of data generated and the difficulty of resolving species based on short sequences means that improved methods need to be developed for characterising microbial diversity and interpreting what this means for interacting organisms.

Using a common garden approach, combined with generation and analysis of deep sequencing data, and development of advanced statistical approaches to characterising biodiversity, the purpose of this multidisciplinary project is to use economically important Brassica napus (oilseed rape, which is used for both biofuel and edible oil production and is a polyploid hybrid that reproduces by self-fertilising) as a model to investigate:?1) the relative ability of plants with different traits to adapt to new environments; 2) the role of the microbial community in plant adaptation;?3) the consequences of the interaction between plant fitness and microbial community diversity for oil seed yield.

Project team: Dr Barbara Mable (Principal investigator), Institute of Biodiversity, Animal Health & Comparative Medicine

Dr Christina Cobbold (Co-investigator), School of Mathematics and Statistics

Dr Bill Mullen (Co-investigator), Institute of Cardiovascular and Medical Sciences

Dr Chris Quince (Co-investigator), School of Engineering

Mr. Stephen Herrington (Project Partner), Curator, Glasgow Botanic Gardens

Application Process: Please contact the Principal investigator (Barbara.mable@glasgow.ac.uk) directly to enquire about applying for this scholarship. ?In the first instance, please send your CV and a written personal statement (no more than 300 words) of why you are interested in applying for this PhD position. ??

Eligibility: There are no citizenship or residency restrictions but applicants should have an equivalent of a UK 2:1 (B average) in a relevant undergraduate degree and/or have passed a Master?s degree with at least a Merit (B average). ? This project requires strong quantitative skills but prior experience with advanced statistics or bioinformatics is not required. An interest in working with plants will be a strong factor in shortlisting applicants but prior experience is again not essential.

Barbara.Mable@glasgow.ac.uk

UGroningen 6PhDPdf OriginOfSpecies

6 PhD / postdoc positions available on eco-evolutionary assembly of ecological communities

At the Centre for Ecological and Evolutionary Studies of the University of Groningen in the Netherlands, there are 6 vacancies for PhD students and/or postdocs, as part of the research program 'On the origin of species assemblages' which is funded by a VICI grant awarded to Prof. Rampal S. Etienne.

Content

This program aims to develop a fully stochastic, dynamical, eco-evolutionary and data-friendly theory of community assembly, and testing and informing this theory with model-oriented experiments and field studies of both macro-organisms and micro-organisms.

The theory will contain models of speciation, extinction, immigration, and evolutionary change that vary in spatial, phylogenetic and biotic complexity, and will be designed for confrontation with data. The models include but are not limited to birth-death models, individual-based simulation models, and models of adaptive dynamics. New modelling directions are encouraged.

The evolutionary experiments will involve the mite Tetranychus urticae (in collaboration with Dries Bonte at the University of Ghent, Belgium) and the bacterium Escherichia coli (in collaboration with Joana Falcao Salles at the University of Groningen) which are ideal model organisms due to their short generation times. The experiments will provide insight into how diversity affects diversification, a great unknown in current macro-evolutionary theory.

The theory will be applied to naturally occurring microlandsnails in South-East Asia (in collaboration with Menno Schilthuizen at Naturalis Biodiversity Center, Leiden, The Netherlands), and micro-organisms in geothermal pools in New Zealand (in collaboration with Gavin Lear at the University of Auckland, New Zealand).

As a general outline, for the theoretical part, both potential PhD students and postdocs can apply. The mite and microsnail projects will each require a PhD student, the E. coli and geothermal pool projects together will require a postdoc. However, candidates who are willing and able to handle a combination of theoretical and empirical work are particularly encouraged to apply.

Profile of candidate

The candidates should - - hold an MSc degree in ecology or evolutionary biology, or an MSc degree in mathematics or physics with experience in applications to biology - -be willing to work in a multidisciplinary team - -have good communication skills in English (speaking and writing)

Information and application

More information can be requested from Prof. Rampal Etienne (r.s.etienne@rug.nl). Applications can be sent to the same address and should contain: - Motivation letter (max. one page) - Up-to-date CV - List of study grades (academic transcripts)

- Names of two references

Incomplete applications will not be considered. Applications will be considered until the positions are filled.

“R.S.Etienne” <r.s.etienne@rug.nl>

ULincoln UK PrimateRelatedness

The University of Lincoln is offering a PhD studentship to work on a project on genetic relatedness and social complexity in the Barbary macaque (Macaca sylvanus), under the supervision of Drs Bonaventura Majolo (http://staff.lincoln.ac.uk/bmajolo) and Malgorzata Pilot (http://staff.lincoln.ac.uk/mpilot). This project aims to investigate the link between inter- and intra-group social behaviour and the modulating effect of kin relationships between individuals in a wild population of macaques in the Middle Atlas Mountains, Morocco.

This is a part of a longitudinal project on the socio-ecology of the Barbary macaque run by Dr Majolo that started in January 2008 (http://-barbarymacaque.blogs.lincoln.ac.uk). Several groups of macaques are habituated for research purposes at the field site. The University of Lincoln is fully equipped for field work and DNA analysis. This project requires the student to spend approximately 13 months in Morocco and the rest of the time in Lincoln for lab work, data analysis and writing up of the PhD thesis.

The work at the field site is physically and mentally demanding. The field site is between 1,400 and 1,900m above sea level and weather conditions can vary dramatically across the year, with temperature ranging between 35oC to -5oC and snow in the winter months. The successful applicant will live in the town of Azrou in an apartment block with basic amenities including internet access.

Applicants should:

- Have a background in animal behaviour, primatology, population genetics, anthropology or related fields;

- Have a strong interest in social behaviour research and motivation to pursue a research career;

- Have some knowledge and experience of behavioural data collection methods and fieldwork;

- Have at least a basic knowledge of population genetics.

The ability to speak French and/or Arabic is desirable but not essential to this post.

The fully-funded studentship (3.5 years) is open to UK and EU citizens. All Candidates must satisfy the University’s minimum doctoral entry criteria for studentships of an honours degree at Upper Second Class (2:1) or an appropriate Masters degree or equivalent. A minimum IELTS (Academic) score of 7 (or equivalent) is essential for candidates for whom English is not their first language. The expected start date is September 2014.

To apply, please send a covering letter outlining your research interests and proposed approach (up to 1 page A4) with an accompanying CV to studentship-scss@lincoln.ac.uk by 5:00pm (UK time) on 18 April 2014. Candidates will be notified w/c 5th May of the outcome of the process and if invited to interview, these are anticipated to take place w/c 26th May. For further details see: http://www.lincoln.ac.uk/-home/studyatlincoln/postgraduateprogrammes/-postgraduate research/studentships/

Dr Malgorzata Pilot School of Life Sciences University of Lincoln Riseholme Park Lincoln LN2 2LG UK mpilot@lincoln.ac.uk

The University of Lincoln, located in the heart of the city of Lincoln, has established an international reputation based on high student satisfaction, excellent graduate employment and world-class research.

The University may monitor email traffic data and content in accordance with its policies and English law. Further information can be found at: http://www.lincoln.ac.uk/legal . mpilot@lincoln.ac.uk

UMarburg ComparativeGenomics

Two PhD-positions in comparative genomics and bioinformatics at the University of Marburg, Germany

The Rensing lab (http://plantco.de) is a joint wetlab/drylab group interested in the evolution of plants. Our main organism is the model moss Physcomitrella patens, our main theme is comparative genomics. We are looking for two PhD students with bioinformatics background.

One position is to be staffed within the ERA-CAPS project “Dimorphic fruits, seeds and seedlings as adaptation mechanisms to abiotic stress in unpredictable environments (SeedAdapt)”. The successful candidate for this project will work on tanscriptomics, phylogenomics and epigenomics of Brassicaceae (mainly Aethionema).

The other position will encompass the analysis of high throughput RNA, DNA and ChIP sequencing data, as well as machine learning/predictive approaches, phylogenetic methods and data visualization.

The positions require an M.Sc. or equivalent in bioinformatics, computer science or biology (bioinformatics skills are mandatory), fluency in English, ability to interact with wetlab and drylab researchers, good communication skills and interest in academic research. Programming skills in Perl or Python are expected, as well as skillful command line use and R or Matlab experience. Good IT/sysadmin skills, knowledge of statistics, experience with data-bases, Gbrowse and handling of high throughput sequencing data, as well as fluency in German are helpful.

Please send your application mentioning the registration number

fb17-0007-wmz-2014 (Comparative genomics)

or

fb17-0008-wmz-2014 (ERA-CAPS)

including a cover letter, recent C.V. with list of publications, two potential referees and list of skills as a single PDF to peterjul@biologie.uni-marburg.de. Application deadline is April 7th 2014.

– Kristian Ullrich

Rensing lab, Plant Cell Biology Faculty of Biology, University of Marburg Karl-von-Frisch-Str. 8, D-35043 Marburg phone +49 6421 28 22040 fax +49 6421 28 22190 mail kristian.ullrich@biologie.uni-marburg.de

Kristian.Ullrich@biologie.uni-marburg.de

UNordland Norway MarineGenomics

PhD Position (3 years) in marine genomics and benthic ecology at University of Nordland A Position as PhD student in marine genomics and benthic ecology is available at the University of Nordland, Faculty of Biosciences and Aquaculture.

About the Position The Faculty of Bioscience and Aquaculture, University of Nordland in Bodø, Norway, opens for applications for a three-year PhD position in marine genomics and benthic ecology. The position is part of the researcher project “Next-generation biodiversity assessment and environmental monitoring of benthic communities using high-throughput DNA metabarcoding”, financed by the Research Council of Norway. The collaborating partners of the project are Ghent University (http://www.ugent.be/en), Akvaplan-niva (www.akvaplan.niva.no/en), and the University of Nordland (www.uin.no). The primary objective of the project is to characterise marine benthic diversity in north Norwegian waters using high-throughput DNA technologies. The project aims to develop effective methods for DNA metabarcoding of benthic communities, and to analyse benthic diversity along natural diversity gradients and in environments influenced by human activities. The PhD candidate will participate in the collection of environmental samples and processing of samples for DNA analysis, including next-generation sequencing and subsequent bioinformatics analyses. The project will seek to develop efficient methods for assessment and monitoring of benthic communities, based on comparison of traditional taxonomic classifications and novel DNA barcoding methods. It also aims to build taxonomic competence and contribute to a molecular reference database with particular focus on marine nematodes. The successful applicant must have a MSc degree, or equivalent, in ecology, genomics, or a related field, and a focus on marine genomics and/or benthic ecology is preferred. Experience in DNA sequence analysis (preferred next-generation sequencing) and bioinformatics is mandatory. Knowledge of marine ecology is mandatory, except if the molecular skills are outstanding. Experience in taxonomic classification of benthic organisms, shipboard field work experience and statistical analysis are desirable, but not required. Good communication skills in English, both oral and written, are required, as the Faculty operates in an international environment with many international visitors and staff members. The PhD position is organized research training, implying that the candidate will obtain the PhD degree. It is required that the PhD student will be admitted to the PhD programme at the Faculty of Biosciences and Aquaculture, and participate in the organized research training programme. Application for admission to the programme must be submitted within three months after admission. For admission requirements and regulations, see www.uin.no . Personal skills The position requires a highly motivated, performance driven person with good capabilities of working independently as well as in teams.

Salary and Working Conditions The start salary for the PhD candidate is set at wage level 50 in the Norwegian State Salary Scale (ca NOK 416 600 per year). As an employee at the University of Nordland you become a member of the Norwegian Public Service Pension Fund and you will also get access to other social benefits. A statutory amount to the Norwegian Public Service Pension Fund will automatically be deducted from the salary. The person who is appointed must abide by the laws, agreements and directives that apply to the position at any time. The responsibilities and duties linked to the position may be altered due to future reorganization at the University of Nordland. According to the employment policy of the institution, our staff should reflect the population in general. We encourage candidates with minority background to apply for the position. The University practices moderate allocation according to sex quotas in accordance with the Basic Agreement for the Civil Service.

Contact Information For further information, prospective applicants can direct their questions to Truls Moum (truls.moum@uin.no, phone +47 75517422/+47 90095956) or Henning Reiss (henning.reiss@uin.no , phone +47 75517576).

Application (until 16. March 2014) For more information and online application forms see: http://www.uin.no/omuin/ledigestillinger/Pages/-default.aspx Henning Reiss <Henning.Reiss@uin.no>

UOslo 2 ComparativeGenomics

Department of Biosciences PhD Research Fellowship in comparative genomics Position as PhD Research Fellow in comparative genomics is available at the Centre for Computational Inference in Evolutionary Life Sciences (CELS), Faculty of Mathematics and Natural Sciences.

The fellowship will be for a period of up to 4 years, with 25 % compulsory work (e.g. teaching responsibilities at Department of Biosciences) if the Department finds the candidate suited. Otherwise, the fellowship will be for a period of up to 3 years, with no compulsory work. Starting date no later than 01.10.2014. The PhD research fellowship will be linked to CELS and to the project “Unravelling the impact of genome duplications on the evolution and diversification of gene function in non-model organisms”. The position will be affiliated to Department of Biosciences. This is position is one of four positions within CELS, one at Department of Informatics, one at Department of Mathematics and two at Department of Biosciences.

CELS CELS is a multidisciplinary centre within life sciences comprising strong research environments in biology and statistical and computational methods for data analysis. CELS is hosted by the Department of Mathematics, Faculty of Mathematics and Natural Sciences. CELS addresses fundamental biological questions related to the genotype-phenotype paradigm, how the environment affects genome evolution and development of methods for integrated analysis of genomic and other biotic and abiotic data. A main goal is to develop interdisciplinary research activities generating science of true interest for statisticians, bioinformaticians and biologists. Our vision is to be a leading interdisciplinary environment driven by common projects bridging the fields of biology, statistics and informatics.

Job/ project description: Comparative genomics is a powerful tool to examine the function and evolutionary processes that act on genomes through the identification of 1) overall structure of genes/genomic regions, 2) which genes that are conserved, in addition to 3) which genes that are unique for the organisms investigated. Gene and entire genome duplication events seem to be mechanisms leading to functional innovation and evolutionary change. This PhD project will be linked to the recent sequencing of the genome of grayling (Thymallus thymallus) and to studies of genomic and transcriptomic variation in grayling and other species within the genus Coregonus as well as other relevant genomes. The project will involve investigations of the genomic landscape at the species and population level (related to the genome duplication in these species) as well as development of efficient methods for comparative genomics. The successful applicant will be working an interdisciplinary environment together with biologists, bioinformaticians and statisticians.

Requirements/qualifications: The Faculty of Mathematics and Natural Sciences has a strategic ambition of being a leading research faculty. Candidates for these fellowships will be selected in accordance with this, and expected to be in the upper segment of their class with respect to academic credentials. Applicants must hold a Master's degree (or equivalent) in biology (evolutionary genomics), bioinformatics or statistics. Experience with next generation sequencing and bioinformatic analysis of such data will be an advantage. Applicants with a biology background are expected to have a keen interest in statistical and bioinformatics methods and applicants with a computational background are expected to have strong motivation for biological questions. We seek a highly motivated and enthusiastic person with good communications skills and with ambitions to work together with an interdisciplinary research team. Candidates without a Master's degree have until 30 June, 2014, to complete the final exam. A good command of English is required.

The purpose of the fellowship is research training leading to the successful completion of a PhD degree. The fellowship require admission to the PhD program at the Faculty of Mathematics and Natural Sciences. The application to the PhD program must be submitted to the department no later than two months after taking up the position. For more information see: http://www.uio.no/english/research/doctoral-degree-and-career/phd/application/ http://www.mn.uio.no/english/research/doctoral-degree-and-career/phd-programme/index.html Salary: Position code 1017, pay grade: 50 - 57 (NOK 421 100 - 473 400 per year)

The application must include:

* Application letter (maximum one A4 page) * CV (summarizing education, positions and academic work - scientific publications) * Copies of educational certificates, transcript of records and

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UOslo LifeHistory Evolution

A PhD Research fellow in Ecotoxicology is available at the Department of Biosciences, Section of Aquatic Biology and Toxicology, Faculty of Mathematics and Natural Sciences, University of Oslo.

The main objective of this PhD project is to investigate how differences in life history strategies affect food web bioaccumulation of environmental contaminants. Understanding how variations in animals' life-history strategies influence contaminant accumulation is a key to address our larger goal. Life history strategies of animals inhabiting Arctic waters will change with climate change due to altered species composition, particularly due to more southern species, with their different life histories, becoming established at high latitudes, and due to flexible behavioural and life-history responses to climate changes in true Arctic species, particularly concerning energy storage and reproductive strategies.

The project combines knowledge from ecotoxicology, marine biology, and evolutionary ecology. The successful candidate will compile and work with large data sets, using both statistical and mechanistic modeling. Field studies or experiments may be conducted to complement the existing data.

We seek and independent and motivated candidate with strong interest in (eco)toxicology, ecology and evolutionary biology, statistics and/or ecological/environmental modeling, and a solid academic background. The successful candidate should have strong quantitative skills and interests, and will be required to perform statistical and mechanistic modelling. Prior experience with data treatment and statistics, life history theory, and/or contaminant bioaccumulation is relevant. The fellow will interact within a network of researchers and students, and needs to possess collaborative abilities and a personality to do so. Applicants should include a short text that outlines the candidate's motivation and ideas for a project within the described field of research (1-2 pages).

The project will be conducted in collaboration with the Department of Biosciences' prioritized research group "Life-history variation under multiple stressors: separating the effects on development, growth, maturation and survival - LUMS".

Application deadline April 20th 2014.

For more information such as requirements and conditions please visit:

http://uio.easycruit.com/vacancy/1149335/-96323?iso=no or contact Professor Katrine Borga: Katrine.borga@ibv.uio.no

Oystein Varpe <oystein.varpe@akvaplan.niva.no>

USC Australia DolphinSociality

Primary supervisor: Dr Celine Frere, The University of the Sunshine Coast, Australia Secondary supervisor: Professor Janet Mann, Georgetown University, USA.

Despite a growing body of theoretical and empirical research on the evolution of mammalian social systems, the development of a unified theoretical framework remains a significant challenge. Most agree that variation in mammalian social systems can be attributed to four main factors: predation pressure (Dunbar 1988; van Schaik and van Hooff 1983); distributions of resources (e.g. food, water, nesting sites, mates) and levels of competition for them (Clutton-Brock and Harvey 1977; Krebs and Davies 1993); sexual selection (Clutton-Brock and Parker 1995; Clutton-Brock 1989; Smuts and Smuts 1993; van Schaik and Janson 2000; van Schaik, et al. 2004); and inbreeding avoidance (Perrin and Mazalov 2000). While it is widely accepted that these four factors interact with each other to influence patterns of mammalian group living within and between species (Aureli, et al. 2008; Sueur, et al. 2011), we still know very little about whether and how the selective pressures resulting from these four factors influence the spatial and temporal nature of social interactions.

To better understand the ecological basis of mammalian sociality, this PhD project will focus on the hypothesis that individuals within a population can ultimately use conspecifics to balance responses to the four main factors described above and thus increase their own fitness (Frère, et al. 2010). This hypothesis will be investigated using the long-term behavioural and genetic dataset (>27 years) from the bottlenose dolphin population found in the eastern gulf of Shark Bay, Western Australia. Shark Bay dolphins do not live in stable groups, but have a dynamic fission-fusion society characterized by frequent changes in group composition (e.g., Mann et al. 2000, 2012). Underlying these fluid relationships are very strong bonds, but these too vary. This longitudinal dataset provides us with the unique opportunity to investigate the ways by which female bottlenose dolphins temporally and spatially adapt their social networks to maximize their own fitness.

The student will be based in the Genecolgy research centre at the University of the Sunshine Coast in Dr Celine Frere lab and will be co-supervised by Professor Janet Mann from Georgetown University. It is expected that the student will spend several months per year in Shark Bay to conduct field work. Please visit monkeymiadolphins.org for more information on the long term study.

Applicants will need to have an extremely competitive academic record and obtain an Australian Postgraduate Award or International Research and Fee Remission Scholarships (for details and scholarship application forms http://www.usc.edu.au/research/research-students/hdr-scholarships). The main application deadlines for these scholarships are 11th of April (domestic only) and October (Domestic and International). Interested students are invited to email their CV to Celine Frere (cfrere@usc.edu.au).

Cheers Celine

Celine Frere PhD

Research Fellow GeneCology Research Centre University of the Sunshine Coast mobile: 0423312893

celinefrerelab.com

Celine Frere <cfrere@usc.edu.au>

UVienna Phylogenetics EcolGenomics

A 3 years PhD student position is available in the Department of Botany and Biodiversity Research of the University of Vienna, Austria (http://systematics.univie.ac.at/) to work on a project funded by the Austrian Science Fund (FWF) starting from 1st of May 2014. The project employs latest methodological developments (including NGS) to investigate the plant community structure in a tropical forest at Kuala Belalong Brunei Darussalam and the factors (i.e., geographic, edaphic, climatic) influencing it. For DNA barcoding, we will sequence plastid regions rbcL and matK. The reconstructed phylogenetic trees will be compared to the distribution and frequency of different species to confirm the presence of phylogenetic clustering or overdispersion. Barcoded species of well represented Angiosperm families of these plots will be incorporated into available sequence matrices to get the molecular phylogeny of the family concerned. Phylocom will be used to analyse the phylogenetic community structure and quantify community indices for each subplot. Correlations between community indices and ecological parameters will be examined to determine the influence of abiotic parameters on the community structure. We will further apply a genome-wide RAD (restriction site associated DNA) sequencing for a detailed phylogenetic reconstruction of relationships between dipterocarps and to evaluate the structure of their community. The sampling will be completed with additional accessions from other parts of Brunei, Malaysia and Thailand. This will allow us to understand the ecological and evolutionary processes that influence community assembly at local and regional level.

The student will be part of a larger consortium including the following national and international partners: Prof. Dr. Rosabelle Samuel (Project leader), Dr. Ovidiu Paun, Dr. Michael Barfuss (all University of Vienna, Austria), Prof. Dr. Mark W. Chase FRS (Jodrell laboratory, Royal Botanic Gardens, Kew, UK), Prof. Toby Pennington (Tropical Diversity, Royal Botanic Garden Edinburgh, UK), and Dr Kamariah Abu Salim (University of Brunei Darussalam, Brunei). The position offers a competitive salary (of ca. £á28,000 per year before tax according to FWF regulations, including social and health security), the opportunity to attend two international conferences, and if necessary to shortly visit one of the labs of our collaborators.

The working language in the department at the University of Vienna is English. German skills are not essential, but can be helpful for everyday life in Vienna. Vienna is a highly attractive city in beautiful surroundings, with a multinational population, and many educational and recreational opportunities. The presence of several outstanding research groups (see www.univie.ac.at/evolvienna/) make Vienna a hot spot of evolutionary research and offers ample opportunities for interactions with peers.

Expect qualifications of the suitable candidate.

- We are looking for a highly motivated candidate with an excellent academic track record. A MSc degree (or equivalent) in a related discipline (e.g., taxonomy, phylogenetics, evolution, molecular ecology) is required.

- Field experience is a plus (especially in tropical forests). The selected candidate will have to spend two to three months during the first and the second year in the field in Brunei for collecting material as well as ecological observations. A good knowledge of tropical plant species will be therefore of advantage.

- The successful candidate is expected to be able to demonstrate some previous laboratory experience, at least with PCR and Sanger DNA sequencing. Previous experience with phylogenetic analyses and/or next generation sequencing methodology (e.g., RADseq wet lab and/or bioinformatics) is a significant advantage.

- The PhD student should be fluent in English (both speaking and writing) and s/he is expected to have excellent organization skills.

To apply please send your electronic application (motivation letter V up to 2 pages) explaining why would you be interested in/qualified for this position together with a Curriculum Vitae, and the names and contact details of two academic referees to mary.rosabella.samuel@univie.ac.at before the end of March 2014. PLEASE NOTE: we will NOT consider any incomplete application.

Ovidiu Paun <ovidiu.paun@univie.ac.at>

UppsalaUniversity ButterflyGenomics

PhD-position in butterfly genomics

A 4-year Ph.D. position in butterfly genomics is available in the research group of Dr. Niclas Backström at the Evolutionary Biology Centre in Uppsala, Sweden. Starting date as soon as possible or as agreed upon. The successful applicant will work with genome assemblies, population genomic analysis using re-sequencing data from several populations and species, and management of captive butterfly populations for crossing and linkage mapping experiments.

Background: Getting detailed understanding about proximate and ultimate causes to formation of reproductive isolation between diverging lineages is one of the major challenges in evolutionary biology. The genomic revolution is at full swing and brings about the necessary tools to investigate the genomic architecture of population differentiation and speciation in almost any wild organisms. In this project, we will use butterflies of the genus Leptidea as a model system to investigate the role of chromosome rearrangements in the formation of barriers to gene flow and to investigate the genetic basis of traits that may play a role in for example species recognition, mate choice and local adaptation.

Uppsala University is an international research university with 40,000 students and 6,500 employees. The Evolutionary Biology Centre (http://www.ebc.uu.se/-) is one of the world's leading research institutions in evolutionary biology. Our lab is part of the Department of Ecology and Genetics that excels in many aspects of genetics and evolution and offers an inspiring international atmosphere. As a member of the Science for Life Laboratory (http://www.scilifelab.se/) we have excellent access to advanced laboratory infrastructure, high performance computing resources and bioinformatic support. It is placed in Uppsala, a town that offers opportunities for both cultural and outdoor activities and the capital of Sweden, Stockholm, is less than an hour away.

If you are enthusiastic about evolutionary biology, have a good understanding of population genetics and evolution theory, and/or are skilled in bioinformatics you are most welcome to apply for the position. To apply for the position you must hold a master of science (or your national equivalent) in Biology or a related field.

Informal inquiries can be addressed to Niclas Backström: niclas.backstrom[at]ebc.uu.se

Formal applications should be made using our online application form: http://www.uu.se/en/jobs/-jobs-detail-page/?positionId=34085 Niclas Backström niclas.backstrom@ebc.uu.se

Jobs

CAS Beijing PopulationGenomics

Our research group is now looking for an Assistant Professor in the fields of population and evolutionary genomics.

The Institute of Zoology of Chinese Academy of Sciences (CAS) is located at Beijing and is one of the leading research institutes in CAS. Please see http:/-/ www.ioz.ac.cn for more information.

Our research interests focus on evolutionary (e.g. the climate driven adaptation) and functional genomics in wild and domestic sheep using the high throughput genomic data (high-density ovine Beadchip SNP, whole-genome re-sequencing and mRNA and microRNA data etc.)

Applications are sought from individuals with a strong background and research record in population, evolutionary and functional genomics. Knowledge of Chinese will be viewed as advantageous.

This position can be filled from July or August of 2014. The emolument and relevant benefit will be implemented according to the scales of CAS.

To apply for the post, please send a c.v. (including names of 3 referees) and a cover letter to Prof. Menghua LI (menghua.li@ioz.ac.cn), Institute of Zoology, Chinese Academy of Sciences, Beijing.

ÀîÃÏ≫£Meng-Hua LI£© <menghua.li@ioz.ac.cn>

ChongqingU EvolutionaryGenetics

Academic positions available at CQU

School of Life Sciences of Chongqing University (CQU) (http://life.cqu.edu.cn/), located in ChongqingCity of China, has 2-3 academic positions available at the level of full professor. Applications are invited from fields including but not limited to evolutionary genetics, comparative genomics, bioinformatics and population genetics. Applicants should have a Ph.D. degree and outstanding research accomplishments.

Successful candidates are expected to develop their own research programs and establish their labs. The University provides successful candidates with startup funding and very good salary and benefits. Only applications from oversea Chinese scholars are considered.

Applicants should submit their CV, biography, future plan, and names/addresses of three references, to Dr. Ze Zhang, zezhang@cqu.edu.cn, Tel: +86-23-65122685). These positions will be "OPEN UNTILL FILLED".

Thanks!

Best wishes,

Ze

Ze Zhang, Ph.D., Professor of Genetics Room 606, Life Science Building, Chongqing University Campus B School of Life Sciences, Chongqing University No. 174 Shazheng Rd., Shapingba District Chongqing 400044 China Tel/Fax: +86-23-65122685 Email: ze_zhang@126.com; zezhang@cqu.edu.cn http://life.cqu.edu.cn/labs/zezhang/ ze_zhang <ze_zhang@126.com>

Colorado MolecularEvolution

We are seeking a molecular evolutionist.

Evolutionary Genomics, Inc. (EG) seeks candidates for the position of Director/Senior Scientist. He/she will use state-of the art genomic and molecular biology technologies, including EG's proprietary gene discovery tools to identify and characterize agriculturally valuable genes in several commercial crops (soybeans, tomato, maize, cannabis, and rice). He/she will also develop and analyze 'high value' targets. Strong organizational skills and the ability to work independently in a team environment are required. Excellent communication skills, both written and verbal are essential.

An ideal candidate should have a Ph.D. in Molecular Biology, Molecular Evolution, Plant Genetics, or Agricultural Sciences. Qualified candidates will be highly motivated, with experience in plant genetics, genomics and molecular biology. He/she must have publications in peer reviewed journals. He/she should have superior skills in bio-informatics and ideally in statistical methods. In addition, technical skills in molecular biology, including significant expertise in DNA/RNA techniques, specifically, cloning and manipulation of large DNA constructs, gene stacking, sequence analysis, transgenic plant characterization (including assays for pest resistance), cell culture, and gene expression analysis, are preferred. Prior experience in an industry setting is highly desirable.

Evolutionary Genomics is based near Boulder, Colorado.

Education, Knowledge, Skills and Abilities:

* Ph.D. with at least 2+ years of molecular biology work experience * Post-doc experience required * Knowledge of wide range of plant molecular and cell biology techniques * Proven rigor in experimental design, optimization, data interpretation, and analysis * High level of organization, attention to detail, and ability to complete tasks * Demonstrated record of creative and innovative thinking * Demonstrated ability to work independently, as well as part of a team * Good interpersonal and communication skills, both written and verbal

Application Process:

Submit a cover letter and CV with the names of at least three references. Apply to wmessier@evolgen.com

Walter Messier <wmessier@evolgen.com>

DukeU ResAssist EvolutionaryAnthropology

The Nunn Lab at Duke University (http://people.nunn-lab.org) is looking for a part-time or fulltime Associate in Research. The position will provide unique opportunities to participate in research first-hand, with an emphasis on statistics and phylogenetic comparative methods in R, development of online resources, and construction of original databases on primate behavior, ecology and morphology. Training will be provided as needed. The ideal candidate would be an upcoming (or recent) graduate from an undergraduate program in evolutionary anthropology, biology, statistics, or computational biology. Applicants should have basic skills in statistics, computer programming, or phylogenetics, and an interest in developing those skills for future research endeavors. The initial duration will be one year, with possibilities for a second year of employment based on performance; start date is between May and August, 2014. The position is funded through the National Science Foundation for research on 'Using Primate Comparative Biology to Understand Human Uniqueness' (BCS-1355902). Applications should include a cover letter, name and contact information for two references, and a CV. Applications will be evaluated starting on April 1, 2014, and will continue until the position is filled. Please send application materials and questions to Prof. Charles Nunn, charles.nunn@duke.edu.

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

Charles Nunn Department of Evolutionary Anthropology & Duke Global Health Institute Biological Sciences 107 Duke University Durham NC 27708

people.nunn-lab.org http://www.anthrotreeworkshop.info Office: (919) 660-7281 Cell: (510) 206-5716

Charles Nunn <charleslnunn@gmail.com>

KarlFranzensU Austria EvolutionaryBiol

Full-time Assistant Professor opening in Evolutionary Biology at the Department of Zoology, Karl Franzens University Graz, Austria. The position is non-tenure track, provides a 4 year fixed-term contract and is research oriented, with a ca. 25% teaching obligation. The candidate is expected to conduct independent research in organismic biology with a clear evolutionary context including the use of molecular and/or genetic/genomic methodologies. Within the department the position is assigned to the Biodiversity and Evolution division (http://zoologie.uni-graz.at/de/forschen/biodiversitaet-und-evolution). The candidate must have a Doctorate or PhD, publications in international, peer-reviewed journals and command of written and spoken English; experience in genome or transcriptome analysis, teaching, and international research cooperation is desired. Graz is the second largest city in Austria, with a population of ca. 300,000, with six universities and over 40,000 students. The city center is among the best preserved in Central Europe and as such is a UNESCO cultural site. Graz is located in the southeast of the country outside of the Alps and near the borders of Slovenia, Italy and Hungary. Due to mediterranean climatic influence Graz is notably sunnier and drier than most other Austrian cities. The official job description can be found here (in German - http://jobs.uni-graz.at/de/MB/73/99; in English http://jobs.uni-graz.at/en/MB/73/99). Applications should consist of a short cover letter, CV, publication list and a photo; this can be sent as an e-mail attachment to bewerbung@uni-graz.at or post to Karl-Franzens University Graz, Personalressort, Universit?tsplatz 3, 8010 Graz. Please include the job id number in all communications (MB/73/99). The application deadline is April 19, 2014 and the position can begin as early as 01.07.2014. Specific questions for those unfamiliar with the University system, the institute or the region can be directed to (steven.weiss@uni-graz.at or kristina.sefc@uni-graz.at).

"Weiss, Steven (steven.weiss@uni-graz.at)" <steven.weiss@uni-graz.at>

LeibnizInst EvolutionaryBacteriology

The Leibniz Institute for Zoo and Wildlife Research (IZW) in Berlin is Germany's premier wildlife research institute, one of eight research institutes in the Forschungsverbund Berlin e. V., a member of the Leibniz Association and jointly funded by the German federal and state governments. The IZW focuses on the life histories and mechanisms of evolutionary adaptations of mammals, their limits and their conservation in natural and anthropogenically influenced environments. The institute operates within the fields of wildlife health and diseases, reproductive biology and medicine, and evolutionary ecology and genetics. The Department of Wildlife Diseases offers (beginning 1st May 2014) the following staff scientist position:

bacteriologist (f/m) (Reference number 14/2014) Specific tasks include

§responsibility for the bacteriology laboratory;

§to develop and expand our current research on the interactions of bacterial pathogens and their wildlife hosts using classical and advanced techniques, including microbial genomic approaches;

§to provide excellent diagnostic services to the pathology unit and field projects.

The successful candidate will have extensive experience in veterinary bacteriology, will interact with scientists from a wide variety of fields, and have a strong interest in wildlife, conservation and evolutionary biology. A completed doctoral degree is required. A German (Fachtierarzt), European or American diplomate in veterinary bacteriology or microbiology and/or previous experience with wildlife will be an advantage. Experience or a willingness to develop genomic approaches to wildlife bacteriology will also be an advantage.

We offer state-of-the-art methodology and a stimulating international research environment in an interdisciplinary, collaborative institute, a contract initially limited to three years, starting on the 1st May 2014 at the earliest, and reimbursement according to the TVöD pay scale.

As a member of the Leibniz Association, the IZW is an equal opportunity employer, determined to increase the proportion of women in successful scientific careers, and particularly encourages women to apply. Preference will be given to disabled applicants with the same qualifications. Enquiries or questions should be directed to Prof. Alex Greenwood, phone: +49 (0)30 5168-255, email: greenwood@izw-berlin.de.

Please email complete application documents as a single pdf-file including the position reference number 14/2014, a letter of motivation, CV, copies of relevant degrees, and names and contact details of two referees as soon as possible but no later than April 14th, 2014 to

Leibniz Institute for Zoo & Wildlife Research, in the Forschungsverbund Berlin e.V. Personalabteilung, Frau Stephanie Vollberg, (personal@izw-berlin.de), PO Box 70 04 30, 10324 Berlin, Germany, www.izw-berlin.de Freundliche Grüße Stephanie Vollberg

Stephanie Vollberg

Personalsachbearbeiterin Leibniz-Institut für Zoo- und Wildtierforschung (IZW) Alfred-Kowalke-Str. 17 10315 Berlin (Friedrichsfelde)

Tel. 030- 5168 107 Fax. 030-5126 104 vollberg@izw-berlin.de www.izw-berlin.de P Please consider the environment before printing this email!

"Vollberg, Stephanie" <vollberg@izw-berlin.de>

MPIEVA Leipzig StudentAssist AfricanPhylo

African Phylogeography - Student assistants at MPI EVA, Leipzig

We are looking for highly motivated students who are interested in improving their hands-on experience in nucleotide databases, molecular phylogenetics and phylogeography.

The selected students will participate in the initial stages of an ambitious comparative phylogeography research project involving the Max Planck Institute for Evolutionary Anthropology as well as national and international research institutions. Our research aims to test paleoenvironmental hypotheses for sub-Saharan Africa by synthesizing existing sequence data for a large number of animal (mostly mammals) and plant species.

Your primary task will be to compile sequence data from Genebank and published sources for developing a database of georeferenced DNA sequences for a wide range of African species. Dr. Paolo Gratton (senior PostDoc) will advise you and supervise your work.

Familiarity with spreadsheet software applications (e.g. MS Excel) will be highly advantageous. Previous experience with DNA databases and at least one programming language (e.g. R, Perl, Python) will be a plus. The start of work will be in May 2014, for a duration initially limited to 6 months.

The position is open to students currently enrolled at a German University and to students who already obtained a Master level degree in any country.

The salary will depend on qualification, up to an equivalent of a PhD stipend.

We will start reviewing applications about March 25, but we will accept new candidates until the position is filled.

Please send your application, including a short motivation letter and CV to Dr. Paolo Gratton (paolo.gratton@gmail.com). Please indicate 'African Phylogeography' in the subject line.

Paolo Gratton <paolo.gratton@gmail.com>

MPI Tuebingen ResAssistant GeneticsMolecularBiology

A scientific research assistant position in genetics and molecular biology is available in the Jones Lab at the Max Planck Institute in Tuebingen, Germany as part of a prestigious 2M EURO European Research Council funded grant investigating the evolution of recombination in adaptation.

The goal of this particular project is to use cutting-edge techniques to characterize, quantify, map and manipulate meiotic recombination hotspots at unprecedented resolution across the genome, among individuals, and between species. This ground-breaking research will elucidate how a fundamental biological process shapes the genomic basis of adaptive divergence in natural populations. It forms part of a broader research focus in the lab that centers around the molecular mechanisms underlying adaptation and speciation.

Your role: You will be a central team member working closely with two postdocs and one PhD student on this ERC funded research project. You will be responsible for a variety of molecular biology assays including preparation of complex genomic DNA libraries, cloning, transgenic microinjection, yeast-one hybrid and fluorescent in situ hybridisation assays. In addition to your own research role, you will share lab management duties that include ordering and equipment maintenance with other existing lab members.

Requirements: You should hold a Masters, or equivalent degree in the areas of genetics, molecular biology. We are looking for someone with a strong track-record of research experience and training particularly in genetics and molecular biology. The successful candidate will demonstrate experience in techniques such as cloning, DNA library preparation, fluorescent in situ hybridisation, and yeast one hybrid assays. Passion for research, team spirit and enthusiasm are essential. English is required.

Our Team: You will work in a multidisciplinary team that uses population genomics, genetics, molecular, developmental, and evolutionary biology to study the molecular mechanisms underlying adaptation and speciation in the threespine stickleback fish. Our research group is funded by the European Research Council (ERC) and the Max Planck Society and is located on the Max Planck campus in Tuebingen, Germany. Our campus hosts world-class research groups, including 7 other ERC-funded teams, and operates state-of-the-art sequencing and other core facilities. English is the working language. All seminars and communications are in English.

Our Offer: The position is available for an initial 2 years with the possibility of extension to 5 years based on performance. Salary and benefits are according to the German public service pay scale (TVöD Bund) and are commensurate with training and experience.

The Max Planck Society seeks to increase the number of women in areas, where they are underrepresented, and therefore explicitly encourages women to apply. Disabled applicants with equal qualifications will be given preferential treatment.

For more information please see: fml.tuebingen.mpg.de/jones-group/open-positions

To Apply: Consideration of applications will begin on April 15th 2014, and will remain open until filled. Please send your application with 1. a statement of research interests and why you have applied for this position, 2. your CV, and 3. three reference letters to Dr Felicity Jones at fcjones@tuebingen.mpg.de or the postal address below. Incomplete applications will not be considered.

Dr. Felicity Jones Friedrich Miescher Laboratory of the Max Planck Society Spemannstrasse 39 72076 Tuebingen Germany

jones.floss@gmail.com

MaxPlanck AvianFieldTrainee

FIELD TRAINEE

needed in fulltime for monitoring and catching breeding passerines at the Max Planck Institute for Ornithology. Website: http://www.orn.mpg.de/159079/-Research_Group_Dingemanse Location: Seewiesen, Bayern, Germany.

Job description: The field Trainee will help collect breeding and behavioural data on Great Tits (Parus major) from approximately mid-March 2014 to end of July 2014. The research focuses primarily on identifying how natural and sexual selection act on animal personalities and behavioural plasticity. The trainee will work closely with a large, international team consisting of several post-docs, PhD and Master students, as well as other trainees. Field work is physically demanding, and involves walking over hilly terrain for long days outdoors in all weather conditions. The breeding season is intense and with typically only 1 day off per week. Duties include behavioural observations, nest monitoring, bird handling, data entry and data management.

Qualifications/Experience: Candidates should study Biology or a related field. We are especially interested in candidates with experience in independent bird handling (preferably with small passerines), including ringing and measuring. Ideal candidates are highly motivated, well organized, while at the same time, able to function well in a big group. Applicants must have a valid drivers license and be experienced in operating vehicles with manual transmission. Non-EU candidates are not eligible for this position (Swiss and UK citizens are eligible). A small financial compensation and housing in shared accommodation will be provided. The accepted assistant should be vaccinated against Tick Borne Encephalitis (TBE or FSME) before arriving in Seewiesen. Applicants should also be aware that Lyme disease (carried by ticks) is prevalent in the area and should inform themselves about this disease beforehand. In an effort to employ more people with disabilities, the Max-Planck-Society specifically encourages people with disabilities to apply for the position.

Applications: Due to late announcement, review of the applications will begin immediately and applications received until the end of the week will receive full consideration. To apply, please send (1) a statement of relevant experience, (2) a short resume or CV, and (3) contact information for two references to Alexia Mouchet (eMail: amouchet@orn.mpg.de).

alexiamouchet@aol.com

NHM London AmphibianCurator

Curator of Amphibia (Science Family level 2)

Salary: Within the range £27,888 - £29,300 per annum plus benefits

Contract: Permanent

Closing date: May 4th 2014

The Natural History Museum (NHM) is one of the worlds leading museums, internationally recognised as a leader in the scientific study of the natural world through its collections, excellence in scientific research and as a leader in the presentation of natural history through exhibitions, public programmes, publications and outreach. NHM collections are both a resource for investigation of the natural world and a point of reference and authority for wider investigations by scientists around the world.

The Department of Life Sciences is seeking to recruit a Curator of the Museums collections of Recent Amphibia. You will undertake collections activities within agreed guidelines provided by Life Science managers and Heads, and set by NHM science strategy. Activities will include: databasing; curation of historical and newly acquired materials; preparation of loans; supporting the museums efforts in digitisation, scholarly taxonomic research and income generation; answering taxon specific enquiries (both commercial and public); public engagement activities (education and exhibitions), supervision of visitors, and promoting development and use of the collections.

The successful candidate will have a high standard of knowledge and experience of amphibian collections and the needs arising from collections-based research. Demonstrable understanding of collection management, specimen conservation, documentation and databasing, familiarity with the rules of zoological nomenclature and at least a first degree in a biological science (or equivalent experience) are also essential.

Candidates are requested to attach a CV including to a covering letter detailing their suitability for the post.

For a full job description and to apply online please visit the Natural History Museum website at www.nhm.ac.uk/jobs We would like to highlight that, as well as the collection management responsibilities this post also provides scope for independent scholarly research in Amphibian Systematics.

For any informal enquiries regarding Herpetological Research at the Natural History Museum please contact either David Gower (d.gower@nhm.ac.uk) or Mark Wilkinson (m.wilkinson@nhm.ac.uk).

Mark Wilkinson <apodauk@gmail.com>

NHM London LifeScienceResearchers

RESEARCHERS IN LIFE SCIENCES, NATURAL HISTORY MUSEUM, LONDON

This is an opportunity to take up a research-intensive role in a world-renowned institution with a unique scientific mission and public profile.

The NHM is internationally recognized for its dual role as a centre of excellence in taxonomy, systematics, biodiversity and mineralogy and as a leading exponent in the presentation of the natural world to the general public through exhibitions. Its objectives are firstly, to discover and make available to the scientific community the information contained within its collections of natural specimens and secondly, to entertain, interest and educate people of all ages in natural history.

The successful applicants will join a large science group that comprises a group of approximately 300 scientists, that houses some of the largest and most significant scientific collections in the world, that is home to an internationally important natural history library, that includes a suite of advanced analytical and imaging facilities, and that has the opportunity to communicate science to a huge national and international audience.

Applications are open to researchers across the breadth of the NHM's activities in Life Sciences. We are especially interested in applicants that combine disciplinary expertise with a demonstrated ability, or potential, to use that expertise to address interdisciplinary questions of broad significance, including key transitions in the origin and evolution of life; discovery of biodiversity; global environment change; food security and agro-ecosystems; and neglected and emerging diseases.

Areas of particular interest include (but are not restricted to):

- Environmental/Biodiversity Genomics - [informal enquiries to Dr David Bass (d.bass@nhm.ac.uk)] - Freshwater biodiversity - [informal enquiries to Dr Steve Brooks (s.brooks@nhm.ac.uk)] - Parasites / Vectors - [informal enquiries to Dr Martin Hall (m.hall@nhm.ac.uk)] - Flowering plants - [informal enquiries to Dr Sandy Knapp (s.knapp@nhm.ac.uk)] - Insect diversity - [informal enquiries to Dr Paul Williams (p.williams@nhm.ac.uk)] - Diptera larvae - [informal enquiries to Dr Erica McAlister (e.mcalister@nhm.ac.uk)]

Salary: £33,668 - £59,510 per annum plus benefits

Closing date: 4 May, 2014

For a full role specification and to apply online, please visit the Natural History Museum website at www.nhm.ac.uk/jobs (REF: DS/RLS/NHM)

Prof Ian P.F. Owens Director of Science The Natural History Museum Cromwell Road London SW7 5BD

Tel: 0207 942 5299/5374

http://www.nhm.ac.uk i.owens@nhm.ac.uk

NewZealand Bioinformatics

Senior Bioinformatician

AgResearch Grasslands

AgResearch is a Crown Research Institute with the purpose of enhancing the value, productivity and profitability of New Zealand's agricultural sector. The Bioinformatics team supports scientific research in a range of areas to the benefit of the pastoral agricultural sector.

We are seeking a highly motivated individual with excellent training and expertise in Bioinformatics to join our team. The successful candidate will be responsible for providing Bioinformatics consultancy to a range of science projects. Main duties will involve analysing high throughput/high-dimensional 'omics data from mostly non-model organisms, this includes the design, development, implementation and testing of bioinformatics pipelines for Next-Gen Sequencing (NGS) data, assembly and expression analysis of NGS data and contribution towards interpreting the results. Experience in working with Genotyping by Sequencing data would be advantageous. The ideal candidate will also have some experience or an interest in integrating multifaceted 'omics data to understand underlying systems and biological networks. This is a senior and permanent position.

The successful applicant will have a PhD or high level postgraduate qualification in Bioinformatics (or related field) with at least five years of related work experience. A thorough knowledge of Unix, scripting language (Perl/Python or similar) and an understanding of biological databases along with various Bioinformatics tools is required. This is a highly collaborative role, where the incumbent will be working alongside scientists on a regular basis thus requiring a good knowledge of Genetics and Molecular Biology. Strong communication skills, with the ability to effectively articulate complex, technical information to the clients is highly desirable. Other requirements are good organisational abilities along with excellent interpersonal and relationship building skills.

The position will be based at our Grasslands campus in Palmerston North and will be part of the wider Bioinformatics and Statistics team. Palmerston North, a university city, is 30 km from the coast, 2 hours from ski fields, and 2 hours from Wellington. The AgResearch Grasslands campus is situated in pleasant rural surroundings with easy access to the central city. The surrounding area offers many outdoor recreational opportunities.

The position is available immediately and will be open until filled.

For informal inquiries please contact Dr. Nauman Maqbool (nauman.maqbool@agresearch.co.nz). Applications including a CV highlighting relevant research experience, a cover letter and contact details of three referees should be submitted online at: https://careers.sciencenewzealand.org . Applications not submitted online will not be accepted.

Regards, Aurelie Laugraud Bioinformatician T +64 3 321 8626 E aurelie.laugraud@agresearch.co.nz [http://www.agresearch.co.nz/images/agresearch-logo-email.jpg] Lincoln Research Centre Cnr Springs Road and Gerald Street, Private Bag 4749, Christchurch 8140, New Zealand T +64 3 321 8800 F +64 3 321 8811 www.agresearch.co.nz "Laugraud, Aurelie" <Aurelie.LAUGRAUD@agresearch.co.nz>

NorthernPortugal FieldAssist MammalEvolution

Paid field research assistent position available in a new starting project on freshwater mammals' ecology (mostly Iberian desman - and otter - occupancy and river connectivity in the Sabor river, which was the last undammed river in Europe) in Northern Portugal.

Work will start in mid-end of April (2014), there will be a break during August, and will begin again in September and October (and possibly November), with the possibility that it will continue for the next year.

Autonomy, fluent Portuguese speaking, car driving license (and possibly experience in 4x4 car driving) and adaptability to difficult field working conditions are required. Statistics and GIS knowledge and programming skills would be an advantage. Also, we could give priority to people living in or nearby the study area, but people from anywhere are encouraged to apply. Salary and accomodation will be provided, but the selected candidate will have to pay for her/his living expenses.

The candidate will mainly assist with data collection and compilation, and report writing, but opportunities to participate as co-author in scientific papers could arise.

Interested candidates should send me a private email (lorenzo.quaglietta@gmail.com) with their CV, picture, short (no more than 300 words) motivation letter, 1-3 references.

Please note: ONLY selected candidates will be contacted and a Skype meeting will be scheduled for an interview.

Sincerely,

Lorenzo Quaglietta

Post-Doctoral Fellow EDP Chair in Biodiversity Research Center in Biodiversity and Genetic Resources (CIBIO/InBio) - University of Porto Jardim Botânico Tropical/IICT Tv. Conde da Ribeira, 9 1300-142 Lisboa Portugal Tel. +351213616340 (ext. 307)

Lorenzo Quaglietta <lontrenzo@gmail.com>

SLU Uppsala InsectEvolution

Dear Friends and Colleagues,

May I draw your attention to the following position as Professor in Insect Ecology at the Department of Ecology, SLU, Uppsala.

http://www.slu.se/sv/om-slu/fristaende-sidor/-aktuellt/lediga-tjanster/las-mer/?eng=1 The professorship should focus on the ecology and dynamics of insect populations. Of particular interest is basic understanding of the population processes affecting distribution and abundance and how these processes interact with changing environmental conditions. Understanding of how population growth can be controlled is also central.

The professor will develop and lead an eminent research group with the ability to attract external financing. This includes taking advantage of opportunities for collaboration within and outside the department. The professor is expected to carry out research and other activities with a clear connection to the applied part of the insect research in the Department of Ecology, e.g. conservation biology, agricultural and forest entomology. The professor in Insect Ecology is also expected to contribute to the strengthening of cooperation between entomologists and ecologists in and outside the department.

jogstephan@googlemail.com

Turkey AnimalGenetics

Assistant Professor of Molecular Animal Genetics with teaching, research and service responsibilities.

Address: Department of Molecular Biology and Genetics, Faculty of Arts and Sciences, Canakkale 18 Mart University, Canakkale/Turkey The appointment is a renewable 3 year assistant professor position.

The researcher will have access to our research lab: http://molbio.comu.edu.tr/ksayfalar/sayfa/3/-11/research-laboratory Access to an animal facility including mice, rats and rabbits, and is free to collaborate with the biotechnology department, which has Mongolian gerbils and Syrian hamsters. We have ties to a private farm with Jersey cattle and have a university farm with sheep and goats. Other collaboration opportunities include in campus units such as Department of Bioengineering, the School of Medicine, Faculty of Agriculture, and our Science Park: Canakkale Research and Technology Inc.

All teaching is in English and we have a dedicated lab used for teaching: http://molbio.comu.edu.tr/-ksayfalar/sayfa/3/12/student-laboratory Our curriculum can be found under the link: http:/-/molbio.comu.edu.tr/ksayfalar/sayfa/4/13/-undergraduate Responsibilities: The Department is seeking applicants who utilize recent molecular methods to study animal genetics. The appointee is expected to establish a competitively funded research program in animal genetics to come up with significant findings in the field. The appointee will be responsible for teaching undergraduate and graduate courses assigned to meet the teaching needs of departmental curricula. Mentoring of graduate students, undergraduate student advising, curricular development, and performance of departmental and university service is expected. The appointee is expected to conduct fundamental research, train students, and yield both basic biological mechanisms and translatable outcomes and to participate in research and outreach programs.

Qualifications: Ph.D. or equivalent degree in Genetics, Molecular Biology, Molecular Genetics, Animal Science or a closely-related field. Post-doctoral experience is preferred. Research interests focused on animal molecular genetics with a working knowledge of recent molecular methods is preferred. The candidate should have the ability to develop and instruct undergraduate and graduate courses and the ability to develop and conduct extramurally funded research in molecular genetics/genomics. We especially value the ability to work well with others.

Salary: Higher than an average Assistant Professor salary at Canakkale 18 Mart University. The salary can be supplemented by writing projects that involve additional income, by establishing a private R&D company in our Science Park, or by working for such a company.

Application: Pre-application materials should be sent to akin@comu.edu.tr. The position will remain open until filled. To ensure consideration, applications should be received by March 18, 2014. Materials requested to include: 1) curriculum vitae including publications list, 2) up to three key publications in full text, 3) transcripts if the applicant is within five years of his/her Ph.D. degree, 4)statement of research accomplishments, 5) the names, addresses, including e-mail, of three professional references. Additional inquiries should be directed to Professor Dr. A. Pala, Department Head of Mol. Biol. & Genetics. +90 (542)2996560, akin@comu.edu.tr

Prof. Dr. Akin Pala Dept. Head of Mol. Biol. & Genetics

Daniel Montesinos <danimontesinos@gmail.com>

UCLondon Independent Fellowships

University College London - Excellence Fellowship programme

Dear all,

UCL's School of Life and Medical Sciences is calling for applications to its Excellence Fellowship programme. These fellowships offer three years of salary and a generous contribution to research costs to support excellent individuals while they pursue external fellowship funding.

The Department of Genetics, Evolution and Environment is seeking to actively promote outstanding candidates for the Excellence Fellowship scheme. The research of applicants should complement the research themes covered by the Department. We would be particularly interested in candidates working in the fields of *field-based and experimental ecology and population biology, *evolutionary disease ecology, *origins and evolution of eukaryotic complexity, *genome regulation and function.

Expressions of interest should be directed to Dr Max Reuter (m.reuter@ucl.ac.uk) before 20 April (the scheme deadline is 6 May). Please include a cover letter, CV, the names of two referees, and an outline of your research proposal (2 pages maximum in the full proposal). The Department will select a shortlist of candidates to provide support in developing your project, writing the application and preparing for interview.

The call for fellowship applications can be found at http://www.ucl.ac.uk/slms/vacancies/UCL-excellence-fellowships For more information about the Department of Genetics, Evolution and Environment http://www.ucl.ac.uk/gee Best regards,

Max

Max Reuter

Research Department of Genetics, Evolution and Environment Faculty of Life Sciences University College London Darwin Building Gower Street London WC1E 6BT, UK

Phone: +44-20-76792201 (internal 32201)

Lab: http://www.homepages.ucl.ac.uk/ ~ ucbtmre/Labsite/ Department: http://www.ucl.ac.uk/gee Centre for Ecology and Evolution: http://www.ceevol.org.uk m.reuter@ucl.ac.uk

UCalifornia LosAngeles DirectorConservation

University of California, Los Angeles Director, Institute of the Environment & Sustainability

The University of California, Los Angeles (UCLA) seeks outstanding candidates for the position of Director of the Institute of the Environment & Sustainability (IoES). The Director will have the academic rank of Professor and will hold a named chair.

The IoES's primary mission is to identify study and provide solutions for regional and global environmental problems, and to educate the next generation of scholars and leaders. The Institute achieves this mission though its core faculty, affiliated faculty from across UCLA, undergraduate and graduate degree programs, and interdisciplinary centers and off-campus partnerships. Working both locally and globally, the IoES employs innovative cross-disciplinary approaches to address critical environmental challenges including climate change, water and energy sustainability, urban and business sustainability, and ecosystem and biodiversity conservation. Through its eight centers, the institute enables a wide range of research, education, and outreach activities that span the breadth of academic disciplines at UCLA, with the important goal of encouraging interdisciplinary research and policy. For more information about the IoES, please visit http://www.environment.ucla.edu/ The successful candidate should be a distinguished scholar holding a Ph.D. or equivalent degree in any area of environmental research, and should have the ability and desire to cross disciplinary boundaries, demonstrated administrative experience, and a passion for environmental stewardship. The Director will provide vision, leadership and support for IoES research, educational, and outreach programs, and take a strong role in promoting collaborative efforts among faculty and between UCLA and the broader community. The successful candidate will also take a primary role in fundraising and development, building on the strong base of philanthropic and extramural research support that enables many of the Institutes most exciting activities. The incoming Director will have the opportunity to guide several new faculty hires, and is expected to play a leadership role in sustainability and environmental initiatives at UCLA. Therefore, the ability to articulate and develop a strategic plan for the institute's future growth and development is a requirement.

We invite interested applicants to submit a cover letter outlining your interests in and qualifications for the position, including a succinct description of your vision for the future of environment and sustainability in a university setting, as well as a curriculum vita, to UCLA Academic Recruit at: https://recruit.apo.ucla.edu. Please use job number: JPF00184.

For additional information about the IoES or about submitting an application, contact Ms. Karen Lefkowitz (karen@ioes.ucla.edu, 310-794-4908) or see www.environment.ucla.edu. Review of applications will begin on May 15, 2014 and will continue until the position is filled. Please address any questions to Brad Shaffer, Search Committee Chair, at brad.shaffer@ucla.edu. The University of California is an Equal Opportunity/Affirmative Action Employer. All qualified applicants will receive consideration for employment without regard to race, color, religion, sex, national origin, disability, or protected veteran status.

Karen A. Lefkowitz Communications Officer UCLA Institute of the Environment and Sustainability (310) 794-4908 http://www.environment.ucla.edu/ Check out the UCLA Institute of the Environment and Sustainability on Facebook < http://www.facebook.com/-uclaioes > and Twitter < http://twitter.com/-UCLAIoES >

“Lefkowitz, Karen A.” <karen@ioes.ucla.edu>

UCambridge EvolutionaryBiol

Prince Philip Professorship of Ecology and Evolutionary Biology

The Board of Electors to the Prince Philip Professorship of Ecology and Evolutionary Biology invite applications for this Professorship from persons whose work falls within the general field of the Professorship to take up appointment on 1 October 2014 or as soon as possible thereafter.

Candidates will have an outstanding research record of international stature in the broad field of animal ecology and evolution, and the vision, leadership, experience and enthusiasm to build on current strengths in maintaining and developing a leading research presence. They will hold a PhD or equivalent postgraduate qualification.

Standard professorial duties include teaching and research, examining, supervision and administration. The Professor will be based in Cambridge. A competitive salary will be offered.

Further information is available at: www.admin.cam.ac.uk/offices/academic/secretary/-professorships/ or contact the Academic Secretary, University Offices, The Old Schools, Cambridge, CB2 1TT, (email: ibise@admin.cam.ac.uk).

Applications, consisting of a letter of application, a statement of current and future research plans, a curriculum vitae and a publications list, along with details of three referees should be made online no later than Wednesday 30 April 2014. The Department would particularly welcome applications from women as it has an historic imbalance in the number of women holding academic staff positions.

Informal enquiries may be made to Professor Michael Akam, Head of the Department of Zoology, Cambridge, telephone +44 (0)1223) 336601 or email HOD@zoo.cam.ac.uk.

Please quote reference PF03005 on your application and in any correspondence about this vacancy.

The University values diversity and is committed to equality of opportunity.

The University has a responsibility to ensure that all employees are eligible to live and work in the UK.

Department/Location

Department of Zoology

Reference

PF03005

Closing date

30 April 2014

To apply please click on the link below. This will route you to the University's Web Recruitment System, where you will need to register an account (if you have not already) and log in before completing the online application form.

Please quote reference PF03005 on your application and in any correspondence about this vacancy.

http://www.jobs.cam.ac.uk/job/3517/

Mrs Anastasia Nezhentseva

HR & Grants Administrator Department of Zoology University of Cambridge Downing Street Cambridge CB2 3EJ

Tel.: +44 (0)1223 (3)30117 +44 (0)1223 (7)69413

Email: an286@cam.ac.uk

Anastasia Nezhentseva <an286@cam.ac.uk>

UColorado MNH AssistDirector

Greetings - please feel free to share this position announcement with potentially interested individuals.

Kind regards, Erin

Position Announcement: Assistant Director of the University of Colorado Museum of Natural History

Application due date: April 15

Come help guide the future of a teaching museum that hosts a free public museum, a museum and field studies graduate program, and world class collections in Anthropology and the Natural Sciences. The University of Colorado Museum of Natural History is a dynamic and innovative institution with a vibrant faculty research community that seeks an assistant director who will help take the public museum to the next level. The Assistant Director will develop and manage the vision and projects of the Public Section of the museum, which is responsible for exhibitions, public programs, and mentoring students in these areas. The Assistant Director is expected to teach one class per year, to engage the campus and broader community, and will report directly to the museum director.

For more information and how to apply: http://www.jobsatcu.com/postings/79374 erin.tripp@colorado.edu

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UEssex ChairHumanGenomics

PROFESSOR IN HUMAN GENETICS, School of Biological Sciences, University of Essex

The School of Biological Sciences is seeking to appoint a Professor in Human Genetics to establish and lead a Genomics Research Group. You should have a proven track record in using modern genomic approaches, specializing in genome-wide analysis, bioinformatics, epigenetics or cutting edge molecular genetic approaches to address questions relating to the study of disease mechanisms or susceptibility, complex traits or social behaviour. We encourage applications from those whose interests align with key areas of research within the School including ageing, health, immunity or cancer. In addition, we would welcome applications from candidates with an interest in exploiting the ESRC-supported Understanding Society project (in the Institute for Social and Economic Research at Essex) a longitudinal survey interviewing individuals in 40,000 households across the UK and for which there are accompanying biological samples providing a unique data source for human genomic research.

The School of Biological Sciences at Essex (www.essex.ac.uk/bs) is one of the largest in the University. Research activity in the School is supported by external funding from a variety of sources including the ESRC, BBSRC, NERC, EPSRC, Wellcome Trust, European Commission, Unilever and the National Institute of Health, USA. We provide a multi-disciplinary research environment with access to a range of core facilities from fully equipped cell and molecular biology laboratories to state-of-the-art bio-imaging, proteomics and biophysical facilities. The University has invested significantly in this research initiative including funding for technical support, laboratory refurbishment and equipment to underpin the establishment of a research group in the area of human genetics and genomics. Candidates for this post should have an outstanding international reputation including both an excellent publication record and a track record in obtaining significant external grant support.

This Professorial appointment is part of a planned expansion of Biological Sciences at Essex and represents a unique opportunity to shape the development of a new area of research.

We are offering an attractive remuneration package commensurate with experience of the individual, together with a generous removal and relocation grant.

We particularly welcome female applicants and those from an ethnic minority group, as they are underrepresented at this level.

Salary will be commensurate with the skills and experience of the successful candidate. Please use the link below for a full job description, person specification and further information relating to this post. Please read this information carefully before applying for this post as it contains details of documents that must be attached to your application. Applications should be made on-line, but if you would like advice or help in making an application, or need information in a different format, please telephone (01206 874588/873521).

Further information about this post and application forms at: http://jobs.essex.ac.uk/fe/tpl_essex01.asp?s=4A515F4E5A565B1A&jobid=76078,4058543399 amarco.bio@gmail.com

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UKansas Metagenomics

The University of Kansas is hiring a POSTDOCTORAL RESEARCHER and a RESEARCH TECHNICIAN to support the development of the Center for Metagenomic Microbial Community Analysis (www.kansasmetagenome.org).

This new Center is funded by a KU Strategic Initiative grant, and involves a multidisciplinary research team from several units on campus with diverse interests in microbial communities, from microbial ecology and ecosystem management, to wastewater treatment and water quality, to ecophysiology and soil science, to geomicrobiology. The Center seeks to use next-generation sequencing to investigate an array of projects in these areas.

In the first instance we are hiring a postdoc and a research technician. Full details of the positions are provided below. Enquires from potential applications are welcome, and can be directed to any of the team leaders:

Belinda Sturm (PI) - Civil, Environmental & Architectural Engineering (bmcswain@ku.edu)

Sharon Billings - Ecology & Evolutionary Biology / Kansas Biological Survey (sharonb@ku.edu)

Stuart Macdonald - Molecular Biosciences / Director of K-INBRE Bioinformatics Core at KU (sjmac@ku.edu)

Jennifer Roberts - Geology (jaroberts@ku.edu)

Benjamin Sikes - Ecology & Evolutionary Biology / Kansas Biological Survey (ben.sikes@ku.edu)

OFFICIAL POSITION ANNOUNCEMENT The University of Kansas is hiring a Postdoctoral Researcher and a Research Assistant to support the development of a Center for Metagenomic Microbial Community Analysis. A key goal of the proposed Center is to bring together researchers across the university to advance metagenomics methods for diverse research programs at KU. The University of Kansas has significant expertise in microbial ecology applications in Ecology, Biology, Geology, and Environmental Engineering. Faculty comprising this multidisciplinary realm link microbial ecology to the removal of pollutants and excess nutrients from stormwater, wastewater systems, and soils (Belinda Sturm, Environmental Engineering; Sharon Billings, Ecology and Evolutionary Biology/Kansas Biological Survey), the production of greenhouse gases in carbon and nitrogen biogeochemical cycles (Sharon Billings, EEB/ KBS; Jennifer Roberts, Geology), the microbial generation and destruction of porosity in petroleum carbonate reservoirs and their modern analogues (Jennifer Roberts, Geology), and the restoration of plant-microbe-soil ecosystems (Ben Sikes, EEB/KBS). Successful applicants will work in this interdisciplinary team to analyze diverse communities using the Illumina HiSeq platform. Visit our webpage at www.kansasmetagenome.org . We are hiring a motivated Postdoctoral Researcher with prior experience in any field of environmental community analysis. We are specifically interested in candidates with a strong background in the computational analysis of next-generation sequencing-based metagenomics studies. For specific requirements and application materials see http://employment.ku.edu/jobs/4904 . We are also hiring a Research Assistant with strong molecular skills to generate next-generation sequencing libraries from environmental samples. We are particularly interested in an individual with prior experience with metagenomic applications or with any form of next-generation sequencing. For specific requirements and application materials see http://employment.ku.edu/jobs/4903 . Applicants should submit the application at the link provided above, along with a curriculum vitae, the names and contact information for 3 references, and a brief statement of research interests and skills.

A start date of May 2014 is preferred. Any inquiries can be directed to Dr. Belinda Sturm.

Belinda Sturm, PhD Associate Professor Dept of Civil, Environmental & Architectural Engineering University of Kansas bmcswain@ku.edu http://people.ku.edu/~bmcswain Dr. Stuart J. Macdonald Department of Molecular Biosciences 4043 Haworth Hall 1200 Sunnyside Avenue University of Kansas Lawrence KS 66045 office: 785-864-5362 lab: 785-864-5777 fax: 785-864-5321 email: sjmac@ku.edu

sjmac@ku.edu

UKansas ResTech DrosophilaVariation

A Research Technician position is available in Stuart Macdonald's lab in the Department of Molecular Biosciences at the University of Kansas. The Macdonald lab explores the genetic basis of complex phenotypic variation within and between species using Drosophila as a model system. We seek an enthusiastic individual to supervise and carry out large-scale genetics/genomics projects, and to oversee various lab activities. The responsibilities of the technician will include helping to maintain and use a large panel of Drosophila strains (see King et al. 2012), and running a range of quantitative genetic experiments to uncover the genetic basis of stress- and drug-resistance, and the genetics of male sexual trait variation (see McNeil et al. 2011). The successful candidate should be motivated, organized, and careful, and should have excellent oral and written communication skills. Salary will be commensurate with experience and will include benefits.

Required qualifications are a Bachelors degree in biology or a related field, and lab experience with a (broadly-defined) "model" genetic system such as Drosophila, C. elegans, mouse, Arabidopsis, and so on. Preference will be given to candidates with significant experience in the laboratory (including troubleshooting and optimizing protocols, and managing projects), and individuals holding a Masters degree.

The position is open and review of applications will begin on March 24th and continue until the position is filled. Informal inquires are welcome and can be directed to Stuart Macdonald (sjmac@ku.edu). To apply, complete an online application at https://employment.ku.edu/jobs/4958. Attach a cover letter (describing your interest in the position and any relevant expertise), a full CV, and complete contact information for 3 referees. EO/AA Employer.

McNeil et al. 2011 http://www.g3journal.org/content/1/5/343.full King et al. 2012 http://genome.cshlp.org/content/early/2012/04/10/gr.134031.111.abstract Dr. Stuart J. Macdonald Department of Molecular Biosciences 4043 Haworth Hall 1200 Sunnyside Avenue University of Kansas Lawrence KS 66045

office: 785-864-5362 lab: 785-864-5777 fax: 785-864-5321

sjmac@ku.edu

ULeicester GenomeDynamics

Dear evoldir,

The University of Leicester wishes to take the opportunity to recognise Emeritus Prof Alec Jeffreys' tremendous contribution to genetics by establishing a prestigious academic post that maintains critical mass in the area of genome dynamics, which he has influenced so much. We therefore wish to appoint a senior research scientist with an outstanding international research profile to join the Department of Genetics as the Jeffreys Professor of Genetics.

Jeffreys Professor of Genetics You will have a clear research vision to undertake high-impact research in any aspect of genetics, genomics and diversity. Research interests can be focused on any eukaryotic organism, although a focus on human genetics may be favoured. You will consolidate Leicester's reputation for undertaking world-class research in this area, and would be expected to secure external research funding and deliver high-impact publications. You will act as a focus to attract further talented researchers, and be able to take a strategic view of the field and its position within the UK and beyond. This appointment reinforces the University's strong commitment to genetics research over many years and is pivotal to the Genome Science Research Theme of the College, linking strongly with other themes, notably Cancer and Population Science. You may wish to establish collaborations, not only within the Genome Science Theme, but also exploit opportunities to collaborate across the University with other departments.

Closing date 24 April 2014.

For further information see: http://www.jobs.ac.uk/job/AIK573/jeffreys-professor-of-genetics/ Ed Hollox, PhD Lecturer in Genetics, University of Leicester

Research group pages http://tinyurl.com/hollox Departmental staff page http://www2.le.ac.uk/departments/genetics/people/hollox Room G6, Department of Genetics, **** note new office ***

Adrian Building University Road, Leicester LE1 7RH UK

Tel: +44 (0)116 252 3407 (office G6) +44 (0)116 223 1366 (lab G3)

"Hollox, Ed (Dr.)" <ejh33@leicester.ac.uk>

UManchester ChairEvolutionaryBiology

Professorial Chair in Evolutionary Biology

We are seeking to appoint to a new chair in Evolutionary Biology, based in the Faculty of Life Sciences (FLS) at The University of Manchester. FLS has a large number of researchers studying the full range of evolutionary biology, from fossils to genomics, from population genetics to evolutionary ecology, who focus on all levels of biology - viruses, genes, organisms and societies. Candidates must be internationally leading scientists with an appropriate level of academic achievement in relevant fields of evolutionary biology.

This is a high-profile role for which a vigorous research programme is expected. We are seeking individuals with a strong commitment to developing both individual and team-based research programmes, and who could inspire the next generation of researchers through their teaching.

To succeed, you will need to have an outstanding track record of published research and a demonstrated ability to lead. A strong track record in the supervision of doctoral/postgraduate students and an ability to secure major competitive grant funding is expected.

informal enquiry: Daniela Delneri: d.delneri@manchester.ac.uk

Catherine.Walton@manchester.ac.uk

UMemphis ResTech Genetics

Plant Ecological Genetics Research Technician Start date (estimate): March 15

Job Description

The Mandel Lab at the University of Memphis will be hiring a full time research laboratory technician with a tentative start date of March 15, 2014. Research in the lab centers around the desire to understand the processes and mechanisms that lead to genetic, phenotypic, and ecological diversity. The technician will carry out greenhouse, field, and molecular lab studies. Duties will include: DNA/RNA extraction, PCR, genotyping; plant care in the greenhouse; data collection on plants in the greenhouse; supervising undergraduate researchers; general lab maintenance.

The candidate should have an associates degree in biology, genetics, horticulture or plant sciences, or similar and previous experience performing research, the ability to work well in a group environment, and the willingness to supervise undergraduates. The preferred candidate will have experience with nucleic acid isolation, PCR, RT-PCR, and molecular cloning. Experience with Illumina sequencing library prep and plant/greenhouse work is desired, but not necessary. The ideal candidate will have good organizational skills, attention to detail, and a strong ability to multi-task. This technician position is ideal for a motivated, organized person interested in gaining greenhouse and laboratory skills prior to starting graduate school.

Candidates can apply to this position through the University of Memphis employee job posting system, https://workforum.memphis.edu. This is a full-time, one-year position with the possibility of additional years subject to performance review and funding. Salary is commensurate with experience and includes benefits. The University of Memphis is an equal opportunity employer.

www.mandel-lab.org Jennifer Mandel, Assistant Professor The University of Memphis Department of Biological Sciences 3700 Walker Avenue Memphis, TN 38152 (p) 901-678-5130 (f) 901-678-0639

"Jennifer Mandel (jmandel)" <jmandel@memphis.edu>

UMichigan ResTech MicrobialViralEvol

RESEARCH TECHNICIAN/LAB MANAGER POSITION: ECOLOGICAL GENOMCIS OF ENVIRONMENTAL MICROBES, UNIVERSITY OF MICHIGAN, ANN ARBOR, MI

A full-time (12 month) technician position is available in the Duhaime Lab in the Ecology and Evolutionary Biology Dept at the University of Michigan in Ann Arbor, MI (http://www-personal.umich.edu/~duhaimem/). The lab focuses on (i) aquatic virus-microbe interactions, using lab-based culture approaches and environmental genomics, and (ii) microbial biofilms of aquatic plastic debris. Immediate responsibilities will include: maintenance of microbial cultures and long-term host-virus experiments, specialized methods for environmental virology (fluorescent/electron microscopy, metagenome library prep, virus isolation) and general lab maintenance (ordering, inventory, organization) on UM main campus, with likely summer fieldwork on the Great Lakes (possibly Mediterranean Sea). Previous experience with basic molecular/microbial techniques, such as DNA extractions, PCR, culturing (sterile technique), plaque assays, as well as exposure to microbial sequence analysis (e.g., 16S tag sequencing, al la Mothur/QIIME), is ideal. The candidate should have a BA or BS in biology, microbiology, environmental science, or bioinformatics, previous experience performing research in a wet lab, the ability to work well in a group, and the willingness to supervise undergraduates. The position is ideal for a motivated, organized person interested in gaining field, laboratory, and informatics skills, e.g., prior to starting graduate school. Candidates can apply to this position using the following link (http://umjobs.org/job_detail/92422/research_lab_tech_intermediate) and are welcome to email duhaimem@umich.edu with questions. Review of applications will begin immediately (March 2014) and continue until a suitable candidate is found, with hiring date ASAP. Salary is commensurate with experience and includes benefits. The position is initially available for 1 year. The University of Michigan is an equal opportunity employer.

Melissa Duhaime 2037 Kraus Natural Science Building Department of Ecology and Evolutionary Biology University of Michigan Ann Arbor, MI duhaimem@umich.edu

Melissa B. Duhaime Assistant Research Scientist Ecology and Evolutionary Biology University of Michigan Office: 2037 Kraus Natural Science Bldg Office Phone: (734) 763-5612 Lab: 1008 Kraus Natural Science Bldg Lab Phone: (734) 763-8161 http://www.lsa.umich.edu/eeb/directory/faculty/duhaimem duhaimem@umich.edu

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UMontana GenomicsLabManager

Genomics Core Laboratory Manager, University of Montana

The Division of Biological Sciences at the University of Montana seeks to hire a laboratory manager for the new Genomics research and training core facility. The core manager will be in charge of evaluating and establishing technologies in support of genomic research, supervising associated technical staff, training core users in molecular protocols and supporting instrumentation, the production of genomic data using next-generation sequencing technologies, and maintaining core operating and billing procedures.

The candidate will be expected to effectively manage a multi-user core facility. As such, the ideal candidate will possess a strong foundation in molecular biology or genomics including experimental design. A bachelor's degree (BS or BA) in molecular biology, genetics, or a related field is required. An advanced degree in molecular biology or a related field is preferred. The candidate will also have a demonstrated track record of strong technical, analytical, and organizational skills, and will be willing and enthusiastic about staying up-to-date with the technologies associated with genomics including through travel to scientific meetings and/or training workshops. Previous teaching experience in a laboratory setting and analytical experience with bioinformatics or other large datasets is highly desired.

The Division of Biological Sciences and the University of Montana is home to a diverse and highly interactive collection of faculty with expertise in ecology, evolution, genetics, genomics, physiology, wildlife biology, and behavior. Missoula is a great college town with an exceptional quality of life and is located in the Rocky Mountains of western Montana.

To apply, please visit http://umjobs.silkroad.com and click the job title for this position under "Current Openings: Professional". Candidates must apply online, and will be asked to upload the following application materials: a cover letter describing your interests and qualifications, a CV, and the names and contact information for three references. Review of applications will begin on March 31 and the position will remain open until filled. The position is full time and available immediately. Any questions regarding the position can be sent to Jeff Good (jeffrey.good@umontana.edu).

University of Montana is an ADA/EOE/AA/Veteran's Preference Employer

jeffrey.m.good@gmail.com

UMontana LabTech PopGenetics

LAB TECHNICIAN JOB - for POPULATION GENETICS/GENOMICS RESEARCH

Projects: (1) Predicting Climate Change Impacts on fish populations (2) Quantifying introgression from non-native or hatchery fish into wild populations (3) Testing for genes associated with body size and disease susceptibility in moose and elk

Principal Investigators: Dr. Gordon Luikart, Conservation Geneticist/Ecologist, Flathead Lake Biological Station, The University of Montana, 406-982-3301 x249, gordon.luikart@umontana.edu. Steve Amish, Division of Biological Sciences, The University of Montana, 406-243-6749, stephen.amish@mso.umt.edu

Note: We have several exciting research projects that the technician (or perhaps postdoc) could help publish. We need help with genetic data production (library preparation, exon capture, and RAD) and perhaps data analysis (RADs, exon capture), and publishing. The successful candidate could participate directly in multiple projects. See below for information on some of our projects (funded by NSF; USGS, and NASA).

Start Date & Duration: March 2014 (or until filled); One Year with likely extension

(1) Project #1 Description/Summary: We need a lab technician to help produce RAD and exon capture data for 100s of fish for research to understand how species and habitats will respond to climate warming. This is critical for developing sustainable management strategies for freshwater systems. This research builds on existing climate change research projects focused on how hydrologic, thermal, and habitat change influences native salmonids (e.g., threatened Chinook salmon, threatened bull trout, and westslope cutthroat trout). This could involve testing for genomic signatures of local adaptation and adaptation to captivity.

(2) Project#2 Summary: We need to conduct RAD-capture and exon capture on 1000s of cutthroat trout from many streams. We will study hybridization between native cutthroat trout and introduced rainbow trout in the northern Rocky Mountains. Our primary goal is to understand how genetic, evolutionary, an ecological processes (dispersal/straying) influence hybridization within and among populations. There will be opportunities to conduct field work (fish trapping, hook and line fishing).

(3) Project #3 Summary: We need a lab technician for DNA extraction from moose bones and teeth, followed by library preparation and exon capture. An extensive historical collection of samples will be used to investigate genetic signatures of osteo-arthritis using next-generation sequencing approaches.

Skills required: The technician should have experience preparing DNA libraries for NGS analyses. Ideally, the person would have experience conducting exon capture or using capture arrays. Understanding of basic population genetics, NGS data analysis, and being able to write well would be advantageous. There would be opportunities to participate in field work and other projects (e.g. eDNA). We also need help conducting qPCR tests on eDNA (water) samples to detect invasive species (e.g. mussels, plants, and trout), for which qPCR skills would help.

Applications: Send a brief letter describing your motivation and background, your CV, and the names and contact information for three references to both G Luikart and S Amish. Review of applications will start February 20th and remain open until a suitable candidate is hired.

Salary: Approximately $28,000 to >$35,000 the first year depending on experience (cost of living in Montana is relatively low)

Key references: see our web pages and contact us

gordon.luikart@mso.umt.edu

UNAM Mexico SystematicEntomologist

Position opening - Instituto de Biología, Universidad Nacional Autónoma de México Systematic Entomologist. The Instituto de Biología, Universidad Nacional Autónoma de México (IB-UNAM), is the leading Mexican institution for the study of biodiversity and houses the national biological collections. The Department of Zoology at IB-UNAM is inviting applications for a tenure- track, full time position of Associate Researcher level "C" in systematic entomology at the National Collection of Insects (CNIN) in main University campus in

Mexico City.

Requirements for candidates include:

1. A PhD degree or equivalent, preferably in entomology, systematics, evolutionary biology, or a related discipline.

2. Research experience in insect systematics, preferably, but not restricted, to Lepidoptera or Diptera. This experience must be demonstrated by original, high quality publications, which will be evaluated according to age and academic trajectory of the candidate.

3. Knowledge of a group of insects in Mexico and/or the Neotropics, particularly a group with high diversity in Mexico.

4. Experience and/or complete disposition for the curation of scientific collections and carry out field work.

5. Knowledge and/or entire disposition to carry out integrative systematic studies employing morphological, molecular, ethological and/ or niche modelling research.

5. A commitment to be permanently involved in educational programs at UNAM, including teaching, direction of theses at the undergraduate and graduate level, activities of science outreach, as well as institutional duties.

6. Willingness to participate in the academic activities of the IB- UNAM and demonstrate capacity to become part of a research group at the CNIN.

7. Demonstrable proficiency in Spanish.

Applicants must submit a letter of intent directed to the Academic Secretary of the IB-UNAM with a detailed statement of purpose, a full curriculum vitae with contact information (supporting documentation is not necessary at this stage), PDF reprints of three publications that the applicant considers the most important of their professional trajectory, a synthetic outline of research goals for the first year (5 pages maximum), and a letter of recommendation. The required documentation must be received by May 30, 2014. Shortlisted candidates will be contacted for a personal interview.

Inquiries regarding this announcement should be addressed to the Curator of the Entomological Collection, Dr. Alejandro Zaldivar- Riverón (azaldivar@ib.unam.mx) or Dr. Atilano Contreras-Ramos, Academic Secretary of IB-UNAM (acontreras@ib.unam.mx). Applications must be emailed to Dr. Atilano Contreras-Ramos (sacademica@ib.unam.mx).

Alejandro Zaldívar Riverón Colección Nacional de Insectos Departamento de Zoología Instituto de Biología Universidad Nacional Autónoma de Mexico 3er. Circuito Exterior Cd. Universitaria Apartado Postal 70-153 C.P. 04510 México, D.F. México

Alejandro <azaldivar@ibiologia.unam.mx> Alejandro <azaldivar@ibiologia.unam.mx>

UNebraska MuseumDirector

DIRECTOR

UNIVERSITY OF NEBRASKA STATE MUSEUM

The University of Nebraska State Museum (UNSM), the natural history museum located at the University of Nebraska-Lincoln, seeks a Director to provide dynamic leadership for the UNSM.

We invite nominations and applications for Director of the University of Nebraska State Museum, a large comprehensive museum of natural history with a faculty and staff of 40 and research collections in paleontology, parasitology, entomology, zoology, botany and anthropology of more than 15 million specimens.

UNSM also has active, federally-funded education and outreach programs and close collaborations with university programs and school districts. It is accredited by the American Alliance of Museums and is a Smithsonian Affiliate.

The Director provides leadership and is responsible for developing external funding and partnerships, and enhancing facilities and collections. The Director will also develop and implement a new strategic plan to grow the Museum's research, collections, and education programs.

The successful applicant will have an earned doctorate in science with a strong research and funding record meriting a tenured faculty position. It is expected that the Director will be tenured in an appropriate department. The Director will have museum experience, effective management and organizational skills, the ability to work well on collaborative teams and excellent interpersonal and fundraising skills.

We are accepting nominations and applications for this position. To nominate someone please email UNLresearch@unl.edu. To apply, go to http://employment.unl.edu, search for requisition number F_130241. Click on "Apply to this job." Complete the application and attach a letter of interest, an up-to-date vita, and names/addresses of five references. Please email Peg Filliez at pfilliez1@unl.edu for further information. Applications will be reviewed beginning February 17, 2014 and will remain open until filled. For more information about this position and UNSM, please visit http://research.unl.edu/museumdirector . The University of Nebraska has an active National Science Foundation ADVANCE gender equity program, and is committed to a pluralistic campus community through affirmative action, equal opportunity, work-life balance, and dual careers.

Jay Storz <jstorz2@unl.edu>

UNewEngland Australia EvolutionaryZoology

http://www.une.edu.au/jobs-at-une/current-vacancies UNIVERSITY OF NEW ENGLAND

Lecturer/Senior Lecturer in Zoology (Fixed-term, 3 years)

School of Environmental and Rural Science

The School of Environmental and Rural Science is a major research and teaching group within the University of New England (Armidale, NSW). It has rated very highly (4) in the most recent Excellence in Research Australia Rankings for both its Zoology and Palaeontology research disciplines, and is one of very few Australian universities to offer degrees in both fields. The school is very well-resourced with new or recently updated facilities, which include state of the art CT, microCT and surface scanning equipment.

The responsibilities of the position will include both research and undergraduate teaching in Zoology. Candidates with a demonstrated capacity to independently develop and complete projects will be favoured. Applicants must have a PhD in Zoology or a related discipline, competence in the areas of geometric morphometrics and/or biomechanics, a strong record of research and research publication and well-developed communication skills.

This full time, fixedterm, Level B or Level C position is available for three years initially, with the possibility of further appointment, subject to satisfactory performance and the availability of funding.

Armidale, a vibrant university city recognised as a centre of culture, is well served with art, music, theatre, sport and public and private education. While UNE has a long history and strong tradition of academic distinction, our outlook is dynamic and fresh (visit: www.armidaleregion.com.au/ and/or http://www.experiencethehighs.com.au/)

Informal enquiries may be directed to Associate Professor Stephen Wroe, phone: (02) 6773 2930 or email: swroe@une.edu.au. For further information about the School/Directorate visit: www.une.edu.au/ers/ and the Function, Evolution and Anatomy Research lab: http://www.thefearlab.com/#&panel1-2 . Salary: $82,123 to $97,329 per annum (Lecturer Level B) $100,369 to $115,578 per annum (Senior Lecturer Level C) plus 17% employer superannuation and optional salary packaging

Closing Date: 31st of March 2014

Reference No: 214064

Best wishes,

Steve Associate Professor Stephen Wroe ARC Discovery Outstanding Research Award Fellow Director of The Function, Evolution & Anatomy Research (FEAR) Lab < http://www.thefearlab.com/ > Zoology, School of Environmental and Rural Science, University of New England, Armidale, NSW, Australia, 2351 Conjoint A/Prof School of Engineering, University of Newcastle, NSW, Australia, 2308 Email swroe@une.edu.au Phone 61 2 67733261 or 61 [0]432349049

GOOGLE SCHOLAR http://scholar.google.com/citations?hl=en&user=c65t4cwAAAAJ&view_op=list_works&cstart ACADEMIA http://une-au.academia.edu/StephenWroe Facebook: https://www.facebook.com/stephen.wroe.359?ref=tn_tnmn University of New England: CRICOS 00003G

Stephen Wroe <swroe@une.edu.au>

UOregon ResAssistant MicrobialEcol

Research Assistant Institute of Ecology and Evolution Posting: 14064 Location: Eugene Closes: Open Until Filled

The Institute of Ecology and Evolution at the University of Oregon currently has an opening for a full time Research Assistant to work in the area of microbial ecology. The successful candidate will play a key role in the Biology and Built Environment (BioBE) Center (http://biobe.uoregon.edu/), funded by the Alfred P. Sloan Foundation. The BioBE Center is training a new generation of innovators to study the built environment microbiome - the diversity of indoor microbial life, their genetic elements and their interactions. The vision of this national research center is to understand buildings as complex ecosystems and to explore how architectural design mediates urban microbial ecology and evolution. For a description of partner projects see http://www.microbe.net/ . The initial appointment is for one year, with the possibility of extension dependent on funding and satisfactory performance. The University of Oregon is located in Eugene, Oregon, recently rated in the top 10 “Best Places to Live” (livability.com).

Extensive experience using molecular techniques is required, including some combination of skills in DNA/RNA extraction, PCR, cloning, next-generation DNA sequencing, bioinformatics, and phylogenetic analysis. Ability to work in a team atmosphere is a must. A Master’s degree in biology is desirable, but individuals with a bachelor in biology or related field and extensive experience are also encouraged to apply. The successful candidate will be responsible for conducting laboratory research under the direction of Principle Investigators Jessica Green (pages.uoregon.edu/green) and Brendan Bohannan (http://pages.uoregon.edu/bohannanlab/). Salary will be commensurate with education and experience. We invite applications from qualified candidates who share our commitment to diversity.

Please e-mail a cover letter and current CV with names and contact information of three references to: ie2jobs@uoregon.edu Subject: Posting 14064

Or mail to:

Posting 14064, 5289 University of Oregon, Eugene, OR 97403-5289.

To ensure consideration, please submit applications by April 25, 2014, but position will remain open until filled. EO/AA/ADA institution committed to cultural diversity.

http://jobs.uoregon.edu/unclassified.php?id=4620
http://jobs.uoregon.edu/unclassified.php?id=4621
Postdoctoral Research Associate Institute of Ecology and Evolution Posting: 14066 Location: Eugene Closes: Open Until Filled

Position in Bioinformatics/Microbial Ecology

Jessica Green (http://pages.uoregon.edu/green/) and Brendan Bohannan (http://pages.uoregon.edu/bohannanlab/) are currently seeking a bioinformatics postdoctoral researcher to explore fundamental questions in microbial ecology and evolution. Applicants should have a PhD with extensive training using bioinformatics to understand the ecology and/or evolution of complex biological communities, and strong writing skills. The ideal candidate will have experience developing and applying quantitative community and population ecological methods to the analysis of environmental sequence data and next-generation sequence data.

The successful candidate will play a key role in the Biology and Built Environment (BioBE) Center (http://biobe.uoregon.edu/), funded by the Alfred P. Sloan Foundation. The BioBE Center is training a new generation of innovators to study the built environment microbiome - the diversity of indoor microbial life, their genetic elements and their interactions. The vision of this national research center is to understand buildings as complex ecosystems and to explore how architectural design mediates urban microbial ecology and evolution. For a description of partner projects see http://www.microbe.net/ . The position is available for 1 year with the possibility for renewal depending on performance. The start date is flexible. Please email questions regarding the position to Jessica Green (jlgreen@uoregon.edu).

To apply

A complete application will consist of the following materials:

(1) a brief cover letter explaining your background and career interests

(2) CV (including publications)

(3) names and contact information for three references

Submit materials to ie2jobs@uoregon.edu. Subject: Posting 14066

To ensure consideration, please submit applications by April 25, 2014, but position will remain open until filled.

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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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UParis13 EvolutionaryEthology 2

Full Professor - Ethology

The /Laboratory of Experimental and Comparative

Ethology (LEEC) – EA 4443/, University of Paris 13, is inviting applications for the position of a Professor in Ethology (69 PR 0949), with tenure status and salary commensurate with qualifications and experience.

The successful candidate will succeed Professor Dominique Fresneau, who has recently announced his retirement. Applicants should have a strong track record of international excellence and external grant funding. The successful candidate will be expected to develop an innovative research program in ethology and must demonstrate the ability to successfully mentor young researchers.

The research activities at the Laboratory of Experimental and Comparative Ethology cover various aspects of social behaviour using mechanistic, functional and evolutionary approaches. The position also remains open to other topics as long as they are located within the field of ethology.

The position includes teaching at the bachelor (psychophysiology) and master level (Master in Ethology). The latter is nationally recognized for its significant role in the formation in basic and applied ethology.

Application is electronic via a national portal (/Galaxie/; deadline for application: 01. April 2014, 16:00 h).). Interested candidates should contact us as soon as possible for further information on the position and on electronic application procedure. In addition to the obligatory application via /Galaxie/, please send curriculum vitae and list of publications to: Heiko.Rodel@leec.univ-paris13.fr

Contact:

Prof. Heiko G. Rödel, Director of the LEEC (Heiko.Rodel@leec.univ-paris13.fr); Prof. Patrizia d'Ettorre, Head of the teaching department of psychophysiology (Patrizia.dEttorre@leec.univ-paris13.fr); Prof. Dominique Fresneau (Dominique.Fresneau@leec.univ-paris13.fr), President of the Selection Committee

Laboratoire d'Ethologie Expérimentale et Comparée EA 4443, Université Paris 13, Sorbonne Paris Cité, 99 avenue J.B. Clément, F-93430 Villetaneuse, France. Phone:+ 33 (0)14940 3259; Fax: + 33 (0)14940 3975; http://leec.univ-paris13.fr/ The University of Paris 13is an Equal Opportunity Employer. http://www.univ-paris13.fr/ Heiko Rödel <heiko.rodel@googlemail.com>

USheffield BioinformaticsResAssist

Biostatistician/ Bioinformatician Research Assistant

University of Sheffield -Department of Animal and Plant Sciences

The Animal and Plant Sciences is one of the leading research departments for whole-organism biology in the UK. The department research projects going on in locations from the polar regions to the tropics, at scales from within cells up to entire ecosystems. Through our research we aim both to understand the fundamental processes that drive biological systems and solve pressing environmental problems. The Bioinformatics Hub is a new establishment aiming to carry develop novel computational tools and carry bio statistical analyses. Dr. Elhaik's lab has a diverse range of activities from Molecular Evolution to Paleo-genomics (see www.eranelhaiklab.org).

You will have a good honours degree in biostatistics, epidemiology, statistical genetics or relevant experience and experience of conducting research e.g. through a qualification or through a previous research assistant post or through working towards a PhD. Ideally you will have experience of analysing qualitative data and a relevant postgraduate qualification (or relevant experience) featuring research methods.

Contract Type: Fixed Term with a start date of 1 April 2014 and an end date of 30 September 2015.

Faculty: Faculty of Science

Salary: Grade 6 pounds 24,289 to pounds 28,132 per annum

Closing Date: 7 April 2014

Please apply here: http://www.jobs.ac.uk/job/-AII502/biostatistician-bioinformatician-research-assistant/

Many thanks

Eran Elhaik, Ph.D.

http://www.eranelhaiklab.org/ Department of Animal & Plant Sciences, Alfred Denny Building University of Sheffield, Western Bank Sheffield, S10 2TN, UK

Phone: 01142222837 Fax: 0114 2220002

Email: e.elhaik@sheffield.ac.uk

Eran Elhaik <e.elhaik@sheffield.ac.uk>

UTexas-Arlington BiologyDepartmentChair

Department Chair, The University of Texas at Arlington, Department of Biology

POSITION DESCRIPTION: The University of Texas ' Arlington^{1}s Department of Biology seeks an individual with outstanding academic credentials in any field of Biology to serve as the Department Chair. The successful candidate must hold a Ph.D. and have proven management and leadership skills, as well as a track record of extramurally funded internationally recognized research and a demonstrated commitment to excellence in teaching and mentoring. Applicants should present a compelling vision for guiding the future trajectory of the department ' one that capitalizes on recent departmental and institutional investments in faculty and research infrastructure to foster UT Arlington^{1}s explicit goal of becoming a Tier 1 research university.

The new chair will lead a department comprised of 22 faculty, 7 full-time lecturers and 12 staff. With over 2,029 majors across 4 undergraduate degrees, 55 M.S. students, and 52 Ph.D. students, Biology has the largest enrollment in the College of Science. Broad areas of faculty strength include: aquatic and plant ecology, genomics, molecular evolution, microbiology, and herpetology. The department offers teaching loads commensurate with a predominant research focus, as well as competitive salaries and startup packages. Information about research facilities within the department is available at www.uta.edu/biology/facilities/index.htm. The department benefits from significant recent institutional investment in imaging, proteomics and analytical chemistry capabilities through the Shimadzu Institute for Research Technologies, a $25.2 million partnership between UT Arlington and Shimadzu Scientific Instruments. Furthermore, as a University of Texas member institution the department enjoys excellent access to core facility resources at UT Southwestern Medical Center and the Texas Advanced Computing Center (TACC) ' one of the leading advanced computing centers in the United States. Additional information about the department can be found at www.uta.edu/biology/home.html . APPLICATION PROCEDURES: The Search Committee invites applications, inquiries, and nominations for this position. Applications should be accompanied by a letter of interest, curriculum vitae, and the names and contact details of at least five professional references. Applications and nominations will be accepted until the position is filled, and review of applications will begin immediately. Interested candidates are encouraged to submit materials prior to April 14, 2014 to the search firm assisting UT Arlington at the following address (electronic submissions preferred):

Ryan Crawford, Principal Parker Executive Search rcrawford@parkersearch.com 770-307-7031 | Fax: 770-804-1917

ADDITIONAL INFORMATION ABOUT UTA AND THE AREA

THE UNIVERSITY: With a commitment to innovative research, teaching excellence and service to the community, The University of Texas ' Arlington is an educational leader in the heart of the Dallas-Fort Worth Metroplex. Founded in 1895 as a private liberal arts institution, UT-Arlington achieved senior college status in 1959 and became a part of The University of Texas System in 1965.

UT Arlington is the second largest of the fifteen-campus University of Texas System. It is a comprehensive teaching, research and public-service university organized into 12 colleges and schools offering more than 180 degree programs to over 33,000 students. Located in downtown Fort Worth, the UT-Arlington Fort Worth Center offers master^{1}s degrees and continuing education programs tailored for the working professional.

The Carnegie Foundation for the Advancement of Teaching ranks UT Arlington as a Research University/High Activity. Since 2001, research expenditures have increased more than three-fold to $77 million in FY 2012-2013. As research grants and contracts have increased, so have the number of invention disclosures, patent applications and licensing agreements. U.S. News and World Report lists UT Arlington as one of the 15 most diverse universities in the country and the New America Foundation lists UT Arlington as one of six public Next Generation Universities that are ^{3}breaking the mold.^{2}

The Hispanic Outlook in Higher Education magazine selected UT Arlington as one of the top 100 four-year colleges for Hispanics in 2006.

U.S. News & World Report recently named three of UT Arlington^{1}s distance education programs among the best in the nation.

Many of the University^{1}s faculty members are recognized nationally and internationally for their teaching and research expertise as well as their community service.

Partnerships between UT Arlington and UT Southwestern Medical Center, UT Austin, Rice University, UT Dallas, Northlake College and other

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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

UWisconsin Whitewater EvolutionarySciOutreach

Hello,

The College of Letters & Sciences at the University of Wisconsin-Whitewater invites applications for a Science Outreach Coordinator. The successful candidate will be expected to continue to develop a strong and visible science outreach program that will advance and assist science education throughout the region, engage K-12 students, and attract them to careers in science.

Please see the Job Announcement copied below for additional information.

If you have any questions, please feel free to contact the search chair, Dr. Jessica L. Menke (menkej@uww.edu).

ANNOUNCEMENT OF SCIENCE OUTREACH POSITION

Position Title: Science Outreach Coordinator (Outreach Program Manager I) Appointment: Full-time, 12-month Starting Date: July 1, 2014, or sooner

Position Description: The College of Letters & Sciences at the University of Wisconsin- Whitewater invites applications for a Science Outreach Coordinator. The successful candidate will be expected to continue to develop a strong and visible science outreach program that will advance and assist science education throughout the region, engage K-12 students, and attract them to careers in science. A detailed list of the current UW-Whitewater Science Outreach Goals & Mission Statement can be found at http://uww-scienceoutreach.blogspot.com/p/blog-page.html Teaching may comprise a small portion of the position's responsibilities. Support in the form of a part-time administrative assistant and student workers will be provided by the college. The candidate will be expected to acquire extramural funding to support the program. The program serves a diverse population of students and embraces the principles and practices of Inclusive Excellence that are reflected in UW System's commitment to diversity and educational opportunity.

Qualifications: Advanced degree in a natural or physical science (M.S. or Ph.D.) required with significant experience in K-12 education/administration or science outreach as well as teaching experience strongly preferred. The successful candidate must demonstrate the potential to be an enthusiastic and motivated promoter of science and science education and to serve as a liaison between the sciences at UW-Whitewater and local/regional school districts and the public at large.

University & Community: Founded in 1868, UW-Whitewater is a premier public regional university with an enrollment of approximately 12,000 students in 50 undergraduate majors and 13 master's degree programs, and one specialist degree program. It offers high-quality career-oriented programs integrated with a model general education curriculum. UW-Whitewater is part of the 26- campus University of Wisconsin System. Located in a community of 14,622 residents near the scenic Kettle Moraine State Forest in southeastern Wisconsin, Whitewater is within convenient driving distance to the metropolitan areas of Milwaukee, Madison and Chicago. Visit our website at http://www.uww.edu . Application: Interested persons should apply electronically to: SO-search@uww.edu c/o Dr. Jessica Menke

Chair, Science Outreach Coordinator Search 265 Upham Hall University of Wisconsin-Whitewater Whitewater, WI 53190 (262) 472-1088 menkej@uww.edu

A complete application packet consists of a letter of application, curriculum vitae, official copies of all transcripts, a brief statement summarizing previous experience in outreach, grant-getting, and program administration all as a single Word or pdf. file and three current letters of recommendation.

Applications received by April 21, 2014 are ensured consideration; the position is considered open until otherwise indicated. The University of Wisconsin-Whitewater is an Equal Opportunity and Affirmative Action Employer, and actively seeks and encourages applications from women, members of minority groups, persons with disabilities, and all veterans. Names of applicants may be disclosed unless requested otherwise. Names of finalists will be released. UW-Whitewater conducts criminal background checks as a contingency to employment. A criminal background check will be conducted prior to an offer of employment.

lisberga@uww.edu

WillametteU EvolutionaryBiol

The Department of Biology at Willamette University welcomes applications for a non-tenure-track, visiting assistant professor position to begin August 2014. The appointment will be for one year, with potential for renewal up to three years depending on successful teaching.

We are seeking a broadly trained biologist who is strongly committed to excellence in both teaching and research in a liberal arts college environment. The successful candidate will be expected to teach 6 course units a year (1.0 unit/lecture, 0.5 unit/lab). The teaching assignments will include an introductory non-majors biology course (BIOL 110 Principles of Biology) and an introductory course for biology majors in EITHER Cellular Biology and Genetics OR Ecology and Evolutionary Biology. The candidate will also be asked to teach intermediate and advanced courses in his or her area of expertise. These might include: Microbiology, Gene Structure and Function, Molecular Genetics, General Ecology, Evolutionary Biology, Molecular Ecology, or Behavioral Ecology. Course sizes range from 12 to 48 students.

Our faculty are dedicated teacher-scholars, many of whom are successfully funding their research programs with extramural grants. Teaching in our department is inspired by Vision and Change (NSF, AAC&U, 2011) and research training is deeply embedded in the curriculum at all levels. The Departmental culture encourages extramural funding for research and pedagogical projects and candidates may expect support for their initiatives if they can create opportunities for our students. For more information about the Department of Biology, please visit http://www.willamette.edu/cla/biology . Applicants must have a Ph.D. in an appropriate area of biology. A.B.D candidates will be considered, but the Ph.D. must be completed before beginning the appointment. Prior teaching experience is preferred but not required.

To apply visit the following URL: https://jobs.willamette.edu/postings/1088 The following materials will need to be uploaded as part of your online application:

1. A cover letter describing your interest in the position and indicating which of the two introductory courses you would teach (Cell Biology and Genetics OR Ecology, Evolution and Diversity) 2. A copy of your CV 3. A teaching statement describing your teaching philosophy and practice, and identifying advanced courses that you would be interested in teaching. 4. A research statement describing your current and future research goals, and how you might involve undergraduates in your work. 5. A diversity statement describing your experience with diverse populations and importance of diversity in teaching and research communities. 6. A copy of your graduate transcripts. 7. Three reference letters that address both research and teaching potential.*

*As part of the online application, please include three references and notify them that they will be contacted electronically. The email from Human Resources will include a link where they will be able to submit a letter of recommendation/reference on your behalf. Please note letters will only be accessible to the search committee.

Inquiries may be addressed to: David Craig, dpcraig@willamette.edu.

Open until finalists are selected. For optimal consideration, all application materials should be received by March 21, 2014.

If you need assistance applying for this position please contact Human Resources, human-resources@willamette.edu or 503.370.6210

Willamette University, founded in 1842, is the oldest institution of higher education in the Far West. Willamette University is a selective residential liberal arts college in the heart of the Willamette Valley. Situated in Oregon's capital city, Willamette includes the College of Liberal Arts (approximately 2000 students), and graduate programs in Education, Law, and Management. The academic year is divided into two semesters, beginning in late August and ending in May. The academic undergraduate profile is competitive, with a GPA of 3.84 and average composite SAT scores of 1260. Willamette students are recipients of prestigious national awards annually, such as NSF, Watson, Truman, Fulbright and Goldwater fellowships. Salem is located in the center of the Willamette Valley, approximately an hour's drive from the Pacific Coast, the Cascade Mountains, and the cities of Portland and Eugene. To learn more about Willamette University, please visit http://www.willamette.edu . Believing that diversity contributes to academic excellence and to rich and rewarding communities, Willamette University is committed to recruiting and retaining a diverse faculty, staff and student body. We seek candidates, particularly those from historically under-represented groups, whose work furthers diversity and who bring to campus varied

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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

Other

AFLPOP question

Hi,

Does anyone know if AFLPOP outputs the probability of assignment to each source population, or does it only output the probability for the allocated population? I'd like to know the probability of local assignment (to its nominal population) for each individual.

Also, how does one specify separate populations in the input files? It's not clear to me from the demo data, but I'm not entirely sure these have been downloaded correctly or that the software isn't having a problem because of my current browser, excel and OS versions.

Any help is appreciated.

Thanks, Shannon

Shannon Corrigan, PhD Postdoctoral Researcher Hollings Marine Laboratory 331 Fort Johnson Charleston, SC 29412 Phone: +1 843-725-4886 Fax: +1 843-762-8737 Cell: +1 415-359-7970 http://prosper.cofc.edu/ ~ sharkevolution/ shancorrigan1@gmail.com

Allendorf Fund

Wildlife Biology Program - University of Montana - www.cfc.umt.edu/wbio - wbio@cfc.umt.edu March 4, 2014

Dear friends, As you may know, our dear friend and colleague Fred Allendorf has been through a tragedy. Last Friday, February 28, an avalanche was triggered in a gully on Mount Jumbo that ends at the home where Fred, Michel (his wife), and children have lived for over 20 years. The avalanche demolished the home, and buried Fred, Michel, and an 8-year old boy from a neighboring house. All three people were recovered from the snow and wreckage in the following hours, and rushed to the hospital. The boy, Phoenix, has since been released from the hospital. Fred remains in serious condition with 17 broken ribs, several broken vertebrae, and some internal bleeding, but prospects for his recovery are good. Sadly, Michel passed away on Sunday night. Michel was the first woman to earn a degree in Wildlife Biology at the University of Montana after it became an interdisciplinary program in 1965. She was a wonderful, caring, and adventurous person. She will be sorely missed by all who knew her, and it breaks all of our hearts to think of what Fred is going through. Since the avalanche, there has been a wave of support for Fred and Michel from people all over the world. This support means a lot to Fred, and will continue to be important in the coming days and weeks. Also, "The Allendorf Family Fund" has been established for those wishing to make financial contributions to help Fred and his family recover. Donations can be made directly at any branch of the Missoula Federal Credit Union (MFCU), sent to MFCU at 3600 Brooks St., Missoula MT 59801, made over the phone by calling (406) 523-3300, or by e-banking to MFCU account 277580. You can also make contact through the "Contact Us" link on the MFCU website, http://www.missoulafcu.org. On behalf of all of Fred's friends and colleagues at the University of Montana, thank you for your support during this difficult time.

Sincerely, Winsor Lowe Charlie Janson Mike Mitchell Interim Director, Wildlife Biology Program Associate Dean Unit Leader Associate Professor, Biological Sciences Division of Biological Sciences Coop. Wildlife Research Unit (406) 243-4375 (406) 243-5122 (406) 243-4390 winsor.lowe@umontana.edu charles.janson@mso.umt.edu Michael.Mitchell@mso.umt.edu

Steven Orzack

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

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

BryanClarke FRS

It is with great sadness that we have to report to the evolution community the death of Professor Bryan Clarke FRS on Thursday, the 27th February 2014.

Bryan Clarke was a leader in our understanding of the process of evolution for more than four decades. He made fundamental contributions, both empirical and theoretical, particularly in elucidating the forces that maintain genetic variation in populations, and in throwing light on the process of speciation.

Bryan was born on the 24th June 1932, and, following service in the Royal Air Force, was educated at Magdalen College Oxford, from where he received both his BA in 1956 and DPhil in 1961. From 1959 to 1971 he worked at the University of Edinburgh, starting as Assistant Lecturer and rising to a Readership. In 1971 he was the Foundation Professor at the new Department of Genetics at the University of Nottingham, and remained until 1997, when he became Professor Emeritus.

The Darwinian theory of evolution by natural selection identifies genetic differences in populations - polymorphisms, as the key to evolutionary change. It is of fundamental interest whether polymorphisms are affected by natural selection, or solely by genetic drift. Bryan's research focussed on polymorphisms in snails, including members of the genus Cepaea, the shells of which vary greatly in colour and in their banding patterns. While some had naively suggested that this variation might have no effect on the organisms' fitness, earlier experiments and observations, from Cain and Sheppard in particular, had demonstrated that these variants were indeed subject to natural selection. But, if there is selection operating on this genetic variation, why does the population not come to consist of only a single, best-adapted, type? The answer is that selection can, in some circumstances, maintain variation rather than destroying it. One mechanism for the maintenance of genetic variation is heterozygote advantage, which explains, for example, the high frequency of the allele causing sickle cell anaemia. Bryan knew that the patterns of inheritance of the polymorphisms in Cepaea could not be explained by heterozygote advantage. Rather, he was able to demonstrate that these are maintained by a different mechanism, frequency-dependent selection, in which the fitness of genetic types increases if their frequencies in the population diminish, thereby creating a stable equilibrium in which multiple genetic types are maintained. His studies of frequency-dependent selection were able to demonstrate the near-ubiquity of this phenomenon when visible polymorphisms are studied in wild populations, and also showed the selective agents which brought this about. The frequencies of polymorphic variants in snails can vary greatly in space, without any obvious environmental correlates. An important and influential step in the understanding of such "area effects" came from Bryan's models of morph-ratio clines in his 1966 American Naturalist paper.

Studies of visible polymorphisms were augmented, from the 1960s, by the study of polymorphisms in the amino acid sequences in proteins, investigated initially through electrophoretic detection of differences in the electric change on enzyme molecules. As with the visual polymorphisms in Cepaea, some assumed that the changes were invisible to natural selection. Bryan Clarke advocated the view that a large proportion of the changes were indeed subject to natural selection and demonstrated experimental support for this view, particularly for variants in the enzyme alcohol dehydrogenase in Drosophila melanogaster. The study of selection acting on polymorphic differences in amino acid sequences is a direct way to obtain evidence about whether the long-term evolution of the amino acid sequences of proteins is shaped by natural selection. Some believe that protein evolution is almost completely dominated by random forces in which the successful variants were so not because of the advantages they gave to their bearers, but as a result of genetic drift. Bryan Clarke was one of the main advocates of the view that a large part of the evolutionary changes in the amino acid sequences of proteins were indeed driven by Darwinian natural selection, a view that results from large-scale DNA sequencing are confirming in many species.

Bryan Clarke also played a large part in developing our understanding of the process through which species form. He carried out a long-term study of species of the land snail Partula on the South Pacific island of Moorea and neighbouring islands. He appreciated that, in the early stages of speciation, matings between members of populations undergoing speciation do not stop instantly- some hybridisation persists. Species stay distinct notwithstanding there being some gene flow between them. Thus, selectively important genetic differences between species, such as those determining form, colour and behaviour, are maintained as

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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

CLUMPP and DISTRUCT

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.

Best, Jenny Ovenden

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

Jennifer Ovenden http://molecularfisherieslaboratory.com.au http://www.uq.edu.au/sbms/staff/jennifer-ovenden j.ovenden@uq.edu.au

Drawing pedigrees

Dear All: Can anyone recommend a (preferably free and easy to use) program for drawing pedigrees? In particular, I'd like the option of being able to choose the style and colour of intergenerational connecting lines. I've explored Genopro and Pedigraph, which aren't bad but they are limited. Thanks, Bill Chapco.

Dr. William Chapco Professor Emeritus Department of Biology University of Regina Regina, SK, S4S 0A2 Canada 306-585-4478 306-337-2410 (FAX) chapco@uregina.ca

William.Chapco@uregina.ca

EDEN ResearchFunding 2

Dear Colleague,

(Apologies if you have received this email more than once.)

This email is to remind you that the upcoming deadline for research exchange grants from the Evo-Devo-Eco Network (EDEN) is April 30, 2014. EDEN is a program funded by the National Science Foundation Research Coordination (http://edenrcn.com/).

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

Please note that the updated eligibility for EDEN funding is as follows:

Researchers based anywhere in the world can apply for funding to visit labs in the US.

Researchers based in the US are eligible for funding to visit labs anywhere in the world.

This spring EDEN will award approximately five research exchanges to be held in 2014-2015. Each exchange will consist of an award of up to $3,000 per researcher toward travel, lodging and subsistence costs. You can find out more about this program at http://edenrcn.com/funding/index.html .If you know of outstanding lab personnel who would be interested, please forward this announcement to them.

You can read more about EDEN's activities and opportunities at http://www.edenrcn.com, where you will be able to obtain protocols for evo-devo-eco work developed with EDEN funding.

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

Best wishes,

Cassandra Extavour

Dr. Cassandra Extavour

EDEN Lead PI EDEN: Evo-Devo-Eco Network http://www.edenrcn.com edenrcn@fas.harvard.edu

EDEN Administration: Barbara Perlo perlo@fas.harvard.edu

Department of Organismic and Evolutionary Biology Harvard University 16 Divinity Avenue, BioLabs 4103 Cambridge, MA 02138, USA

Extavour Lab: http://www.extavourlab.com edenrcn@fas.harvard.edu

EthidiumBromide alternative

Dear EvolDir Members:

I would be very grateful to all those that could suggest me some (non toxic) products to efficiently stain DNA on agarose gel in place of the ethidium bromide (toxic)

We have tried a few but with no success so far (Euroclone, BioRad, SYBR Green...)

Thank you very much,

Regards

Filippo Barbanera

Dept. of Biology University of Pisa, Italy filippo.barbanera@unipi.it

MY NEW EMAIL ADDRESS IS: filippo.barbanera@unipi.it

Filippo Barbanera

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

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

FILIPPO BARBANERA <filippo.barbanera@unipi.it>

EvoDevoEcoNetwork ResearchFunding

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This email is to remind you that the upcoming deadline for research exchange grants from the Evo-Devo-Eco Network (EDEN) is April 30, 2014. EDEN is a program funded by the National Science Foundation Research Coordination (http://edenrcn.com/).

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Researchers based in the US are eligible for funding to visit labs anywhere in the world.

This spring EDEN will award approximately five research exchanges to be held in 2014-2015. Each exchange will consist of an award of up to $3,000 per researcher toward travel, lodging and subsistence costs. You can find out more about this program at http://-edenrcn.com/funding/index.html. If you know of outstanding lab personnel who would be interested, please forward this announcement to them.

You can read more about EDEN's activities and opportunities at http://www.edenrcn.com, where you will be able to obtain protocols for evo-devo-eco work developed with EDEN funding.

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

Best wishes,

Cassandra Extavour

edenrcn@fas.harvard.edu

Fst Structure answers

Dear all,

I recently posted this question:

I'm working on population genetics of reef fishes; I've used microsatellite loci to detect population structure and I've found significant Fst value among different sampling locations. However, when running STRUCTURE I failed finding any partition among samples. Does anybody has a clue about why is this happening??

Answers are listed below:

Answers

1) with polymorphic enough data, Fst tests are powerful to detect weak differentiation between a priori groups. STRUCTURE tries to find a structure in a dataset without a priori groups, which is much more challenging, and will often fail when the Fst between real groups is too low (e.g. Fst <0.03).

2) Your experience is not unique. For example, we recently published a paper in Molecular Ecology on our work on collared lizards. We found significant isolation by distance and an fst, but STRUCTURE gave us nothing. We then used a different Bayesian assignment program that also incorporates spatial information, BAPS, and got beautiful results. In this case, I had translocated these populations into an area in which they had gone extinct, and we have followed in detail their entire colonization and dispersal history for over 30 years. BAPS reconstructed this known history very accurately. The BAPS results are in our paper (Neuwald, J. L., and A. R. Templeton. 2013. Genetic restoration in the eastern collared lizard under prescribed woodland burning. Molecular Ecology 22:3666-3679). Right now I'm in Israel working on an endangered salamander. When we applied STRUCTURE to our data, we got just two divisions (the Galilee and Mt. Carmel, which are isolated from one another and show extreme genetic differentiation). However, when we applied BAPS, in addition to this major subdivision, it subdivided the Galilee into 10 subpopulations, all of which made excellent sense given the topography of the area and our previous studies on dispersal. Using these 10 subpopulations, we had highly significant results with fst and AMOVA - all completely invisible to STRUCTURE.

I have also had experience with STRUCTURE in my work in human genetics, and have found I can get just about any result I want by playing with K, which is notoriously hard to estimate in a statistically meaningful fashion. I truly do not understand the popularity of STRUCTURE. I advise you to simply avoid its use, and go to other programs such as BAPS. A non-parametric alternative that has been used mostly in the human genetic literature is with the program Awclust (http:/-/awclust.sourceforge.net/docs/index.html).

3)My guess is that you are looking at two different scales in your data (also I am not sure what parameters you used in structure) - if you find a local structure (it could be that your individuals are more related and then detect significant Fst between populations) whereas you have enough migration (in the sense of genetic exchange) between groups which lead structure to consider your population as panmictic.

I would suggest that you have a look at: Gauffre B, Estoup A, Bretagnolle V, Cosson JF (2008) Spatial genetic structure of a small rodent in a heterogeneous landscape. Mol Ecol 17:4619-4629 and maybe who cites this paper.

4)Personally I only use Bayesian clustering when I am desperate, e.g. I suspect strong FIS to come from Wahlund effects but have no clue to find the origin of it. The assumptions of panmixia and Linkage equilibrium (the last being impossible to reach in real populations), and also because I really do not understand what these kind of softwares really do, are constraints that make me quite reluctant. I prefer using old stuffs that are directly connected to demography in a way I can understand.

In your case, you might have a continuous (or nearly so) increase of differentiation with some factor(s), the most obvious being geographic distance. You might also have multi-hierarchical levels. All factors that might prevent STRUCTURE finding anything.

Try to study isolation by distance and, if it works, you will get much more information than STRUCTURE will ever give you.

A good thing also is checking that all your loci behave the same (for both FST and FIS). If one or two loci display unusual behaviour as compared to all others, this might represent the signature of some technical or non-neutral factors that may also disturb STRUCTURE functioning.

5)Fst can become significant also for very small value if the sample size turns larger. In fact, and that is true for most statistical applications, if you increase your sample size enough you get significant results eventually - even though they will be biologically irrelevant.

It is difficult to evaluate your question without having seen your structure results, or knowing your runtime settings. Maybe you have performed

— / —

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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Homidae skull data

Dear Friends,

I am teaching Biostatistics for Biology students and I would like to explore human evolution during the classes. I would like to compare skull measurements from apes, fossil hominids and modern humans and also explore skull evolution by using simple linear models. I was looking in Google but I cannot find good spreadsheets. Maybe there are good data set examples in some textbooks but I don't know.

My idea is always to bring new data and ideas for the students because most of them don't like numbers and using a more applied approach is creating much more interest among them.

Thanks for any help!

Prof. Dr. J. C. VOLTOLINI Grupo de Pesquisa e Ensino em Biologia da Conservação - ECOTROP Universidade de Taubaté, Departamento de Biologia Taubaté, SP. 12030-010. E-Mail: jcvoltol@uol.com.br * Grupo de pesquisa ECOTROP CNPq: http://dgp.cnpq.br/buscaoperacional/detalhepesq.jsp?pesq=8137155809735635 * Currículo Lattes: http://lattes.cnpq.br/8137155809735635 * Assessoria Estatística: http://assessoria-estatistica.blogspot.com.br/ * Fotos de Cursos e Projetos: http://www.facebook.com/VoltoliniJC?v=info VOLTOLINI <jcvoltol@uol.com.br>

Indel aa selection

Dear Brian and Evoldir,

During a class, I was asked to show some examples of insertions in the protein level during evolution. The idea is to show some examples of aa insertions that will be easily visible in a pairwise alighment (e.g. human - mouse) and will have some functional role.

I tried to find such examples using google, blast etc. but it doesn't see to be such a trivial task. Could you please suggest any specific examples that clearly show insertions (or deletions) in the alignment of a homologous protein between two species and this indel to have a functional role?

kind regards, pavlos

–

Pavlos Pavlidis, PhD

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

pavlidisp@gmail.com

JHeredity pageCharges

The Journal of Heredity now waives page charges of one 8-page article per volume for all authors. Current members of the American Genetic Association receive 10 free pages. For details about submission to Journal of Heredity, please visit http://-jhered.oxfordjournals.org/ .

KBS MichiganStateU VisitingScholars

The W.K. Kellogg Biological Station (KBS) of Michigan State University invites applications for short term Visiting Scholars to be in residence fall 2014-spring 2015 semesters. KBS will provide Visiting Scholars with desk space in the academic building and family-friendly housing in the Caretakers Cottage on the KBS grounds for visits of one to eight weeks. Visiting Scholars can use their time at KBS to pursue collaborations with KBS and other MSU faculty and to work on their own projects. The KBS environment provides an ideal place for scholars to pursue new and ongoing projects away from the distractions of their home institutions. Visiting Scholars are expected to give a research seminar and otherwise participate in the academic life of the KBS community while in residence.

To apply, first identify and contact a KBS faculty member to serve as a host. Then send to vistingscholars@kbs.msu.edu your CV and a letter explaining the goals of your visit, how you might contribute to the KBS academic environment while in residence, and a range of dates youre available. Indicate any specific needs (research or housing) you may have. Arrange to have your KBS faculty host send a letter to the same address in support of your visit. Preference will be given to applicants with the most potential to contribute to KBS academic life (research expertise, potential for collaborative research, offering a short course or public lecture, etc.). Visiting Scholars should have a Ph.D. or equivalent experience.

Applications for visits for Fall Semester 2014 (October 1-December 19, 2014) are due April 1, 2014, with decisions made by April 30, 2014. Applications for visits for Winter/Spring 2015 (January 1-April 30, 2015) are due June 1, 2014, with decisions made by June 30, 2014. Early applications are encouraged. Applications received after the deadline will be considered on a first-come, first-served basis, given availability. A few opportunities are available for Visiting Scholars before April 30, 2014; please inquire about availability.

Contact vistingscholars@kbs.msu.edu for further information.

– Christopher Klausmeier Kellogg Biological Station Department of Plant Biology Michigan State University Hickory Corners MI 49060

Phone: (269) 671-4330 Web: http://-preston.kbs.msu.edu/ Email: klausme1@msu.edu

Christopher Klausmeier <klausme1@msu.edu>

MissouriBotanicalGarden REU opportunity

The Missouri Botanical Garden is currently recruiting students for a Research Experience for Undergraduates program (REU). This NSF-funded program provides full support for 10 students to work on mentored research projects for 10 weeks during the summer of 2014, from May 19 to July 25.

The MBG REU program focuses on the areas of plant systematics, conservation biology, and ethnobotany. Potential projects for this year include taxonomic description of new species of tropical aroids (Araceae), study of a cryptic species complex in Hypericum, DNA barcoding, pollen analysis and imaging, effects of climate change on threatened species, morphometrics of native Vitis species, edge effects on microclimate and vegetation, economically important Bolivian palms, fruit types and seed characters in Burmeistera (Campanulaceae), pollen characters and pollination syndromes in Anthurium, and population genetics of an endangered species of Polygala. REU students have access to a herbarium of 6.3 million specimens, an excellent botanical library, rich garden collections, a 2,400 acre natural area, and a laboratory with facilities for plant anatomy, microscopy, digital imaging, SEM, and DNA analysis. Students are expected to work full-time on research and participate in weekly lunch-time seminars and workshops, including subjects on botany, conservation, career development, ethics in research, writing, communication skills, and preparation for graduate school, and also participate in a final poster session and symposium.

Students receive lodging near the Garden, an allowance for food and research expenses, plus a $500/week stipend.

The deadline for application is March 30, 2014.

For more information and application procedures please see the program website at http://www.mobot.org/mobot/research/reu/reu.shtml or contact the REU Coordinator at reu@mobot.org , or the PI David Bogler (david.bogler@mobot.org).

David J. Bogler, PhD

Missouri Botanical Garden

P.O. Box 299, St. Louis, MO 63166-0299

Office: 314-577-0831 Email david.bogler@mobot.org

David Bogler <david.bogler@mobot.org>

New RAxML Citation

Dear Community,

When using RAxML please cite the following paper describing the current version from now on, if possible:

A. Stamatakis: "RAxML Version 8: A tool for Phylogenetic Analysis and Post-Analysis of Large Phylogenies". In Bioinformatics, 2014.

http://bioinformatics.oxfordjournals.org/content/early/2014/02/07/bioinformatics.btu033 Thank you very much,

Alexis

– Alexandros (Alexis) Stamatakis

Research Group Leader, Heidelberg Institute for Theoretical Studies Full Professor, Dept. of Informatics, Karlsruhe Institute of Technology Adjunct Professor, Dept. of Ecology and Evolutionary Biology, University of Arizona at Tucson

www.exelixis-lab.org alexandros.stamatakis@gmail.com

New Raccoon Conservation Group

Greetings. I want to make you aware of a new nonprofit conservation organization: *Save the Ringtails*. Please inform those you know about this via email, Facebook (we will have a page soon), etc. - and check our website. Feel free to attach the following to any posts: *Save the Ringtails is a new conservation group for threatened members of the raccoon family:* www.savetheringtails.com Many thanks,

Sam

Dr. Sam Zeveloff, Ph.D. Presidential Distinguished Professor of Zoology Department of Zoology Weber State University Ogden, UT 84408-2505 U.S.A.

telephone: 801 626-6655 fax: 801 626-7445

Websites: http://www.weber.edu/drsamzeveloff/default.html http://www.savetheringtails.com/ szeveloff@weber.edu

OmennPrize EvolutionMedicine 2

The Evolution, Medicine, & Public Health Foundation (http://evolutionarymedicine.org) invites nominations for the Omenn Prize for the best article published in 2013 in any scientific journal on a topic related to evolution in the context of medicine and public health. The $5000 prize is made possible by a generous donation from Gilbert S Omenn. It will be awarded in April 2014 to the first author of the winning article.

Any relevant peer-reviewed article is eligible, but the prize is intended for work that uses evolutionary principles to advance understanding of a disease or disease process. The prize committee will give priority to articles with implications for human health, but many basic science or theoretical articles have such implications.

Nominations should include a copy of the article (if distribution is permitted) or an abstract and link to the article, and a brief nominating statement (<250 words) in the body of an email to OmennPrize@evolutionarymedicine.org. Authors are encouraged to nominate their own articles, but nominations of articles by others are also welcome.

The Prize Committee is chaired by Allen Rodrigo, and its members are Carl Bergstrom and Sarah Tishkoff. Papers by committee members, their students and lab group members are not eligible, and articles by their co-authors or close associates are subject to special conditions.

Nominations will be accepted at OmennPrize@evoluitonarymedicine.org until 5pm, 28 February, 2014 US Eastern Standard Time.

Randolph M. Nesse < http://randolphnesse.com/- > Arizona State University Center for Evolution, Medicine, & Public Health< https://sites.google.com/a/asu.edu/cemph/ > The Evolution & Medicine Review < http://EvMedReview.com > (480) 965 3518 office

rmnesse@gmail.com

Other phylogenetics evolution resources

Dear Evoldir list subscribers,

As an “old school” mailing list user who has had the same email address since 1984, I still think traditional mail lists such as this one can have advantages over newer and theoretically better technologies such as wikis, “chat rooms”, social media services and so on.

However, one of the best parts of a mail list is maintaining a “user culture” that maintains traditions in the group. One example that seems to be slipping away in the evoldir list is having users ask a good question, the members send answers or suggestions to that user and then after a week or so the user replies back to the whole list with a summary of the best replies.

In recent years, several other phylogenetics/evolution groups have become available, but I am not sure any can replace evoldir just yet. Some examples are:

phylobabble.org New site with participation from quite a few very good software developers, such as the RAXML and BEAST developers.

http://treebase.org/treebase-web/home.html Site for depositing phylogenetic trees and the data used to build the trees. Does not have a “discussion group” section.

https://www.researchgate.net/home.Home.html ResearchGate has discussions on phylogenetics, evolution and other topics, but so far tends to be dominated by low level questions and not very well-informed answers.

The user groups for each software package, such as http://groups.google.com/group/beast-users/topics http://groups.google.com/group/raxml/topics are of course limited to discussion only of the use of one package each.

http://bodegaphylo.wikispot.org/ The TreeThinkers group seems to have a very good thing going with their wiki, but I am not sure it has the “critical mass” to really expand, and it also seems to be designed specifically for this group’s own phylogenetics workshops and not inviting public input.

http://www.mendeley.com/groups/726401/-phylogenetics-discussion-group/ Mendeley seems to have a lot of potential for serving discussion groups, but there are several phlylogenetics and evolution groups in it, and none of them are so far getting the critical mass needed to become the “go to” place for phylogeny discussions.

If I have missed what any of you consider to be one of the best places to share phylogenetics and evolution discussions, please add to my list.

Brian Foley, PhD HIV Databases http://-www.hiv.lanl.gov btf(_at_)lanl.gov

“Foley, Brian T” <btf@lanl.gov>

Phylogenies from vcfs

Can anyone point us towards software for making phylogenetic trees from .vcf files? We are aware of SNPhylo, but it is not working for us.

Thanks, Paul

Paul Marjoram Research Assoc. Prof. Division of Biostatistics U.S.C., Dept. of Prev. Med. 2001 N. Soto St., SSB 202V, MC-9234 Los Angeles CA 90089-9234 pmarjora@usc.edu 323-442-0111

pmarjora@usc.edu

Pyrenees VolFieldAssist EvolBiol

Field assistants summer 2014: Volunteer positions in evolutionary biology

Nick Barton's group at the Institute of Science and Technology (IST) Austria requires volunteers to assist with field work on plant speciation in the Pyrenees (Spain) this coming summer (June - July).

The project: We are studying the evolutionary dynamics underlying species diversification in the genus Antirrhinum (snapdragons). We are using ecological, molecular and population genetic tools to investigate the dynamics of speciation in hybrid zones between two species with different flower colours. At the field site, our main goal is to build a long-term pedigree for the population, which involves mapping the location of individual plants (GPS), tagging and sampling them for leaves and flowers, measuring quantitative traits and processing leaves for later DNA extraction. There may also be opportunities to be involved other tasks such as work we are doing on plant-pollinator interactions. Most of the work is outdoors, however we do spend some time indoors processing samples. The work is highly team orientated. This is a great opportunity for anybody looking to obtain experience in field work relating to evolutionary biology, plant ecology and plant-animal interactions. You will also be part of a large multidisciplinary team including researchers from IST Austria (Vienna), John Innes Centre (Norwich, UK) and the University of Toulouse.

The field site is located near Ripoll in a beautiful part of the Pyrenees of Northern Eastern Spain (Catalonia). We stay in comfortable apartments overlooking a picturesque valley, with close access to hiking trails and small villages. All food, accommodation and travel (within Europe) are covered. However, we cannot offer any further stipend.

For these positions we are looking for hard working and enthusiastic biology students with a strong interest in working outdoors with plants. You must also be comfortable working as part of a team. Experience with field-based projects and plants is preferred but not essential.

We require assistance between early June and the end of July. Length of stay is flexible but a minimum stay of 3 weeks is required.

How to apply? Please send by the closing date of 14th April, a statement of your background, CV, why you are interested and the length of time you would be available via email to:

david.field@ist.ac.at

Dr. David Field Postdoctoral Fellow Barton Group IST Austria AM Campus 1 Klosterneuburg 3400 Phone: +432243 9000 3008 Web: http://ist.ac.at/-research-groups-pages/barton-group/team/david-field/ david.field@ist.ac.at

Question Pippin size selection service

Dear EvolDir members,

As part of a project investigating the population genomics of the Spadefoot Toad, we are looking for a facility within the USA that offers restriction digest fragment size selection services by Pippin Prep or BluePippin.

If anyone can recommend a good, reliable service we would be very grateful.

Best regards,

Heidi Seears

Postdoctoral Research Associate, Rice lab, Lehigh University, PA, USA.

heidiseears@lehigh.edu

Heidi Seears <has313@lehigh.edu>

Question phylogenetic comparative methods

Dear EvolDir community,

I am a biological anthropologist working on the functional morphology of

human and non-human primates. I am interested in learning how to use phylogenetic comparative methods to analyse morphological traits. I deal with continuous traits that may span from articular and/or diaphyseal linear dimensions, indices and cross-sectional geometric properties.

In particular, I need to learn how: 1) to add fossils to an already

built phylogenetic tree (given that primate phylogenies can be already found on the 10kTrees website); 2) how to use the tree/trees to compare

the morphological traits I collected.

I was advised by some colleagues to look into the software Mesquite for the first task and into R for the second one. I have been trying to learn by myself how to solve the problem but I have failed so far.

I was wondering if anybody is willing to give me advises as for how to perform these analyses and/or collaborate on the papers where they are necessary.

Any help is welcome!

Best regards,

Damiano Marchi

Damiano Marchi <damiano.marchi@unipi.it>

SmithsonianTropicalResInst REU

We are calling for applicants for a summer research program for undergraduates at the Smithsonian Tropical Research Institute in Panama. The research projects comprehend different fields of sciences including evolutionary biology and population genomics.

Paola Gómez García, MSc

Smithsonian Tropical Research Institute - Research Experience for Undergraduates (STRI-REU) summer program 2014.

2014 Program Dates: Jun. 9-Aug. 15 Application deadline: March 30

We are currently recruiting applicants for the *Research Experience For Undergraduates in Integrative Biology* (REU-STRI) program 2014 (http://www.stri.si.edu/reu/english/). This 10-week summer program is directed to 3rd or 4th year undergraduates enrolled in the traditional life science departments (e.g. biology, ecology, botany, etc.), as well as, engineering, mathematics, and computer science departments. We also encourage applications from groups under-represented in the sciences. Applicants must be US or Latin American citizens or permanent residents (See eligibility criteria here http://www.stri.si.edu/reu/english/elegibility.php). This unique internship opportunity offers airfare, housing, food allowance, and a $5,000 USD stipend. If you would like to apply, you should first browse through the list of potential mentors and project descriptions and identify up to three distinct projects/mentors that align with your own scientific interests here (http://www.stri.si.edu/reu/english/REU%20projects%20and%20mentors%20summary_2014.pdf). *There is no need to contact the mentor before submitting you application.*Interested students must fill out the application form found here (http://www.stri.si.edu/reu/english/REU_internship%20application%20form.pdf). All application materials, with the exception of the recommendation letters, must be compiled into a single electronic pdf file. The file should be named as follows: SURNAME_FIRST INITIAL_REU.pdf and sent to strireu@si.edu

For further questions about the application process please contact us:

strireu@si.edu or check our website (http://www.stri.si.edu/reu/english/) and program flyer: http://www.stri.si.edu/reu/english/STRIInternshipFlyer2014.pdf Phone: (507) 212-8281 or from USA: (202) 633-4700 x28281

Paola Gomez <paolaonca@gmail.com>

Software Bayesian analysesofMacroevolution BAMM

Evoldir community:

We announce the release of BAMM and BAMMtools, a Bayesian framework for the analysis of speciation, extinction, and trait evolution on phylogenetic trees (www.bamm-project.org). BAMM is oriented entirely towards detecting and quantifying heterogeneity in evolutionary rates. It uses reversible jump Markov chain Monte Carlo to automatically explore a large number of candidate models of lineage diversification and trait evolution. BAMM is a command line program written in C++.

We have also created BAMMtools, an R package for the analysis and visualization of BAMM output. The package is available for installation via CRAN or through the project website.

BAMM / BAMMtools functionality includes a number of novel methods for visualization and analysis of complex macroevolutionary dynamics, including:

- Inference on evolutionary rate variation through time and among clades - Visualization of dynamic rates on phylogenetic trees with BAMMtools - Estimation of credible sets of macroevolutionary rate configurations - Estimation of the "best" (maximum a posteriori probability) macroevolutionary rate configuration - Bayes factors for inferring numbers of evolutionary rate regimes on phylogenies - Summarize marginal distributions of evolutionary rates for individual clades - Analyze diversification rates with incomplete and phylogenetically non-random taxon sampling

The documentation includes a graph gallery illustrating some of data visualizations and analyses that can be done "out of the box" with BAMMtools (www.bamm-project.org/bammgraph.html). A conceptual discussion how the BAMM framework differs from stepwise AIC-based approaches can be found at http://bamm-project.org/rateshifts.html . A complete description of the general model that underlies BAMM (and a performance evaluation) is available at:

** Rabosky, DL. 2014. Automatic detection of key innovations, rate shifts, and diversity-dependence on phylogenetic trees. PLoS ONE.http://www.plosone.org/article/info%3Adoi%2F10.1371%2Fjournal.pone.0089543
*** If you previously installed BAMM or BAMMtools, please download the latest versions. The code for both has changed during the past month and we cannot guarantee compatibility.

~Dan Rabosky

Dan Rabosky <drabosky@umich.edu>

Software CLUMPAK

A few days ago Jennifer Ovenden has posted a question on whether anyone has a suggestion for a user-friendly way of inputting data into CLUMPP and DISTRUCT. Together with colleagues, I have developed CLUMPAK, a web-server that takes as input the results of STRUCTURE runs for a range of K values, and with any number of replicates for each K, and provides a full pipeline for clustering, summarizing, and visualizing these results. The Evanno method is also implemented by CLUMPAK. Our paper will be submitted in the next few weeks. Meanwhile, please feel free to try our web-server at http://clumpak.tau.ac.il. A manual is available online.

If you have any questions, comments, or suggestions, don't hesitate to contact me. Your feedback would be highly appreciated.

Best, Naama Kopelman

Naama M. Kopelman Tel Aviv University <naamakop@post.tau.ac.il>

naama.kopelman@gmail.com

Software LargeScale BayesianTreeInference

Dear evoldir members,

we introduce ExaBayes, a user-friendly software package for large-scale Bayesian tree inference. ExaBayes provides the most widely used evolutionary models and implements proposals similar to (and as efficient as) MrBayes.

ExaBayes allows for efficient parallel analyses on any multi-core machine (only prerequisite: MPI). The focus of ExaBayes lies on scalability: we managed to compute a tree from a genome-size alignment (200 taxa, 2*10E8 characters) using up to 32,000 CPU cores. Furthermore, we successfully tested our code on alignments with up to 10,000 partitions.

For further information, please visit : http://exelixis-lab.org/web/software/exabayes/ Best regards, Andre Aberer

PreDoc (Bioinformatics) in the Exelixis Lab, Heidelberg Institute for Theoretical Studies

andre.aberer@googlemail.com

Software bPTP GMYC

Dear evoldir members,

We introduce bPTP -a Bayesian implementation of the PTP model for species delimitation, and a web server for PTP and the GMYC model. bPTP is an updated version of the original maximal likelihood PTP (maximal likelihood PTP search result is part of the bPTP results), it adds Bayesian support (BS) values to delimited species, it is now both available as a standalone version and as a web server. Our web server also features an interface for the original R implementation of the GMYC model authored by Tomochika Fujisawa and Tim Barraclough

For further information, please visit:

http://species.h-its.org/ Best,

Jiajie Zhang

PhD student in the Exelixis Lab, Heidelberg Institute for Theoretical Studies

bestzhangjiajie@gmail.com

bestzhangjiajie@gmail.com

Software pophelper R package

I work with population genetics and population structure of honey bees. Therefore I had been writing some R scripts for my personal use and someone recently suggested that I make it into a package that can be shared. Therefore I have recently put together some useful stuff into an R package called pophelper.

Basically, this R package does what STRUCTURE HARVESTER does. pophelper works with structure and TESS output files. I think it may be useful for people working with STRUCTURE, TESS and R. This package requires some basic R skills to use. pophelper can be used to tabulate runs, summarise them, perform Evanno method, export to CLUMPP format, generate barplot figures etc.

The package can be installed from github for the moment. Once a stable version is established, it will be uploaded to CRAN.

https://github.com/royfrancis/pophelper I would very much appreciate if you could share this with the community. I am also hoping people are willing to give this a try and provide some feedback/comments/suggestions/criticisms etc. Feel free to contact me at roy.m.francis@outlook.com if you run into any issues or have any questions etc.

Sincerely,Roy Francis

Roy Francis <roy.m.francis@outlook.com>

SouthAfrica Volunteers SmallMammalEvolution

Several volunteers needed from July / August 2014 onwards

as field assistants for the project:

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

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

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

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

Work of volunteer field assistants: Trapping, marking and radio-tracking of striped mice; direct behavioral observations in the field. Volunteers will also see how blood samples are collected for physiological measurements. Volunteers are expected to help with maintenance of the research station (water pump, solar power, etc.).

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

Costs: Students have to arrange their transport to the field site themselves. Per month, an amount of Rand 1300 (around 180 US$, 110 Euro) must be paid for accommodation at the research station. Students must buy their own food etc in Springbok (costs of about R 3000, approx. 360 US$ or 250 Euro/month). Including extras (going out for dinner; shopping), you should expect costs of about 600 US$ / 450 Euros per month. Students get an invitation letter which they can use to apply for funding in their home country.

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

When and how long: At the moment we are looking for several volunteers starting in July / August 2014. Volunteers are expected to stay at least three months, but longer periods of up to 6months are preferred.

How to apply? Send a short motivation letter stating why and for which period you are interested and your CV via email to succulent.karooo.research.station@kabelbw.de.

More information under

http://stripedmouse.com/site1_3_5.htm http://www.youtube.com/watch?v=w6rvF5XrVn0&list=UUd12oFYqs5OobiiKMhDnFtw&index=1

Contact via e-mail: succulent.karoo.research.station@kabelbw.de

Succulent Karoo Research Station

a registered South African non-profit organization

Dr. Carsten Schradin (Director)

South Africa

WORKING AS A FIELD ASSISTANT IN GOEGAP NATURE RESERVE

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

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

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

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

— / —

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

Structure Fst question

dear all,

I'm working on population genetics of reef fishes; I've used microsatellite loci to detect population structure and I've found significant Fst value among different sampling locations. However, when running STRUCTURE I failed finding any partition among samples. Does anybody has a clue about why is this happening??

Thank you very much

Jessy

Jessy Castellanos Gell Genética para la Conservación Centro de Investigaciones Marinas Calle 16 No.114 entre 1ra. y 3ra. Miramar, Playa, Ciudad de la Habana CP 10300. CUBA. Tel.(537)203 06 17

jessy@cim.uh.cu

jessy@fbio.uh.cu jessy@fbio.uh.cu

WageningenU VolFieldAssist AvianPhenotypicVariation 2

Volunteer field assistant position to study the maintenance of phenotypic variation in great tits in the Netherlands We are looking for a research assistant for the upcoming breeding season to join our project investigating sexual selection and reproductive investment in great tits (Parus major). The research will be conducted in the Netherlands near Arnhem and will last throughout the breeding season, from April until the end of June. Our project investigates the potential of individual differences in mate choice and reproductive investment to maintain phenotypic variation in great tits. During the breeding season we will study parental investment of the great tits breeding in the study area in relation to plumage characters and partner quality. The project is based at the Wageningen University and is in collaboration with the Netherlands Institute of Ecology. The volunteer will help the PhD student working on the project in the field. The work will involve monitoring the breeding birds in the study area, cross fostering of chicks, making video and audio recordings of the nest and banding the offspring.

We ask:

- Candidates should preferably have a BSc or higher in biology, behavioural ecology or a similar qualification

- Ability to work in a team, good social and organizational skills

- Willingness to work long days and if needed during weekends

- Experience in handling and banding birds preferred

- Driving license

- Proficient level of English language

We offer: This is a voluntary position but we may be able to offer travel and accommodation costs to the right candidate.

For further information, please contact Lies Zandberg (lies.zandberg@wur.nl) or Dr. Camilla Hinde (camilla.hinde@wur.nl) or check the website of the research group (www. bhe.wur.nl).

Application: Applications consisting of a CV and a motivation letter should be sent to Lies Zandberg (lies.zandberg@wur.nl)

lies.zandberg@wur.nl

PostDocs

AMU Poznan ModellingMHCEvolution

PostDoc:AMU_Poznan.ModellingMhcEvolution

Evolutionary Biology Group of Professor Jacek Radwan at Adam Mickiewicz University, Poznan, is looking for a Post-Doc in an NCN-funded project investigating evolution of MHC copy number using both empirical and theoretical approaches. The post-doc will perform computer simulations exploring alternative evolutionary mechanisms potentially shaping the number of expressed MHC genes.

The candidate should hold PhD degree in biological sciences, computer sciences or mathematics and should have significant achievements in theoretical modelling of biological processes, documented by publications in international scientific journals. Competence in computer programming is essential.

The employment is offered for three years, starting ideally in May 2014, but it is negotiable. Application deadline is 1st April 2014. Further information can be obtained from the project leader via email: jradwan@amu.edu.pl

Prof. Jacek Radwan Institute of Environmental Biology Adam Mickiewicz University ul. Umultowska 89 61-614 Poznan

j.w.radwan@gmail.com

AMU Poznan UEA CardiffU MHCEvolutionGuppy

Postdoc: AMU_Poznan_UEA_CardiffU.MHCEvolutionGuppy

Post-doc position in evolutionary biology is available for three years, preferably starting from 1st June 2014 in a project “Testing new MHC allele advantage in semi-natural populations of the guppy, Poecillia reticulata”. This collaborative project is led by Professor Jacek Radwan (Adam Mickiewicz University, Poznan), Dr Cock van Oosterhout (University of East Anglia) and Dr Joanne Cable (Cardiff University, School of Biosciences), and is funded by Polish Science Centre (NCN).

Genes of the Major Histocompatibility Complex (MHC), involved in parasite recognition, are crucial for the adaptive immune response in vertebrates. While theories explaining maintenance of MHC polymorphism have been proposed decades ago, empirical tests of some of the most influential hypotheses are scant. Most notably, predictions about frequency-dependent selection (i.e. the hypothesis that rare MHC alleles should be selected for because fast-evolving parasites will adapt to evade immune recognition by common MHC alleles) have not been rigorously tested. The aim of this project is to test crucial predictions of this hypothesis using semi-natural populations of the guppy, Poecilia reticulata. The project will be based on Tobago and will use mesocosm setups to trace frequencies of MHC alleles, and infection levels associated with them, over several generations.

The post-doc will be will be responsible for running the field experiment, which will imply his/her stay at Tobago during the first year of the project and recurrent trips in the second and third year. He will collaborate with other team members and with a PhD student who will be responsible for molecular work.

The candidate should hold PhD degree in biological sciences and should have significant achievements in evolutionary biology, ecology as documented by publications in international scientific journals. S/he should be able to work well as part of a team, have good planning, analytical, statistical and writing skills, and should be ready to work hard in the field. Experience in field work will be considered an advantage.

Further information can be obtained from the project leader via email: jradwan@amu.edu.pl

j.w.radwan@gmail.com

ANU Canberra 2 PopulationGenomics

Postdoctoral positions in population and landscape genomics at the Australian National University, Canberra (http://cba.anu.edu.au/opportunities/employment/-anu-postdocs-genomic-signatures-adaptation-climatic-variation)

We are seeking two postdoctoral researchers who will employ evolutionary genomics to understand adaptation to climate variation. Projects will focus on rainforest lizards and foundation species of Eucalypts, with relevance to conservation and restoration strategies.

We intend to appoint 2 postdoctoral researchers to investigate genomic signatures of adaptation to climatic variation. One appointee will focus on adaptive divergence of populations of lizards in peripheral vs central rainforest isolates, and the other on landscape genomics of two Eucalyptus species (E. melliodora) and E. marginata that are the focus of restoration efforts. Experience in bioinformatics and population genomics inference is required, as is evidence of ability to conduct and publish high quality research.

Further information on the projects can be found at http://biology.anu.edu.au/craig_moritz/ (lizard project) and borevitzlab.anu.edu.au (Eucalyptus project). Appointees will join large dynamic labs and interact broadly through the Centre for Biodiversity Analysis (cba.anu.edu.au) and the new Centre for Plant Energy Biology.

Enquiries from highly qualified candidates should be sent to craig.moritz@anu.edu.au (lizard project) and Justin.borevitz@anu.edu.au (Eucalyptus project). Each appointment will be for 2 years at ANU academic level A8 ($79,294 p.a. plus benefits).

To apply please visit http://jobs.anu.edu.au/-PositionDetail.aspx?p=3828 Please submit a CV, including names of three referees, and a letter outlining your relevant experience. Applications will be reviewed from April 9th and the positions will remain open until filled.

Claire Stephens Coordinator | Centre for Biodiversity Analysis

Research School of Biology | Evolution, Ecology & Genetics Gould Building (Bldg 116 Rm 223), Daley Road | The Australian National University | Canberra ACT 0200 T +61 2 612 59492 | E claire.stephens@anu.edu.au | W cba.anu.edu.au

Please note: monday - wednesday only

Claire Stephens <claire.stephens@anu.edu.au>

AarhusU PopulationGenetics

1-year Postdoc position in population genetics at the Centre for Biocultural History, Aarhus University, Denmark

The Bioinformatics Research Center, Aarhus University invites applications for a 1-year postdoc in population genetics at the new interdisciplinary Centre for Biocultural History. The project will focus on demographic inference and data-mining in population-wide genetic data concerning relationships within and between parts of Denmark and explore whether human movement such as urbanization is visible from genetic data. We are seeking a candidate with excellent skills in (1) population genetics and data mining, and (2) a strong interest in human evolutionary studies. The project is based on genome-wide SNP data from 800 Danish high school students combined with data on family origin and background, but the candidate is encouraged to develop specific projects of her or his own choice as long as they are include mining this data and are conducted in collaboration with other members of the group.

The postdoc will be a member of the newly established Centre for Biocultural History, a highly interdisciplinary team seeking anthropological, archaeological, genomic, ecological, and historical insights into human evolution.. The project will be supervised primarily by Associate Professor Thomas Mailund (Bioinformatics Research Centre) and Prof. Mikkel Heide Schierup (Bioinformatics Research Centre), together with Prof. Peter C. Kjærgaard (Department of Culture and Society). The candidate will join researchers at the Bioinformatics Research Center and collaborate closely with the other members at the Centre for Biocultural History.

Candidates should have obtained a university degree in genetics or other related fields. The successful candidate must document a strong research record as well as a broad knowledge of the field of population genetics.

For more information please contact Associate Professor Thomas Mailund (mailund@birc.au.dk) or Professor Mikkel H. Schierup (mheide@birc.au.dk). For information about the Centre for Biocultural History see bioculture.au.dk or contact Professor Peter C. Kjaergaard (Kjaergaard@cas.au.dk), and for the Bioinformatics Research Centre see birc.au.dk

Please submit application including CV and letters from or names of at least two references to Mikkel H. Schierup (mheide@birc.au.dk) as a single pdf file

Deadline for applications: 15 March 2014

Mikkel H. Schierup Bioinformatics Research Center, Aarhus University, CF Mollers Alle Building 1110, 8000 Aarhus C Denmark Ph: +45 8715 6535 Email: mheide@birc.au.dk http://www.birc.au.dk/ ˜ mheide Mikkel Heide Schierup <mheide@birc.au.dk>

Amsterdam Evolution Mutualism

Post-doc in Evolutionary Biology / Ecology / (social) Microbiology for ERC funded project: Amsterdam Netherlands

Applications are welcome from early-career scientists with an outstanding track record in the field of Evolutionary Biology / Ecology / Microbiology.

In an ERC funded project, the Kiers research group at VU University, Amsterdam is using microbial systems to explore how cooperation evolves and is stabilized. We are interested in the emergence of microbial "Biological Markets" in nature (Werner et al. PNAS 2014). We use small-scale tracking, experimental evolution and phylogenetic analysis to identify how mutualisms respond to radical changes in their environment.

See http://www.tobykiers.com/ Our aim is to identify the evolutionary selection pressures that shape symbiont communities and to identify approaches to conserve mutualisms in the face of environmental change. The research group emphasizes an interdisciplinary approach, integrating evolutionary theory, with the exploitation of cutting-edge empirical techniques While we primarily focus on mycorrhizal fungi and nitrogen-fixing symbionts, we are open to exploring new model systems.

Candidates should hold a Ph.D. and are expected to have a solid track record in the field of evolutionary biology, (social) microbiology and/or ecology. Particular preference will be given to those candidates introducing innovative methodologies (molecular, phylogenetic, statistical, theoretical, experimental) to the group.

The position is flexible with regards to approach and methodologies. The post is offered for an initial term of one year, with the possibility of extension. The post covers consumables and access to core facilities. There is flexibility over starting dates, but the successful applicant is expected to take up a post by May, 2014.

Applications (CV, a letter of motivation, and names of two references) should be sent to toby.kiers@vu.nl. Applications should be received before May 30th, 2014.â

toby.kiers@vu.nl

AuburnU MyriapodPhylogenetics

Auburn University Post-Doctoral Associate Position Department of Biological Sciences, College of Sciences and Mathematics

A post-doctoral position in myriapod phylogenetics with an emphasis on diplopod phylogenomics is available in the lab of Jason Bond in the Department of Biological Sciences at Auburn University.

The focus of work in our lab is the study of arthropodevolutionary diversification at multiple hierarchical levels. This 2-year post-doctoral research associate position will be supported by an NSF-funded project that has as its goal the reconstruction of millipede family level relationships primarily using genomic data. The project will include phylogenomics, classical comparative morphology, and extensive bioinformatics analyses employing next generation sequencing data.

The ideal candidate will have a strong background in arthropod systematics (preferably myriapods), bioinformatics, phylogenetics, and standard molecular lab and field collecting techniques. The position is available for two years and includes benefits and a competitive salary; the preferred start date is June 2014. To apply please email a CV, letter of introduction, and contact information for three references to jbond@auburn.edu.

Dr. Jason E. Bond Auburn University Department of Biological Sciences and Auburn University Museum of Natural History Rouse LSB 101 Auburn, AL 36830 USA

phone: 334-844-8713 jbond@auburn.edu

jeb0037@auburn.edu

AustNatlU ReefEvolutionaryGenomics

The Reef Future Genomics Consortium (ReFuGe) is an initiative of the Great Barrier Reef Foundation that endeavours to leverage biomolecular techniques to improve the management and resilience of coral reef ecosystems.

The Sea-quence project is an undertaking of the ReFuGe Consortium and is aimed at generating reference genomic and transcriptomic sequences for ten coral species, their associated microbial communities, and three strains of endosymbiotic algae (dinoflagellates). Three “Great Barrier Reef Foundation Fellowships”, including this position, are being created at the Australian National University and the University of Queensland, to collaborate in the analysis and interpretation of these data. This position will take the lead role with respect to genome-scale analysis of the ten coral genomes and is expected to collaborate closely with the two other groups working on the microbial and dinoglagellate sequences.

This is a fixed term appointment for 3 years. Applicants should possess a PhD in molecular biology, microbiology, genomics, bioinformatics or a related discipline, with significant data-management, computational and statistical components. They should have at least three years’ full-time experience (during the PhD or otherwise), or its equivalent, in a relevant area of molecular biology, microbiology, genomics, bioinformatics or a related field. Experience in scientific programming and scripting is essential. A demonstrated high-level ability to write scientific papers in clear, grammatically correct English is also essential.

Role Statement Under broad direction the Postdoctoral Fellow / Research Fellow will:

1. Coordinate with the sequence provider regarding the data being supplied e.g. biological source, DNA extraction and library preparation methods, sequencing platform and protocols and initial quality control. 2. Establish and carry out computational and bioinformatic procedures including assembly, structural annotation (e.g. repetitive elements) and functional annotation (e.g. genes, gene families, small and non- coding RNAs, pathways) for the coral genomic data. 3. Conduct phylogenomic analysis of the coral genomic data, including a search for gene family expansions 4. Conduct tests for adaptive selection and codon bias based on the coral data. 5. Collaborate with senior staff within the Sea-quence project to assist in preparing research proposals and publications. 6. Assist with supervision of research students whist maintaining high academic standards in all education, research and administration endeavours. 7. Actively contribute to all aspects of the operation of the ReFuGe consortium. 8. Comply with all ANU policies and procedures, and in particular those relating to work health and safety and equal opportunity. 9. Undertake other duties as required consistent with the classification level of the position.

The University actively encourages applications from Aboriginal and Torres Strait Islander people. For more information on employment opportunities, contact our Indigenous Employment Consultant on indigenous.employment@anu.edu.au ANU values diversity and inclusion and believes employment opportunities must not be limited by socio-economic background, race, religion or gender. For more information about staff equity @ ANU, visit http://hr.anu.edu.au/-staff-equity . For further information please contact Dr Sylvain Foret, Phone: 02 6125 0563, Email: sylvain.foret@anu.edu.au.

To apply, visit: http://jobs.anu.edu.au/-PositionDetail.aspx?p=3438 sylvain.foret@anu.edu.au sylvain.foret@anu.edu.au

Belgium CichlidSpeciation

Deadline extended to March 31st 2014

The Royal Belgian Museum for Natural Sciences is looking for a: Post doctoral researcher April 2014 - February 2018

Summary :

The successful candidate will work in the framework of a 4 year project financed by the Belgian science policy, Belspo. Belspo Brain project: “Behavioral and genomic aspects of cichlid speciation; GENBAS - GENetic Basis for Speciation”. The proposal’s two main objectives are to characterize the genomic differentiation that drives the speciation process, and to verify whether/and to what extent the same genomic changes are involved in to maintain the âintegrity’ of the gene pools of the resulting sister species.

We intend to address this question through a dual approach: one that compares the genome wide differentiation within and between sister species, and one that explores the genetic basis of the behavioural aspects (display and acoustic signalling during courtship) that allow female fishes to differentiate between con-specific and hetero-specific males. For this purpose, we have selected the Lake Tanganyika cichlid genus Ophthalmotilapia. More specifically, our experimental design involves the combination of four studies: (1) to explore behavioural and acoustic aspects of mate pairing during con- and hetero-specific interactions among species; (2) to investigate differential gene expression in the female brain associated with pairing behaviour during con- and hetero-specific interactions; (3) to elucidate genetic differences within and among relatively recently diverged and hybridizing species at a genome-wide level; and (4) to examine whether the part of the genome that is expressed during mate recognition in the brains of the female cichlids correspond with one or more of the genomic areas with increased differentiation within or among these species. The project is a collaboration between Erik Verheyen (RBINS), Jos Snoeks (RMCA), Jeroen Van Houdt (KULeuven), Eric Parmentier & Pascal Poncin (ULiège).

Tasks :

- Coordination of the project: organisation of meetings, coordinate the different studies of the project partners, reporting, keeping time lines - Implementation of Next Generation Sequencing (NGS) methods: Genotyping by Sequencing, RNA sequencing - Data-analysis NGS data, Integration of behavioral and accoustic data with genomic results - Supervision and co-operation with partner researchers, students - Publication of results

Profile :

Education : PhD in sciences: Biology, Biotechnology, Genomics Experience : 3-10 years of experience in independent research, experience in genetic/genomic research

Technical competences :

Experienced in molecular genetics: (Sanger & NGS) sequencing, microsatellites Experienced in NGS methods and NGS data analysis Experienced with population genetics and phylogeographic methods Languages: Dutch and/or French, English

Generic competences :

Independent, people management, project management, coordination, co-operation, good interpersonal skills, prepared to travel if required

Extra :

Project coordination Programming skills (perl, python, R, â) Experience working with fish experiments

Offer:

Full time position (maximum 4 years) Remuneration according to education and experience Free public transport (in Belgium) between your place of residence and the Institute

Application

Send (in a single pdf file) an application letter and your CV with contact information of two references before March 31st 2014 to:

Erik.verheyen@natuurwetenschappen.be

Edinburgh 2 LepidopteraGenomics

Two exciting positions to develop database resources for Lepidoptera Genomes. Based in Edinburgh and collaborating with Cambridge and York

POSITION ONE: The Lepidoptera Genome Biologist (LGB) https://www.vacancies.ed.ac.uk/pls/-corehrrecruit/erq_jobspec_version_4.jobspec?p_id=-026852 http://tinyurl.com/blx026852 POSITION TWO: The Lepidoptera Genome Database Bioinformatician (LGDB) https://www.vacancies.ed.ac.uk/-pls/corehrrecruit/erq_jobspec_version_4.jobspec?p_id=026851 http://tinyurl.com/blx026851 Brief advert versions

Bioinformatician (Lepidoptera Genomic Biologist)

Vacancy Ref: : 026852 Closing Date : 01-Apr-2014 Contact Person : Mark Blaxter mark.blaxter@ed.ac.uk £30,728 - £36,661

The Blaxter laboratory, in close collaboration with Dr Chris Jiggins of Cambridge University and Dr Kanchon Dasmahapatra of York University, is developing a public database that will ultimately include all lepidopteran (butterfly and moth) genomes, using the ENSEMBL model. We are seeking a skilled genome biologist, possibly with specific experience in arthropod genomics, to join the project team. The goal of the project is to establish a local ENSEMBL database, collate raw and assembled data, and to deliver resources, such as methods for community annotation, globally. The post will be based in Mark Blaxter's bioinformatics group in Edinburgh alongside other bioinformaticians working on lepidopteran genomics, nematode genomics and other projects.

Applicants must have a strong track record in genome biology of arthropods or similar taxa (including training or experience to PhD level or equivalent). The post is a bioinformatics one, and so experience with Linux or Unix operating systems, and in the integration and analysis of next-generation sequencing data, preferably in arthropods, is also strongly desirable.

The post is fixed term for 36 months

Bioinformatician (Lepidoptera Genomic Databasing)

Vacancy Ref: : 026851 Closing Date : 01-Apr-2014 Contact Person : Mark Blaxter mark.blaxter@ed.ac.uk

£30,728 - £36,661

The Blaxter laboratory, in close collaboration with Dr Chris Jiggins of Cambridge University and Dr Kanchon Dasmahapatra of York University, is developing a public database that will ultimately include all lepidopteran (butterfly and moth) genomes, using the ENSEMBL model. We are seeking a skilled bioinformatician, possibly with specific experience in arthropod genomics, to join the project team. The goal of the project is to establish a local ENSEMBL database, collate raw and assembled data, and to deliver resources, such as methods for community annotation, globally. The post will be based in Mark Blaxter's bioinformatics group in Edinburgh alongside other bioinformaticians working on lepidopteran genomics, nematode genomics and other projects.

Applicants must have a strong track record in bioinformatics (including training or experience to PhD level or equivalent), and experience of working with Linux or Unix operating systems. Experience in the integration and analysis of next-generation sequencing data, preferably in arthropods, is also essential.

The post is fixed term for 36 months

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

Chris Jiggins Reader in Evolution and Biological Diversity Department of Zoology University of Cambridge Tel: (+44)(0)1223 769021 Mob: (+44)(0) 7549-524-481 http://www.heliconius.org/- http://heliconius.zoo.cam.ac.uk/ Fellow of St John's College, Director of Studies in Biological Sciences Cambridge, UK. CB2 1TP

cj107@hermes.cam.ac.uk

Edinburgh PlantConservation

Post-Doctoral Research Assistant: Conserving the Flora of Socotra Full-time, 18 month fixed term appointment, based in Edinburgh Starting salary Â£26,000 (Band D)

The Royal Botanic Garden Edinburgh (RBGE) is one of the world's leading research orientated Botanic Gardens, and is located in a UNESCO World Heritage city famed for its scientific innovation and cultural interest.

Applications are invited for the above vacancy within the Centre for Middle Eastern Plants at The Royal Botanic Garden Edinburgh. This is an 18 month fixed term appointment with start date on 1 October 2014. Key responsibilities will include:

* Generation and analysis of phylogenetic sequence data for specified plant genera; * Contribution to the inclusion of phylogenetic diversity data into conservation strategies; * Authorship of reports and publications.

This position is part of the Leverhulme Trust funded project 'Conserving the Flora of Socotra: integrating evolution into conservation' based at the Centre for Middle Eastern Plants (www.cmep.org.uk). The Socotra Archipelago has a diverse and fascinating flora, characterized by unique plant species of which ca. 35% are endemic, which lead to its' designation as a UNESCO World Heritage Site in 2008. This project has two main themes: (a) the generation of dated phylogenies for a range of small plant genera with significant numbers of endemic species on Socotra, in order to identify the source, time, mode and tempo of insular endemic species evolution, and (b) sequencing each of the ca. 850 species and applying phylogenetic diversity statistics in an explicit spatial context for the design of Protected Areas, alongside distribution, ethnobotanical and functional trait data. Both themes will be directly linked to long-term conservation strategies. The successful applicant will contribute significantly to the first of these themes, with theoretical and developmental input into the wider project. This will be an opportunity to deliver and apply high quality science to a conservation program of global significance.

Applicants should have a PhD in plant science, conservation or related discipline. Demonstrable experience in phylogenetic data generation and analysis, including phylogenetic dating and meta-analyses, will be required. You should have a dynamic and collaborative approach to research, excellent attention to detail, and a strong interest in plant evolution and conservation.

Informal enquires can be made to Dr Alan Forrest (A.Forrest@rbge.org.uk).

Application details can be found at: http://www.rbge.org.uk/about-us/vacancies#vacancy7 Dr Alan Forrest Researcher & Project Manager Centre for Middle Eastern Plants Royal Botanic Garden Edinburgh | 20a Inverleith Row | Edinburgh EH3 5LR | Scotland | UK

Website: www.cmep.org.uk Email: A.Forrest@rbge.org.uk Telephone: +44(0)131 248 2967

Alan Forrest <A.Forrest@rbge.ac.uk>

FieldMuseum Chicago BiodiversityGenomics

Biodiversity Genomics Postdoctoral Research Scientist

The Field Museum of Natural History in Chicago, Illinois, USA is searching for a postdoctoral scientist with expertise in Next Generation Sequencing (NGS) methods and analysis. A Ph.D. in bioinformatics, evolutionary genomics, or a related field is required.

The position will be based in the museum's Pritzker Laboratory, a core multiuser facility dedicated to genetic studies of the world's biodiversity. At any given time there are roughly 30 scientists working in the lab on a wide range of taxa and evolutionary questions. While research to date has emphasized Sanger sequencing, we are moving rapidly into new areas of genomic analysis, and with the acquisition of an Illumina MiSeq system we are now searching for someone with relevant expertise to enhance our genomics research capabilities.

The ideal candidate will have experience in bioinformatics and NGS, as well as the organizational and interpersonal skills needed to assist and collaborate with a diverse group of scientists. We are especially interested in candidates with expertise in some or all of the following: genome assembly and analysis, reduced-representation genome sequencing (RAD, GBS, etc.), and RNA-seq.

The laboratory is overseen by the Pritzker Lab Management Committee (Drs. John Bates, Kevin Feldheim, Shannon Hackett, Thorsten Lumbsch, Corrie Moreau, and Richard Ree) and the postdoc will report to the members of this committee. This position is a one-year term (with a possibility of extension, conditional on funding). Start date is flexible. Please include your preferred start date in your cover letter.

Responsibilities:

1) Instruction and training in bioinformatics analysis (70% of time). These duties will include:

- Develop and lead informational/instructional tutorials on the analysis of NGS data (genome assembly, GBS, RNASeq) - Training Field Museum scientists in NGS laboratory methods for varied biodiversity studies - Installation, administration, and deployment of NGS software on Linux and MacOS systems - Consulting on the experimental design and assist in the execution of NGS-based studies by Pritzker lab members (with opportunities for co-authorship when appropriate) - Assist the lab in long range planning for bioinformatics that leverages the museum's extensive biological collections

2) Opportunities for independent research with $10K in research funding (30% of time).

Application Instructions:

Your application submission must include 1) a CV/resume, 2) a short cover letter outlining your motivation and relevant experience for the position, your preferred start date, and the names and contact information for three professional references. Documents should be in PDF format. Qualified candidates will be contacted for an interview. Application deadline is April 18, 2014.

Applications will only be accepted through the online submission system. To apply search for the position "Postdoctoral Research Scientist, Biodiversity Genomics": http://fieldmuseum.org/about/employment Corrie Saux Moreau, Ph.D. Assistant Curator - Insects Integrative Research Center Department of Science and Education Field Museum of Natural History 1400 South Lake Shore Drive Chicago, IL 60605 USA Office: (312) 665-7743 Fax: (312) 665-7754 Email: cmoreau@fieldmuseum.org Moreau Lab website: www.moreaulab.org FMNH website: http://fieldmuseum.org/users/corrie-moreau Field Museum Women in Science: http://fieldmuseum.org/womeninscience cmoreau@fieldmuseum.org

FieldMuseum Chicago paleontology

The John Caldwell Meeker Postdoctoral Fellow. Applications are invited for the position of the John Caldwell Meeker Postdoctoral Researcher in the Earth Sciences Section, Science & Education, at The Field Museum. The successful candidate will be expected to complement, and/ or participate in any one of the ongoing research programs in the Section. Research projects are being pursued in the areas of Vertebrate Paleontology, Invertebrate Paleontology, and Meteoritics. Individual curators and their research programs are featured on the Field Museum website (http://fieldmuseum.org/-explore/department/geology). Applications will be reviewed both for merit and suitability with the research and collections strengths of the department. Applicants are strongly encouraged to contact curators they are interested in collaborating with prior to submitting an application.

A Ph.D. in a field of research represented in the Earth Sciences Section is required. The term for this position is for a maximum of two years. The appointment is anticipated to begin in the summer of 2014 or soon thereafter.

Please send a statement of research interests and experience, a curriculum vitae including publications list, and names of three referees (with e-mail addresses) to: Olivier Rieppel, Head of Earth Sciences Section, The Field Museum, 1400 S. Lakeshore Dr., Chicago, IL 60605-2496 USA; e-mail: rieppel@fieldmuseum.org; phone: (312) 665-7630. Applications must be received by June 1st, 2014. The Field Museum is an equal opportunity employer.

cheers, Pete

Peter Makovicky <pmakovicky@fieldmuseum.org>

FloridaIntlU EvolutionaryBiology

The Bracken-Grissom Lab at Florida International University in the Department of Biology and Marine Sciences Program is looking for a 1-year postdoctoral fellow with an interest in evolutionary biology and genomics.

The Bracken-Grissom Lab is fundamentally interested in the evolution of marine invertebrates with an emphasis on decapod crustaceans. Present research combines molecular, morphological, and fossil evidence to gain insights into evolutionary relationships (phylogeny), biogeography, biodiversity, ecology, origins, and diversification of crabs, lobsters and shrimp. The successful applicant will be involved in multiple projects that include: 1) large scale phylogenetic/phylogenomic/population genetic studies of decapod crustaceans and 2) the evolution of bioluminescence using RNAseq data. Mentoring of graduate and undergraduate students will be needed as part of these projects. Experience with wet-lab molecular techniques, large data matrices, phylogenetics/population genetic software, next generation sequencing methods (ex. phylogenomics, transcriptomics, RADseq), and bioinformatics is required. Additional experience with decapod crustaceans is a plus. The successful candidate must have completed her/his doctoral degree before taking up the position. Our work requires good organizational and computational skills and the ability to work collaboratively as part of a team. Occasional physically demanding fieldwork may also be required to support research.

As a single PDF, applications must include a 1) cover letter briefly outlining the candidate's fit to the position 2) CV 3) research statement, and 4) contact information for three references, preferably including doctoral advisor and/or postdoctoral advisor (if relevant). All information may be sent directly to Dr. Heather Bracken-Grissom at *hbracken@fiu.edu * AND must be uploaded to *careers.fiu.edu *with reference to Job opening ID 507343.

Additional information on the lab's research, the biology department, and marine sciences program can be found here: and *www.brackengrissomlab.com *http://biology.fiu.edu/ and www.fiu.edu/~marine.

To receive full consideration, applications and required materials should be received by April 1, 2014. Review will continue until position is filled. The position may be taken as early as 1 May 2014, but the start date is flexible (+ or - few months). A competitive salary and benefits package will be included. This position will be based on the Biscayne Bay Campus.

Contact Information

Heather Bracken-Grissom, PhD Assistant Professor Dept. of Biological Sciences Florida International University-Biscayne Bay Campus

3000 NE 151 Street, MSB-353

North Miami, Florida 33181, USA

305 919-4190 (Phone)

Heather Bracken-Grissom, PhD Assistant Professor Dept. of Biological Sciences Florida International University-Biscayne Bay Campus 3000 NE 151 Street, MSB-353 North Miami, Florida

33181, USA 305 919-4190 (Phone) 305 919-4030 (Fax) *http://www.brackengrissomlab.com/ heather.brackengrissom@fiu.edu <Valerie.Hall@fiu.edu> www.fiu.edu/ ˜ marine heather.bracken@gmail.com

HavardUniversity PlantEvolutionaryBiology

Postdoctoral Fellow in plant evolutionary biology and speciation

A postdoctoral position is available in the laboratory of Robin Hopkins, within the Department of Organismic and Evolutionary Biology at Harvard University. The Hopkins lab conducts research on plant speciation and processes of local adaptation. Major areas of research include determining the genetic basis of reproductive isolating mechanisms, understanding the role of natural selection in speciation, investigating the role of pollinators in plant speciation and adaption, and using population genetics to untangle the forces of gene flow and selection during local adaptation.

This opening is for a highly motivated postdoctoral fellow with expertise in some of the following areas: field research, population genetics, plant biology, statistics, and genetics/genomics. All candidates must have received a Ph.D. in a relevant field. The postdoc will be based at the Arnold Arboretum of Harvard University and will have access to all of the resources available through the Organismic and Evolutionary Department. The position is available for 1 year with the possibility of renewal for up to two additional years, and will include a competitive salary and full benefits.

A successful applicant will have:

Extensive independent research experience

Creativity and independence

Field or greenhouse research experience

Genetic or molecular lab experience

Excellent communication skills, both written and oral.

Application review will begin March 15, 2014 and will continue until the position is filled. All applications materials should be submitted to https://academicpositions.harvard.edu/postings/5429 for consideration. Materials should include:

1. Cover letter

2. Curriculum vitae

3. Brief description of past research accomplishments and future research goals. (Maximum of two pages.)

4. Names and contact information of 3 references

Contact Dr. Robin Hopkins, rhopkins@fas.harvard.edu with questions regarding the position or application process. For further information about OEB visit http://www.oeb.harvard.edu. For further information about the Arnold Arboretum visit http://arboretum.harvard.edu/ Harvard University is an Affirmative Action/Equal Opportunity Employer and requires pre-employment reference and background screening.

Robin Hopkins Assistant Professor Dept. of Organismic and Evolutionary Biology Harvard University

Arnold Arboretum 1300 Centre St Roslindale, MA 02131

rhopkins@fas.harvard.edu

INRA France PlantEpidemiologyModeling

Dear colleagues,

A postdoctoral position on forest epidemiology modeling is available at the Agroclim (INRA, Avignon) and Tree/Microorganism Interactions laboratories (INRA, Nancy) in France.

The Agroclim and Tree/Microorganism Interactions (IAM) laboratories are seeking a highly-qualified postdoctoral researcher to work on a joint project assessing the impacts of climate change on the establishment and development of crop and forest pathosystems in France. Climate change largely questions food security, but its impact on fungal diseases has been under explored, resulting in poor anticipation by management strategies designed to limit epidemics. The most significant work on climate change's impact on diseases in France is related to forests, with INRA already having developed research models resulting in a fine description of plant x pathogen x climate interactions, as well as operational approaches largely used in forest health to identify and quantify the risks associated to future bioclimatic niches. The main objective of this postdoctoral appointment will be to improve these existing models and use them on a country-wide scale in order to identify areas favorable to the development of selected diseases, both for present and for future climates. This will be done for two forest foliar pathogens (Dothistroma Needle Blight disease on laricio pine and Diplodia pinea on pine) and two soft and durum wheat aerial fungi (stem and leaf rusts).

The successful candidate should hold a PhD with a background in epidemiology or agronomy/forestry, and also have experience in modeling. Excellent written and spoken skills in French or English are a must. The project is part of the larger framework of the newly started research network CLIF (Climate change and fungal diseases) within the INRA metaprogramme, Adaptation of Agriculture and Forests to Climate Change. The successful candidate would join a group of approximately 30 scientists, including two international leaders in the field. The appointment is for two years, with a provisional start date of July 2014. The candidate's time would be split between the two labs, with 15 months spent at the Agroclim unit in Avignon (http://www6.paca.inra.fr/agroclim) and 9 months at the Tree/Microorganism Interactions unit in Nancy (http://mycor.nancy.inra.fr/IAM/)

Candidates must send their CV and a cover letter to Marie Launay (Agroclim, Avignon) mlaunay@avignon.inra.fr and Benoit Marcais (IAM, Nancy) benoit.marcais@nancy.inra.fr.

Candidates will be encouraged to apply for an AgreenSkills fellowship that will bring the gross monthly salary up to EUR3500. The next call for submission is 5 May 2014, 24:00 CET. To find out more about the programme and whether you are able to apply for a fellowship, visit www.agreenskills.eu One of the AgreenSkills eligibility requirements is not having spent more than 12 months in France within the last 3 years immediately prior to the expected date of recruitment.

Benoit Marçais UMR Interactions Arbres/microorganismes, INRA-Nancy, France

Dr Pascal FREY INRA, University of Lorraine Department of Tree - Microbe Interactions Ecology of Forest Pathogenic Fungi team UMR1136 IAM F-54280 Champenoux FRANCE

Phone: 33 383 394 056 Fax: 33 383 394 069 E-mail: frey@nancy.inra.fr http://mycor.nancy.inra.fr/IAM/?page_id=731 Pascal Frey <frey@nancy.inra.fr>

ImperialCollege London BeeEvolution

Postdoctoral Research Associate in Animal Behaviour, Ecology and Evolutionary Biology

Imperial College London - Department of Life Sciences - Faculty of Natural Sciences

A NERC funded Research Associate position is available to investigate a number of novel, interesting and important axes: i) the effect of systemic pesticides on bee foraging behaviour; ii) does such foraging impairment affect bee pollination service; iii) what is the genetic basis for pesticide resistance in bees; and iv) can we elucidate the selective pressure placed on insect pollinators by pesticides in the environment.

The post holder will investigate the behavioural and molecular responses to pesticide exposure in bees. The research will involve laboratory, mesocosm and field experiments to look at the responses to pesticide exposure at the individual and the colony level. It will also involve detailed observations and monitoring of individual behaviour and colony dynamics using numerous methods including micro-tagging.

The position is in the research group of Dr Richard Gill for a period of three years. The post holder will be based in the Department of Life Sciences at the Silwood Park Campus of Imperial College London, and they will become an active member of the Grand Challenges in Ecosystems and Environment initiative (http://www3.imperial.ac.uk/ecosystemsandenvironment/grandchallenges).

This post will primarily focus on the behavioural aspect of the project but, in close collaboration with Dr Yannick Wurm of Queen Mary University of London, will also assist with the molecular side of the project to ensure an integrated and inter-disciplinary approach to the questions raised. But please also note, that there will soon be a further postdoctoral position advertised as part of this NERC funded project (to join the research group of Dr Wurm), which will focus on the analysis and bioinformatics of bee genomic and transcriptomic data.

You must hold a PhD (or equivalent) in Biology, Ecology, Evolutionary Biology or a related field. Experience in husbandry, handling and monitoring of animals in the laboratory and/or field (preferably invertebrates and more desirably bees) and experience in experimental design and implementation are essential. Knowledge of and/or experience in genetic methods, investigations and application, and experience of handling and analysing large datasets and statistical analyses are desirable. You must also have produced quality published work in peer reviewed journals as first author.

You will have excellent verbal and written communication skills and be able to write clearly and succinctly for publication. You must have experience of working in a team, be able to develop and apply new concepts and have a creative approach to problem-solving. You must also be able to organise and prioritise your work in response to deadlines.

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

Salary scale: £32,750 - £41,540 per annum (maximum starting salary £33,590)

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 048 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: 3 April 2014 (midnight BST)

Committed to equality and valuing diversity. We are also an Athena SWAN Silver Award winner, a Stonewall Diversity Champion and a Two Ticks Employer.

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

JuniataCollege Bioinformatics

Post-Doctoral Associate in Bioinformatics

For a joint position, The Biology Departments at Juniata College, a highly ranked, national liberal arts college of 1,500 students located in the scenic Allegheny Mountains of central Pennsylvania, and nearby (34 miles) Pennsylvania State University seek individuals interested in a career involving both research and teaching to fill a post-doctoral position in the area of Bioinformatics. Teaching experience and experience in performing relevant wet lab and computational analyses associated with RNAseq are preferred. Experience with Linux and Perl or Python are also preferred, as well as experience using compute clusters and Amazon EC2 computing. The Biology Department at Juniata has developed an innovative curriculum with support from NSF and HHMI, a strong tradition of undergraduate research and a rich history of sending students on to graduate studies and productive careers. Further information about the department can be found at http://departments.juniata.edu/biology . Successful candidates will teach one introductory or upper level undergraduate course per semester, and instruct in an HHMI funded faculty development workshop that includes RNAseq. Candidates will support a new national initiative, headquartered on the Juniata campus, to incorporate massively-parallel sequencing technologies into the undergraduate curriculum and research (www.gcat-seek.org). Concurrently, 25% of time will be spent on functional genomics research in the lab of Prof. Jim Marden at Penn State, a leading institution for bioinformatics research. The position will be initially funded for one year, with the expectation of renewal for a second year depending on performance.

Applicants with an earned Ph.D. (required) and postdoctoral and teaching experience (preferred) should submit 1) a brief statement of teaching experience, philosophy, and interests; 2) a succinct two-page summary of research interests; 3) a curriculum vitae; 4) undergraduate and graduate academic transcripts; and 5) three letters of recommendation.

All materials should be addressed to Gail Leiby Ulrich, Director of Human Resources, Juniata College, 1700 Moore Street, Box B, Huntingdon PA 16652. It is the policy of both Juniata College and Penn State to conduct background checks. Review of applications will begin April 7 and continue until the position is filled.

Juniata College and Penn State will take positive steps to enhance the ethnic and gender diversity on their campuses. We commit ourselves to this policy not only because of legal obligations, but because it believes that such practices are basic to human dignity. AA/EOE

Dr. Vincent Buonaccorsi 601 17th St. Juniata College Huntingdon, PA 16652 Phone: 814-641-3579 http://jcsites.juniata.edu/faculty/buonaccorsi/-BUONACCORSI@juniata.edu

Dr. Jim Marden Dept. of Biology 208 Mueller Lab Penn State University University Park, PA 16802 814-863-1384 http://homes.bio.psu.edu/people/-Faculty/Marden/index.html jhm10@psu.edu

Jim Marden <jhm10@psu.edu>

KielU CyanobacteriaEvolutionaryGenomics

The Genomic Microbiology Group at the Institute of Microbiology in Christian-Albrechts University of Kiel, Germany, invites applications for:

Research Assistant (Postdoc) Position in Cyanobacterial Evolutionary Genomics

The Dagan group research interests are focused on microbial genome evolution. Our current research projects include the study of DNA acquisition dynamics in natural environments, the evolution of protein interaction with molecular chaperones and the evolution of phenotypic diversity in cyanobacteria. In our research we use both computational and experimental approaches (see http://www.mikrobio.uni-kiel.de/de/-ag-dagan). The working language of the group is English.

The position offers the opportunity to develop an independent research and teaching profile (including habilitation at the Institute of Microbiology, CAU Kiel). Development of new research proposals and publication of high-quality original scientific research are expected. The teaching load is 4 hours per week. Teaching will be in German and/or English primarily in the M.Sc. Genetics and Microbiology and B.Sc. Biology programs at Kiel University. The research assistant is expected to help in supervising MSc and PhD students within the group.

Candidate qualifications: (1) Doctoral or PhD degree in Microbiology, Post-Doctoral work is an advantage (2) Knowledge and experience in molecular microbiology techniques. Any of following expertise is an advantage: plasmid engineering and generation of knockout mutant strains, work with cyanobacterial strains or environmental samples, running experimental evolution setups, knowledge of DNA and RNA extraction for sequencing projects. (3) a strong publication record, (4) good oral and written communication skills (English is required, German a plus), (5) skills and desire to communicate and interact with other scientists.

Applicants should send a curriculum vitae with a list of publications, a statement of research interests and contact addresses of two referees in a single PDF to Prof. Tal Dagan, email: tdagan@ifam.uni-kiel.de

The position is initially offered for three years at the German TV-L E13 pay scale and may be extended up to five years.

Application deadline: 15.05.2014 or until the position is filled. Interviews will take place during May-July 2014. The planned starting date for the position is September 1st, 2014.

==> SMBE Satellite Meeting on Reticulated Microbial Evolution ==> April 2014 ==> Register now: www.smbeme.org

Prof. Dr. Tal Dagan

Genomic Microbiology Group Institute of Microbiology Christian-Albrechts-University Kiel ZMB, Am Botanischen Garten 11 24118 Kiel, Germany

Tel: +49 431 880 5712 Fax: +49 431 880 5747 e-mail: tdagan@ifam.uni-kiel.de web: http://www.mikrobio.uni-kiel.de/de/ag-dagan

tdagan@ifam.uni-kiel.de

London MicrobialCommunityEvolution

The Marie Curie Industry-Academia Partnerships and Pathways (MC-IAPP) project entitled 'Microbial Community-based sequencing analysis linked to anthropogenic pressures: MicroCoKit' to address water quality is seeking a young researcher at the postdoctoral level for 24 months The candidate will contribute to the project by developing molecular tools to address water quality based on results obtained from generation and analysis of metagenomics data to evaluate community evolution through time and space. The position will be located in the Molecular Biology Division of LGC in London, UK.

Project description MicroCokit is a five partner consortium, which includes two academic/non profit partners from Italy and UK (CNR-IRSA and MBA), two industrial partners from UK and Spain (LGC and NTBC) and the EU-JRC. The project is focused on the identification and characterization of microbial communities (metagenomes) from water samples that are differentially influenced by anthropogenic pressures (, with the aim to develop robust detection tools based on a range of technologies, e,g, FISH and quantitative Real Time PCR.

Required Skills and expertise Professional Experience. The researcher should have less than 10 years postdoctoral experience in molecular biology, microbiology, biotechnology or bioinformatics and should not have worked in the UK during the last 12 months. Experience in techniques like qRT-PCR, protein purification, DNA/RNA extraction from water, cloning and sequencing are required. Experience with analysis of data from Next Generation Sequencing (NGS) Experiments and metagenomics data analysis tools like MG-

RAST or the Integrated Microbial Genomes (IMG) system would also be beneficial.

Education. PhD in molecular microbiology (omics), biotechnology or related field.

Language skills. Good and fluent knowledge of English

The submission should include a letter of motivation and a detailed curriculum including a list of publications and should be sent to teresa.lettieri@jrc.ec.europa.eu and Carole.Foy@lgcgroup.com

Deadline for submission: 15 April 2014

Expected Start Date: 15 August 2014

Linda Medlin <lindli@MBA.ac.uk>

MPI Tuebingen 2 EvolutionRecombination

Recombination Hotspots and Adaptive Evolution

Two postdoctoral positions are available in the Jones Lab at the Max Planck Institute in Tuebingen as part of a prestigious 2M EURO European Research Coucil grant investigating the role of meiotic recombination in adaptive evolution in stickleback fish.

The goal of our research is to use cutting-edge techniques to characterize, quantify, map and manipulate meiotic recombination hotspots at unprecedented resolution across the genome, among individuals, and between species. We will study its genomic co-localization with kilobase resolution maps of adaptive loci and study the effects of recombination variation on individual fitness in the lab and in the field. This ground-breaking research will elucidate how a fundamental biological process shapes the genomic basis of adaptive divergence in natural vertebrate populations.

Postdoc1: Computational and Statistical Genomics of Recombination & Adaptation

Your role: You will use computational and statistical genetic methods to build ultra high-resolution maps of recombination hotspots across the genome and quantify variation in these maps among individuals, between sexes & divergent species. You will intersect these maps with adaptive loci including those you identify from population genomic analyses of species-pairs to investigate how recombination shapes adaptive evolution.

Requirements: You will have a PhD or equivalent degree, in Biostatistics, Bioinformatics or Statistical Genetics, or several years of experience in these fields. You should demonstrate expertise and proficiency in handling large-scale computational data analyses, and advanced skills in statistical inference (e.g. genotype imputation, Hidden Markov Models, and haplotype phasing of whole genome data). Experience with unix and coding in C, C++, Python, or Perl is essential. We are interested in candidates who are keen to apply new and innovative statistical approaches. Passion for research, team spirit and enthusiasm are essential.

Our Team: You will work in a multidisciplinary team that uses population genomics, genetics, molecular, developmental, and evolutionary biology to study the molecular mechanisms underlying adaptation and speciation in the threespine stickleback fish. Our research group is funded by the European Research Council (ERC) and the Max Planck Society and is located on the Max Planck campus in Tuebingen, Germany. Our campus hosts world-class research groups, including 7 other ERC-funded teams, and operates state-of-the-art sequencing and other core facilities. English is the working language. All seminars and communications are in English.

Our Offer: The contracts are for 2-3 years with the possibility of extension. Salary and benefits are according to the German public service pay scale (TVöD Bund).

The Max Planck Society seeks to increase the number of women in areas where they are underrepresented, and therefore explicitly encourages women to apply. Disabled applicants with equal qualifications will be given preferential treatment.

For more information please see: fml.tuebingen.mpg.de/jones-group/open-positions

To Apply: Consideration of applications will begin on April 15th 2014, and will remain open until filled. Please send your application with 1. a statement of research interests and why you have applied for this position, 2. your CV, and 3. three reference letters to Dr Felicity Jones at fcjones@tuebingen.mpg.de or the postal address below. Incomplete applications will not be considered.

Dr. Felicity Jones Friedrich Miescher Laboratory of the Max Planck Society Spemannstrasse 39 72076 Tuebingen Germany

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Recombination Hotspots and Adaptive Evolution

Two postdoctoral positions are available in the Jones Lab at the Max Planck Institute in Tuebingen as part of a prestigious 2M EURO ERC grant investigating the role of meiotic recombination in adaptive evolution in stickleback fish.

The goal of our research is to use cutting-edge techniques to characterize, quantify, map and manipulate meiotic recombination hotspots at unprecedented resolution across the genome, among individuals, and between species. We will functionally dissect and demonstrate the effect of recombination modifiers on individual fitness and adaptive evolution. This groundbreaking research will elucidate how a fundamental biological process shapes the genomic basis of adaptive divergence in natural populations.

Postdoc2: Molecular Genetics of Meiotic Recombination

Your role: You will dissect and demonstrate the molecular mechanisms underlying recombination variation and functionally test evolutionary theory on recombination modifiers in adaptive evolution. You will be responsible for functionally dissecting recombination modifiers using molecular techniques (including fine-mapping, ChIP-seq, yeast-one hybrid assays), and manipulating recombination in vivo using transgenic microinjection techniques.

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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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MPI Tuebingen GenomeBioinformatics

Positions in genome bioinformatics

Two positions at the PhD/Master student and postdoc level are available for developing new algorithms and strategies for analysis of second- and third-generation sequencing data, and for using these data to study a wide array of biological questions, with an emphasis on genome assemblies, annotation and genome comparisons. Initial appointments for PhD students and postdocs will normally be for three years. The positions are available immediately.

Candidates will have demonstrated experience in sequence and genome analyses, with at least some knowledge of primary short read analysis and genome/transcriptome annotation. Proven skills in at least one major programming or scripting language (PERL/PYTHON, Java, C/C++) and Linux/Unix computing environment (Bourne/Bash shell scripting) are a must. Good understanding of molecular biology, experience with assemblies and familiarity with biostatistics including knowledge of R are a plus.

The lab comprises a mix of computational scientists, biologists with strong bioinformatics skills and molecular biologists. It provides unique opportunities, as the lab is not only very well funded, but bioinformaticians are also involved in designing genomic analyses from day one, and often propose their own project ideas. Our work in this and other areas routinely results in high-profile publications, making it an extraordinary place for talented and ambitious students and postdocs.

The lab has been an early adopter of next generation sequencing technologies and has used these for diverse applications, from studying de novo mutations and epimutations to being the first to fine-map and identify a causal mutation using bulk segregant sequencing (Schneeberger et al., Nature Methods 2009; Ossowski et al., Science 2010; Becker et al., Nature 2011). A major effort is in understanding within- and between-species sequence variation, using both resequencing and de novo assembly strategies (Cao et al., Nature Genetics 2011; Hu et al., Nature Genetics 2011; Slotte et al., Nature Genetics 2013). A flagship project is the 1001 Genomes project for Arabidopsis thaliana (http://1001genomes.org). In this area, we have already gathered experience with PacBio data and will have early access to nanopore sequencing.

We are working closely with other groups that are primarily informatically oriented. These include Daniel Huson (Univ. Tuebingen), Bernhard Schölkopf (Max Planck Institute for Intelligent Systems, Tuebingen) and Karsten Borgwardt (currently Max Planck, soon ETH Zurich/Basel). Additional information on the group, the institute, and Tuebingen can be found on our website (http://weigelworld.org).

For Master and PhD students, we expect that you can provide at least two letters of reference and that you describe in detail your practical programming experience.

For postdocs, we expect that you have published (or are close to publishing) at least one first-author paper in a major international journal. Please send a letter that outlines which projects you are particularly interested in.

For both graduates students and postdocs, we hope to see a cover letter that details how your experience and interest would fit with the projects outlined above.

Please send applications, with a statement of purpose, names of references, and the subject line <bioinformatics posting> to Detlef Weigel: weigel@tue.mpg.de

rebecca.schwab@tuebingen.mpg.de

MasseyU ComputerModeling

Research Assistant/Postdoctoral Fellowship in Computer Modeling

My research group is offering a short-term project exploring the human settlement of the Pacific region using genetic data and agent based modeling.

This one-year position is available for either a Research Assistant or Postdoctoral Fellow depending on the level of the candidate. Candidates must have proven experience with agent based models, including their development, implementation and use. Expertise in programming and statistics is required. Some knowledge of genetics would be welcome, but training in the biological aspects of this project can be provided as required.

This position has no fixed start date and will remain open until filled.

The successful candidate will be based in the Computational Biology Research Group at Massey University, New Zealand. My research team is firmly embedded in the international scientific community, with extensive collaborative links to Australia, Indonesia, Europe and the United States. This position offers a rare opportunity to experience New Zealand's unique natural and cultural environment. Palmerston North, a university town with a large international community, offers a full range of social and cultural amenities. The city is located close to both mountains and the sea, and presents regular opportunities for hiking, skiing, surfing and adventure sports.

If you have any questions, please contact Murray Cox (m.p.cox@massey.ac.nz). Information about the Computational Biology Research Group (http://massey.genomicus.com) and the Institute of Fundamental Sciences (http://tinyurl.com/ifsmassey) is available online.

To apply, please send by email (preferably in PDF format):

1. A curriculum vitae 2. A short summary detailing prior experience with agent based models

Informal enquiries are welcome.

Assoc Prof Murray P. Cox Institute of Fundamental Sciences Massey University Private Bag 11 222 Palmerston North 4442 New Zealand

http://massey.genomicus.com m.p.cox@massey.ac.nz

murray.p.cox@gmail.com

McGillU HumanPopulationGenomics

Job title: Postdoctoral position in statistical and population genetics

A new postdoctoral position in statistical and population genetics is available in Simon Gravel's group at McGill University in Montreal, Canada. The group focuses on statistical and population genetics methods to understand human evolution and demography, and on the analysis of high-throughput genomic data. The postdoctoral researcher will be involved in conceptual methods development, implementation, and applications to exciting datasets.

The ideal candidate has experience with genetics, genomics, or population genetics and a strong interest in quantitative biology. Programming experience is preferred. 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. McGill's 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 research statement and a CV, one of which should address programming experience–code samples or links to published/distributed code are welcome. Contact information for three references is required. Review of applications will begin immediately and will continue until the position is filled.

simon.gravel@gmail.com

McMasterU EvolutionaryPhysiology

POSTDOCTORAL POSITION IN EVOLUTIONARY PHYSIOLOGY

We seek a highly motivated individual to fill a two-year fully funded postdoctoral position to uncover the underlying respiratory and metabolic mechanisms of thermogenic capacity in high-altitude deer mice. The successful applicant will take part in our ongoing international collaboration (Canada and USA) to understand the integrative physiological and genomic adaptations to high-altitude hypoxia [1,2,3].

The project involves a collaboration among the following labs:

Graham R. Scott, McMaster University (biology.mcmaster.ca/fcl/scott/web/) Grant McClelland, McMaster University (biology.mcmaster.ca/fcl/grantm/web/index.html) Zac Cheviron, Universitiy of Illinois (life.illinois.edu/cheviron/Cheviron_Lab_/Home.html) Jay Storz, University of Nebraska (storzlab.unl.edu/)

The post-doc would work in the Scott/McClelland labs at McMaster University. Ideal candidates will have experience with techniques in mammalian physiology, including small animal surgery and in vivo respiratory/cardiovascular measurements, and will be familiar with standard molecular techniques. Projected start date is negotiable but ideally Sept. 1, 2014.

All qualified individuals are encouraged to contact: Graham Scott, Ph.D. (scottg2@mcmaster.ca) or Grant McClelland, Ph.D. (grantm@mcmaster.ca) Department of Biology, McMaster University 1280 Main Street West Hamilton, ON L8S 4K1 Canada

1. Cheviron et al. (2014) Evolution. 68:48-62; 2. Cheviron et al. (2012) Proc. Natl. Acad. Sci. 109:8635-8640; 3. Storz et al. (2010) J Exp Biol. 213:4125-4136.

Graham Scott <scottg2@mcmaster.ca>

Paris-MNHN Population Genetics

We offer a post-doctoral position of one year and a half founded by the French Agence Nationale de la Recherche, project “Demochips”. The ideal candidate would be a computational biologist interested in molecular population genetics to study i) the demographic history of Drosophila melanogaster and simulans; ii) the applicability of next generation sequencing data to investigate complex demographic scenarios.

This project is a joint collaboration between four laboratories located in Paris, who share regular meetings. The postdoctoral fellow will be under the responsibility of Stefano Mona and he/she will be based in the team “Génétique des populations, sélection, structuration, spéciation” within the UMR 7205 MNHN-CNRS-EPHE located at the National Museum of Natural History in Paris, France. If interested, please send a CV, a brief description of research interest and the names of at least two referees to Stefano Mona (mona@mnhn.fr), no later than the end of March 2014.

The main focus of the project will be the development and the application of spatially explicit population genetics models (coupled with ABC or MCMC methods) to trace the most likely route of migrations within and out of Africa in both D. melanogaster (using data available in literature) and D. simulans (using data produced in our lab) and date these events. Depending on the experience and the interests of the postdoctoral fellow, several related questions could be also addressed.

Interviews can be arranged by skype and possible starting date is as early as April 2014 and not later than September 2014. Net salary per month will be around 2,000 euros.

Stefano Mona (MCf EPHE)

Museum National d’Histoire Naturelle Laboratoire ISyEB - UMR7205 Batiment de Cryptogamie - CP39 16 rue Buffon 75005 PARIS France

Tel : +33 1 40 79 81 66

mona@mnhn.fr

SLU Sweden EvolutionMosquitoVectors

Recruitment of a Postdoctoral Fellow in the evolution of mosquito vectors, with particular interest in their olfactory systems and host preference.

Modulation of Mosquito Olfaction The Unit of Chemical Ecology, Swedish University of Agricultural Sciences, Sweden is recruiting a postdoc on the above theme. Our research aims to identify how insects use chemical signals to recognize their hosts, and how their behavioural response is modulated by short-term and long-term events, from receptor neuron to CNS. Within the research group we use a broad spectrum of techniques, such as, behavioural bioassays, neurophysiology, molecular biology and genetics.

Project description: The project will investigate molecular mechanisms underlying decision-making during host and oviposition choice in mosquitoes in the light of phenotypic plasticity over development time and as a result of physiological state change. The purpose is to increase our knowledge about mechanisms underlying phenotypic plasticity based on experience to volatile cues from hosts and oviposition sites, but also to know more about mechanisms guiding resource choice in mosquitoes. The project ties in closely to ongoing host- and oviposition seeking studies, both in the laboratory and field, and requires the candidate to work in a team of PhD students, other postdocs and senior researchers.

Qualifications: The successful candidate should hold a PhD in chemical ecology or entomology, not older than three years. Experience with molecular biology and transcriptomics is a merit. S/he should be fluent in spoken and written English and have excellent communication skills. The candidate should furthermore enjoy working tightly together with a group of researchers on different aspects of the same basic research question.

Place: Unit of Chemical Ecology, Dept of Plant Protection Biology, Alnarp, Sweden. http://www.slu.se/sv/institutioner/vaxtskyddsbiologi/forskning/kemisk-ekologi/ . Duration: 1+1 year

Salary: A stipend of 22 000 SEK per month incl. health care.

Application: Applications including a letter of motivation, a CV and 3 potential referees, should be sent to: sharon.hill@slu.se or rickard.ignell@slu.se

Responsible researchers: Professor Rickard Ignell and Associate Professor Sharon Hill

Further information: sharon.hill@slu.se or rickard.ignell@slu.se

Starting date: as soon as possible, the screening of applications will start from 15 April.

Sharon Rose Hill Associate Professor, PhD

Sveriges lantbruksuniversitet Swedish University of Agricultural Sciences

Division of Chemical Ecology / Department of Plant Protection Biology PO Box 102, SE-230 53 ALNARP Visiting address: Sundsvägen 14 Telephone: +46 (0)40-41 51 05, mobile: +46 (0)76-247 91 75 sharon.hill@slu.se, www.slu.se/sharon-hill Sharon Hill <Sharon.Hill@slu.se>

ShizuokaU EvolutionaryModeling

We have a three-year fulltime faculty position in Mathematical and Systems Engineering, broadly defined, including ecological and biological/evolutionary modelling and simulation. Please see below for the detail.-jin yoshimura

The Graduate School of Engineering, Shizuoka University (http://www.eng.shizuoka.ac.jp/en/), invites applications for a faculty position in Mathematical and Systems Engineering, at the associate or assistant professor level, beginning at the earliest possible time in 2014. Applicants should have a doctoral degree and a substantial record of publications in such areas as Mathematical Engineering, Systems Engineering and Computer Science. Applicants must be non-Japanese and capable of offering courses in English. Preference will be given to those applicants fully qualified at the associate professor level. However, the assistant professor level may also be considered for promising candidates with satisfactory qualifications.

The successful candidate will conduct research and teach some major subjects in Mathematical and Systems Engineering in English. Furthermore, the successful candidate is expected to teach 'Academic English for Engineering' which focuses on technical writing and reading, and also speaking and listening in technical English. The English teaching load is two classroom courses per year. Expectations include cooperating with others in developing international exchange programs in both undergraduate and graduate levels. The appointment will be made on a three-year fixed-term contract basis. This three-year fixed-term contract is renewable, only upon mutual agreement, in the form of either a non-renewable two-year fixed-term contract or an indefinite-term (i.e. tenured) employment. Remuneration is commensurate with qualifications and experience, according to Shizuoka University Remuneration Regulations.

Application instructions: Interested candidates should electronically submit Prof. M. Yokozawa (tmyokoz@ipc.shizuoka.ac.jp), a cover letter, curriculum vitae, copies of selected papers, a statement of research and teaching interests, and two letters of recommendation. Shortlisted candidates will be invited to visit Shizuoka University for interview and lecture. The final decision will be made shortly after the interview. Applications should be submitted by 31 May, 2014. Inquiries should be directed to Committee of foreign scholar affairs (tmanaka@ipc.shizuoka.ac.jp). All application documents, which are used only for selecting a qualified candidate, will be destroyed after making the final decision.

We list in the website below: https://jrecin.jst.go.jp/seek/SeekJorDetail?fn=4&ln=1&id=D114021227&ln_jor=1 https://jrecin.jst.go.jp/seek/SeekJorDetail/koubo_A.pdf?fn=99&id=D114021227&ln_jor=1&seqNo=1 Jin Yoshimura, Ph. D., Professor Department of Mathematical Systems Engineering Shizuoka University, Hamamatsu 432-8561 Japan Email: jin@sys.eng.shizuoka.ac.jp Phone/Fax: +81-(0)53-478-1215

jin <jin@sys.eng.shizuoka.ac.jp>

Singapore EvoDevoGenomics

Postdoctoral position in Evolutionary Developmental Genomics Dept. Biological Sciences, National University of Singapore

A postdoctoral position is available in the lab of Antónia Monteiro to study the genetic basis of morphological variation in butterfly wing patterns. The project will involve using comparative genomic data to identify loci involved in producing wing pattern differences across populations of Bicyclus anynana butterflies. Subsequently, once candidate loci are found, the goal will be to use transgenic tools to test the function of these candidate loci in producing the morphological variation.

The position is initially for three years and can start immediately. Salary will be competitive and commensurate with experience. Candidates with experience in bioinformatics and genomics, in particular in using NGS data, are especially welcome to apply.

The Department of Biological Sciences offers world-class research labs and infrastructure and a convivial and collaborative environment. Singapore is a lush, green city offering tropical weather year around, a diversity of food, and nearby exotic locations.

Interested applicants should contact Antónia Monteiro (antonia.monteiro@nus.edu.sg) with a CV, a brief statement of research interests, and the names of three references.

Antónia Monteiro Associate Professor Department of Biological Sciences National University of Singapore 14 Science Drive 4 Singapore 117543

and,

Associate Professor Yale-NUS-College 6 College Avenue East Singapore 138614

web-page: http://www.lepdata.org/monteiro antonia.monteiro@nus.edu.sg

UBern PhD PDF BioticInteractions

The research group 'Biotic Interactions' at the University of Bern is inviting applications for a PhD and a post doc (group leaser) in Plant-Insect Interactions

PhD position:

Background: Our group is investigating the role of secondary metabolites in plant-herbivore interactions. One of our most advanced models is the western corn rootworm Diabrotica virgifera, an important global maize pest. D. virgifera has adapted to the defense system of its host plant and has become fully resistant to benzoxazinoids, the main resistance factors of maize roots. The PhD project will investigate the mechanisms behind benzoxazinoid tolerance in D. virgifera. The PhD candidate will isolate candidate detoxification genes and modulate their expression using a novel form of transient plant-mediated RNAi. The identified enzymes will then be further characterized on a chemical, biochemical and behavioral level.

We look for an enthusiastic PhD student with strong interests in plant-insect interactions. Applicants should have a firm background in one of the following fields: molecular biology, biochemistry, plant physiology, evolutionary biology, analytical chemistry, entomology and ecology. All our projects are highly integrative and require willingness to embrace multiple disciplines within the domain of chemical ecology. Fluent spoken and written English is a prerequisite for this position.

We offer an inspiring research environment, including state-of-the art research facilities, extensive supervision and an exciting project of considerable fundamental and applied relevance. The institute of Plant Sciences is located at the shore of the river Aare, close to the vibrant center of the city of Bern. PhD students are paid according to University standard rates and have the possibility to join the graduate program in Molecular Life Sciences. More information about the current activities of our group can be found here: www.ips.unibe.ch/content/interactions . How to apply: Send a single pdf including a letter of motivation, a CV with University grades and the names and addresses of two referees to christelle.robert@ips.unibe.ch. The position is available from May 2014 and open until filled.

Position 2: Post Doc (Group Leader)

Background: Our group investigates the roles of plant-secondary metabolites in rhizosphere interactions, with a special emphasis on root herbivores. In this context, we have established Dandelion (Taraxacum officinale) and white grubs (Melolontha melolontha) as a native, co-evolved root-herbivore system. Apart from its ecological relevance, the system is well suited for phytochemical investigations due to its defensive lacticifer system and the availability of efficient transformation protocols.

We look for an enthusiastic post-doctoral researcher that leads the Dandelion project on an executive level. A PhD in related disciplines, including phytochemistry, biochemistry, evolutionary biology, molecular biology and/or plant physiology is required. Good communication and supervision skills, including fluent written and oral English, are a must. A minimum of 3 first or senior author papers in peer-reviewed, international journals are expected. Experience in developing new tools and methods is of advantage.

We offer an inspiring research environment, including state-of-the art research facilities and an exciting project of considerable fundamental relevance. The group leader will be able to build his own team, including MSc. and PhD students and will be given the opportunity to develop a competitive profile, including the possibility to acquire additional third party funding, teach and publish.

The institute of Plant Sciences is located at the shore of the river Aare, close to the vibrant center of the city of Bern. Post docs are paid according to University standard rates. The initial contract is 3 years, with the possibility of a 2 year extension, subject to available funding. More information about the current activities of our group can be found here: www.ips.unibe.ch/content/interactions . How to apply: Send a single pdf including a letter of motivation, a CV with University grades, the names and addresses of two referees, a short 1 page research vision and copies of your 3 most important papers to matthias.erb@ips.unibe.ch. The position is available from May 2014 and open until filled.

Christelle Robert <crobert@ice.mpg.de>

UBrasilia Extinction

Postdoctoral Opportunity: Climate-Forced Extinction Risks for the Herpetofauna of Brazil

A postdoctoral position is available at Colli's lab, Department of Zoology, University of Brasília, Brasília, Brazil, to assess climate-driven extinction risks of amphibians and reptiles across the major ecosystems of Brazil. The position is funded by Conselho Nacional do Desenvolvimento Científico e Tecnológico - CNPq (http://www.cnpq.br), through the Science Without Borders program (http://www.cienciasemfronteiras.gov.br/web/csf). It is part of a broader collaborative effort between Brazilian and American scientists, lead respectively by Guarino Colli and Barry Sinervo, and funded by CNPq and the National Science Fundation - NSF.

The successful candidate will work with Dr. Guarino Colli and Dr. Barry Sinervo (UCSC) primarily at UnB, but also at other laboratories and field locations in the Brazilian Cerrado, Caatinga, Amazonia and Atlantic Forest. The major responsibilities of this position include (1) conducting field and laboratory research to obtain preferred and operational temperature data of amphibians and reptiles, (2) participating in the development of paleoclimatic models of range expansion or contraction based on ecophysiological data, 3) contributing to mentoring of graduate and undergraduate students involved in research, and 4) analyzing data and writing manuscripts.

Qualifications This is an equal opportunity program, open to all qualified individuals without regard to race, color, age, sex, religion, national origin, mental or physical disability, genetic information, or sexual orientation. To be eligible, applicants must have received a doctorate degree in ecology, physiology, herpetology, or related field within five years of the starting date. The ability to organize, lead and endure fieldwork in a foreign country, sometimes for prolonged periods, is required. Strong writing skills, basic knowledge of the R software environment, and the ability to work independently will be valued, as well as a working knowledge of Portuguese or Spanish.

Terms of Appointment Monthly salary is R$ 4,100 (annual R$ 49,200), following CNPq payscale for “Bolsa de Pós-Doutorado JÃºnior - PDJ”. Funds are available for one year, and renewable for additional years pending satisfactory progress.

Applications To submit an application for this role, all applicants must supply the following documents: cover letter, CV, statement of research interests/experiences, and names and contact information for three references that are familiar with your work. Applications should be e-mailed to Guarino Colli (grcolli@unb.br) and Barry Sinervo (lizardrps@gmail.com) in PDF format. The position is available starting August 2014. Review of applications will begin April 1, 2014, and continue until a suitable candidate is found.

Prof. Guarino R. Colli Departamento de Zoologia Universidade de Brasília 70910-900 Brasília, DF BRASIL Phone: +55-61-3107-3013 Fax: +55-61-3107-3036 e-mail: grcolli@unb.br Skype: grcolli ResearchID: http://www.researcherid.com/rid/A-5368-2008 Lattes CV: http://lattes.cnpq.br/2272000258230548

Guarino Rinaldi Colli <grcolli@unb.br>

UCalifornia Berkeley TheoPopGenetics

Postdoctoral positions in theoretical population genetics

There are two NIH-funded postdoctoral positions open in my laboratory for theoretical population geneticists. I am looking for people who have training in analytic theory and have programming skills in Python, R or Perl and a low-level language such as C, C++ or Java. Research areas include the population genetics of humans, Neanderthals and Denisovans, models of range expansions, genomic tests of inbreeding and relatedness, and genomic tests of soft and hard selective sweeps. The lab will continue to collaborate on the Neanderthal Genome Project but there will be opportunities to work in other research areas as well. The initial appointment will be for two years with the possibility of renewal for up to two more years. The initial salary will be $50,000 per year with health insurance provided. The starting date is negotiable but must be within three years of when the Ph. D. or equivalent degree was awarded. Qualified applicants should send a current CV and the names and email addresses of three references to slatkin@berkeley.edu.

Montgomery Slatkin, Department of Integrative Biology, University of California, Berkeley.

slatkin@berkeley.edu slatkin@berkeley.edu

UFlorida PDF PhD InsectFungusSymbiosis

The Forest Entomology and Symbiology team at the University of Florida is seeking a POSTDOC and a GRAD STUDENT!

- Be a part of a young, growing team (www.ambrosiasymbiosis.org).

- Work on a hot topic: insect-fungus-microbe symbioses.

- Do relevant research on globally invasive emerging forest pests.

POSTDOC: Assist in the development of RNASeq-based assessment of communities of fungal symbionts in beetles. Experience with next-gen sequencing is required.

GRAD STUDENT: Survey fungi in exotic bark & ambrosia beetles in the US, and test pathogenicity of overseas fungi to American trees. Overseas fieldwork included.

Apply by email to hulcr@ufl.edu with subject header “Symbiology applicant 2014 postdoc” or “Symbiology applicant 2014 grad student”. Please submit your CV (include evidence of ability to get projects finished and papers written) and contacts to three most recent supervisors. Start: any time during 2014, the earlier the better. Application deadline: April 15, 2014 Thank you!

Jiri Hulcr, Assistant Professor University of Florida | School of Forest Resources and Conservation 352-273-0299 | www.ambrosiasymbiosis.org “Hulcr,Jiri” <hulcr@ufl.edu>

UGeorgia Athens SpeciationGenetics

Post-Doctoral Associate Position

A post-doctoral position in plant evolutionary genetics is available in the lab of Andrea Sweigart in the Department of Genetics at the University of Georgia.

Our lab is broadly interested in the genetics of speciation in the model flowering plant Mimulus. The goal of this NSF-funded project is to understand the evolution of interspecific genetic incompatibilities that cause sterility in species hybrids. This research will focus on dissecting the molecular genetic basis of hybrid sterility between two closely related species, Mimulus guttatus and M. nasutus. The project will involve molecular and functional characterization of hybrid sterility genes, and will include a combination of plant transformation experiments, classical genetics approaches, and bioinformatics analyses. For more information about this and other research projects in our lab, go to the following link: http://www.genetics.uga.edu/-sweigartlab/Andrea/Home.html . The University of Georgia has an exceptionally strong group of plant geneticists and evolutionary biologists across campus. Greenhouse, laboratory, and computational facilities are also excellent. UGA is located in Athens, a vibrant college town famous for its music scene and restaurants.

The ideal candidate will have both a strong background in evolutionary biology and experience with molecular genetic techniques. Experience with plant molecular biology, transformation, and microscopy would be particularly valuable. The position is available for up to three years, and includes a competitive salary and full benefits. The start date may be as early as June 2014. To apply, please email a CV, a brief statement of research accomplishments and future goals, and contact information for three academic references to: sweigart@uga.edu.

Andrea L. Sweigart Department of Genetics 120 East Green Street Davison Life Sciences Building, C218 University of Georgia Athens, GA 30602-7223

office phone: (706)-542-7001 sweigart@uga.edu

Andrea Sweigart <sweigart@uga.edu>

UIllinois UC DeerPopGenetics

Post-Doctoral Research Associate Position Announcement

Position: Post-Doctoral Research Associate, full-time, benefit eligible (12-month service basis, renewable for up to two years based on performance and additional funding).

Employer: Illinois Natural History Survey (INHS), and the Department of Animal Sciences, University of Illinois, Urbana-Champaign, Illinois.

Project description: The Chronic Wasting Disease (CWD) research program conducts applied conservation and population genetic analysis of deer, describes patterns of genetic structure, spatial distribution and gene flow, to draw insights into the epidemiology of CWD.

Responsibilities: Develop, direct and coordinate population studies using genetic tools to examine relatedness and parentage of deer in association with landscape and epidemiological variables related to CWD. Actively integrate data analysis and writing of manuscripts to the above efforts. The Post-doctoral candidate is expected to work within a multidisciplinary environment (veterinarians, wildlife biologists, animal scientists and geographers). The position has potential for expansion to other areas of conservation genetics, epidemiology and wildlife health depending on the candidate^{1}s interest. Qualifications: Applicants must have: 1) completed their Ph.D within the past 5 years; 2) experience with high'throughput for large scale genetic analysis, proficiency with contemporary molecular laboratory and analytical skills (DNA extraction, PCR gel electrophoresis, sequencing and microsatellite optimization); 3) strong quantitative skills and proven ability to publish peer-reviewed papers; 4) ability to work independently as a part of a team, 5) strong attention to detail, organizational, interpersonal and communications skills, 6) leadership and supervisory skills. Additional requirements include a valid driver^{1}s license.

Availability and Salary: Proposed starting date May 1, 2014. Salary is $38,000 to $42,000, commensurate with experience. Benefits: Generous vacation, sick, and personal leave, and holidays. State Health, Dental and Life Insurance, and retirement pension program for eligible employees.

Application process: Applications must be received by April 20, 2014. To apply, all candidates must submit an online profile through https://jobs.illinois.edu by the close of the posting period. Qualified candidates must upload a cover letter detailing skills and qualifications noted above; a curriculum vitae or resume^1; a working e-mail address; and the names, addresses, phone numbers, and e-mail addresses of three professional references. All requested information must be submitted for your application to be considered. Incomplete information will not be reviewed. Applications may be reviewed prior to closing. For further information please contact Erica Hanson, Human Resources, at elhanson@inhs.illinois.edu; For technical questions contact, Drs. Nohra Mateus-Pinilla at nohram@illinois.edu or Jan E Novakofski at jnova@illinois.edu. The University of Illinois is an Affirmative Action/Equal Opportunity Employer. The administration, faculty, and staff embrace diversity and are committed to attracting qualified candidates who also embrace and value diversity and inclusivity.

roca@illinois.edu

UKansas EvolutionaryGenomics Lepidoptera

The Walters lab at the University of Kansas is seeking an post-doctoral researcher to pursue research in Lepidopteran Evolutionary Genomics, with an emphasis on sex-chromsome evolution. Further details follow below. Formal applications are submitted through the U of Kansas website (https://employment.ku.edu/-jobs/4906), though informal inquiries may be directed to Jamie Walters (jrwalters@ku.edu).

The position will be in the Ecology & Evolutionary Biology department at the University of Kansas (KU-EEB), in Lawrence. KU-EEB is a large and diverse department with strong ties to both the Kansas Biological Survey and Natural History Museums' Biodiversity Institute. Several labs at KU-EEB are pursuing genomic research in non-model organisms, supported by our own Illumina sequencer and a superbly-maintained, campus-wide computing cluster.

KU is located in Lawrence, a progressively-minded college town located in the rolling hills of eastern Kansas. It is an easy 45 minute drive west of Kansas City and its international airport. It has a high quality of life and low cost of living, with a thriving music & arts scene, twice weekly farmers' market, a vibrant Main street, and countless options for children's recreation/education. Good opportunities for outdoor activities such as trail running, mountain biking, boating, windsurfing, disc golf, fishing, and hiking are supported by nearby Clinton Lake state park and numerous city parks.

Further further details about our lab and research, see www.walterslab.org Sincerely, Jamie Walters

James R. Walters, Ph.D. Assistant Professor Ecology & Evolutionary Biology University of Kansas Lawrence, KS 301-404-2743 www.walterslab.org Position Details: Post-Doctoral Researcher Ecology and Evolutionary Biology The University of Kansas

The Walters Lab in the Department of Ecology and Evolutionary Biology at Kansas University is seeking a Post-Doctoral Researcher to work in the area of comparative and evolutionary genomics in Lepidoptera (butterflies & moths). Research in the Walters lab projects focuses on reproductive protein evolution, sex-chromosome evolution, and lepidopteran comparative genomics using genome-wide population resequencing, transcriptome, and proteomic data sets. Specific research projects are flexible and can be tailored to suit the interests and skills of the successful applicant but will ideally overlap with focal research areas in the Walters lab.

The anticipated start date is April. 15, 2014 or as soon as possible thereafter. Appointment is for one year, with the possibility of renewal for an additional year.

Pay: $42,000 for new postdocs and following the NIH scale for years of experience: http://grants.nih.gov/-grants/guide/notice-files/NOT-OD-14-046.html FTE: 1.0, full time, 40 hours/week

Required Qualifications: 1. A Ph.D. in biology, genetics, bioinformatics, or a related field. 2. Good computer programming/scripting skills, including UNIX, Perl and/or Python, and R. 3. Demonstrated experience analyzing genome-scale data, particularly next-generation sequencing data (e.g., Illumina) 4. Demonstrated ability to work successfully in a collaborative environment. 5. Strong organizational, communication, and time-management skills.

For more detailed information and to apply, go to https://employment.ku.edu/jobs/4906. Submit online application and attach a cover letter explaining your research experience and interest in the position. Include your resume and at least two reference names and contact information. Application review begins 3/15/14 and will continue until a qualified pool has been identified. The University of Kansas is an Equal Opportunity/Affirmative Action employer. All qualified applicants will receive consideration for employment without regard to race, color, religion, sex, national origin, disability or protected Veteran status.

jrwalters@ku.edu

UKansas Metagenomics

The University of Kansas is hiring a POSTDOCTORAL RESEARCHER and a RESEARCH TECHNICIAN to support the development of the Center for Metagenomic Microbial Community Analysis (www.kansasmetagenome.org).

This new Center is funded by a KU Strategic Initiative grant, and involves a multidisciplinary research team from several units on campus with diverse interests in microbial communities, from microbial ecology and ecosystem management, to wastewater treatment and water quality, to ecophysiology and soil science, to geomicrobiology. The Center seeks to use next-generation sequencing to investigate an array of projects in these areas.

In the first instance we are hiring a postdoc and a research technician. Full details of the positions are provided below. Enquires from potential applications are welcome, and can be directed to any of the team leaders:

Belinda Sturm (PI) - Civil, Environmental & Architectural Engineering (bmcswain@ku.edu)

Sharon Billings - Ecology & Evolutionary Biology / Kansas Biological Survey (sharonb@ku.edu)

Stuart Macdonald - Molecular Biosciences / Director of K-INBRE Bioinformatics Core at KU (sjmac@ku.edu)

Jennifer Roberts - Geology (jaroberts@ku.edu)

Benjamin Sikes - Ecology & Evolutionary Biology / Kansas Biological Survey (ben.sikes@ku.edu)

OFFICIAL POSITION ANNOUNCEMENT The University of Kansas is hiring a Postdoctoral Researcher and a Research Assistant to support the development of a Center for Metagenomic Microbial Community Analysis. A key goal of the proposed Center is to bring together researchers across the university to advance metagenomics methods for diverse research programs at KU. The University of Kansas has significant expertise in microbial ecology applications in Ecology, Biology, Geology, and Environmental Engineering. Faculty comprising this multidisciplinary realm link microbial ecology to the removal of pollutants and excess nutrients from stormwater, wastewater systems, and soils (Belinda Sturm, Environmental Engineering; Sharon Billings, Ecology and Evolutionary Biology/Kansas Biological Survey), the production of greenhouse gases in carbon and nitrogen biogeochemical cycles (Sharon Billings, EEB/ KBS; Jennifer Roberts, Geology), the microbial generation and destruction of porosity in petroleum carbonate reservoirs and their modern analogues (Jennifer Roberts, Geology), and the restoration of plant-microbe-soil ecosystems (Ben Sikes, EEB/KBS). Successful applicants will work in this interdisciplinary team to analyze diverse communities using the Illumina HiSeq platform. Visit our webpage at www.kansasmetagenome.org . We are hiring a motivated Postdoctoral Researcher with prior experience in any field of environmental community analysis. We are specifically interested in candidates with a strong background in the computational analysis of next-generation sequencing-based metagenomics studies. For specific requirements and application materials see http://employment.ku.edu/jobs/-4904 . We are also hiring a Research Assistant with strong molecular skills to generate next-generation sequencing libraries from environmental samples. We are particularly interested in an individual with prior experience with metagenomic applications or with any form of next-generation sequencing. For specific requirements and application materials see http:/-/employment.ku.edu/jobs/4903 . Applicants should submit the application at the link provided above, along with a curriculum vitae, the names and contact information for 3 references, and a brief statement of research interests and skills.

A start date of May 2014 is preferred. Any inquiries can be directed to Dr. Belinda Sturm.

Belinda Sturm, PhD Associate Professor Dept of Civil, Environmental & Architectural Engineering University of Kansas bmcswain@ku.edu http://people.ku.edu/-~bmcswain Dr. Stuart J. Macdonald Department of Molecular Biosciences 4043 Haworth Hall 1200 Sunnyside Avenue University of Kansas Lawrence KS 66045

office: 785-864-5362 lab: 785-864-5777 fax: 785-864-5321 email: sjmac@ku.edu

sjmac@ku.edu

UKentucky GenomeEvolutionRearrangements

A postdoctoral position is available in the Smith lab at the University of Kentucky as part of a 5 year NIH-funded project studying the mechanisms, evolution and developmental function of programmed genome rearrangements in the lamprey (Petromyzon marinus). The project will involve the analysis of large nucleic acid and proteomic sequence datasets and functional analysis of genes involved in programmed genome rearrangement. The postdoc will be involved in all aspects of the project, from experimental design to publication, and will be encouraged to pursue side projects that enhance their pursuit of an independent research career.

A PhD in genetics, development or fields related to genome function and evolution is required. Experience with next-generation sequencing, mass spectrometry, bioinformatics or vertebrate embryology is preferred.

The Department of Biology houses several active labs that focus on diverse aspects of evolution, with a strong emphasis on vertebrate genome evolution. The University of Kentucky provides several common use facilities (imaging, sequencing, proteomic, gene expression analysis, high performance computing) that directly facilitate the achievement of the project's research objectives.

To apply for this position, please send a CV, statement of research interests, and three letters of reference to Jeramiah Smith (jjsmit3@uky.edu). The position is available for 2 years with the possibility of renewal up to 5 years depending on research progress. Although the position is available immediately, the start date can be flexible based on the needs of the candidate. The position will remain open until filled.

The University of Kentucky is an Affirmative Action/Equal Opportunity University that values diversity and is located in an increasingly diverse geographical region. It is committed to becoming one of the top public institutions in the country. Women, persons with disabilities, and members of other underrepresented groups are encouraged to apply. The University also supports family-friendly policies.

Jeramiah Smith <jeramiahsmith@gmail.com>

jeramiahsmith@gmail.com

ULausanne FunctionalEvolutionaryGenomics

BIOINFORMATICS POSTDOC IN FUNCTIONAL EVOLUTIONARY GENOMICS

Center for Integrative Genomics, University of Lausanne, Switzerland

A postdoctoral position (2 years with possible extensions up to 5 years) is available immediately in the evolutionary genomics group of Henrik Kaessmann.

We are seeking highly qualified and enthusiastic applicants with strong skills in computational biology/bioinformatics, preferably also with experience in data mining and comparative or evolutionary genome analyses.

We have been interested in a range of topics related to the functional evolution of genomes across mammals. In the framework of our research, we are generating comprehensive sets of RNA-seq data for a large collection of germline and somatic tissues from representatives of all major mammalian lineages (placental mammals, marsupials, and the egg-laying monotremes) and evolutionary outgroups (e.g., birds). In conjunction with various high-throughput genomic and epigenomic datasets, we are using these transcriptome data to study the functional (expression) evolution of mammalian genomes across gene types, lineages, tissues, developmental stages, chromosomes and sexes.

The postdoctoral fellow will perform integrated evolutionary/bioinformatics analyses based on data produced in the lab and available genomic data. The specific project will be developed together with the candidate.

The language of the institute is English, and its members form an international group that is rapidly expanding. The institute is located in Lausanne, a beautiful city at Lake Geneva.

For more information on the group and our institute more generally, please refer to our website: http://www.unil.ch/cig/page7858_en.html Please submit a CV, statement of research interest, and names of three references to: Henrik Kaessmann (Henrik.Kaessmann@unil.ch).

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Henrik Kaessmann, Ph.D.

Associate Professor

Center for Integrative Genomics

University of Lausanne, Switzerland

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Selected recent publications:

Cortez, D., Marin, R., Toledo-Flores, D., Froidevaux, L., Liechti, A., Waters, P.D., Grützner, F., and Kaessmann, H. (2014) Origins and functional evolution of Y chromosomes across mammals. Nature (in press).

Necsulea, A., Soumillon, M., Warnefors, M., Liechti, A., Daish, T., Zeller, U., Baker, J.C., Grützner, F., and Kaessmann, H. (2014) The evolution of lncRNA repertoires and expression patterns in tetrapods. Nature 505: 635-640.

Meunier, J., Lemoine, F., Soumillon, M., Liechti, A., Weier, M., Guschanski, K., Hu, H., Khaitovich, P., and Kaessmann, H. (2013) Birth and expression evolution of mammalian microRNA genes. Genome Res. 23: 34-45.

Soumillon, M., Necsulea, A., Weier, M., Brawand, D., Zhang, X., Gu, H., Barthès, P., Kokkinaki, M., Nef, S., Gnirke, A., Dym, M., de Massy, B., Mikkelsen, T.S., and Kaessmann, H. (2013) Cellular source and mechanisms of high transcriptome complexity in the mammalian testis. Cell Rep. 2179-2190.

Julien, P., Brawand, D., Soumillon, M., Necsulea, A., Liechti, A., Schütz, F., Daish, T., Grützner, F., and Kaessmann, H. (2012) Mechanisms and evolutionary patterns of mammalian and avian dosage compensation PLoS Biol. 5:e1001328.

Brawand, D., Soumillon, M., Necsulea, A., Julien, P., Csárdi, G., Harrigan, P., Weier, M., Liechti, A., Aximu-Petri, A., Kircher, M., Albert, F.W., Zeller, U., Khaitovich, P., Grützner, F., Bergmann, S., Nielsen, R., Pääbo, S., and Kaessmann, H. (2011) The evolution of gene expression levels in mammalian organs. Nature 478: 343-348.

Henrik Kaessmann <Henrik.Kaessmann@unil.ch>

UMaryland AdaptiveSystemsAnthropology

Postdoc in Complex Adaptive Systems and Sustainability

Job Description and Qualifications

The Department of Anthropology at the University of Maryland solicits applications for a Postdoctoral Research Associate for a 12-month term beginning in July 2014, with a possibility of extension contingent upon external funding. The research topic is improving understanding of the sustainability of human-environmental interactions, broadly construed, with a focus on integrating anthropological, archaeological and environmental data, and computational modeling. Candidates should have strong backgrounds in complex adaptive systems, critical transitions, resilience, and/or evolutionary life history, although other theoretical approaches will be considered. The successful candidate will be supervised by Dr. Sean Downey (www.anth.umd.edu/facultyprofile/Downey/Sean). In addition to conducting research on the these topics, the successful candidate will prepare and submit major research proposals, so applications should demonstrate previous funding success and project ideas or proposals in development. The candidate must hold a Ph.D. in a related field and have a demonstrable record of research and publication. Candidates with excellent writing and technical skills (e.g., R, MatLab, Python, HPC) are strongly encouraged to apply.

To Apply

Candidates should compile the following documents into a single PDF in the following order: (1) a letter of intent that details research interest and proposal ideas, (2) current curriculum vitae, (3) writing samples (publications and/or grant proposals), and (4) contact information for three professional references. Electronic submission only. Please address applications and questions to the search coordinator, Sarah Morrow (semorrow@umd.edu, 301.405.9734). Review of applications will begin immediately and interviews will begin on April 15, 2014. The position will remain open until filled. The University of Maryland is an equal opportunity affirmative action employer with a commitment to racial, cultural, and gender diversity. Women and minorities are encouraged to apply.

About the University of Maryland

The University of Maryland, College Park is the flagship campus of the University System of Maryland. With an enrollment of over 30,000 students, it is the largest university in the state, and the largest in the Washington Metropolitan Area. The University is committed to achieving excellence as the State's primary center of research and graduate education. The campus benefits from the close proximity and networked connections with the broader Washington and Baltimore metropolitan communities. The Department of Anthropology has three degree programs B.A., M.A.A., and Ph.D. It is known for its strong theoretical orientation and it is nationally recognized for being an excellent applied program. Our faculty work with and make connections between local peoples, national governments, non- governmental organizations (NGOs), inter-governmental agencies, and academic institutions. We have a strong commitment to preserving and transmitting the knowledge of the past, as well as to illuminating and confronting the challenges of the present.

Dr. Sean S. Downey Assistant Professor Anthropology Department University of Maryland 1106 Woods Hall College Park, MD 20742 sean@codexdata.com <mailto:sean@codexdata.com> http://www.anth.umd.edu/facultyprofile/Downey/-Sean Office: 301-405-1427

Students wanted: Applications due annually on Dec 15. http://terpconnect.umd.edu/ ˜ sdowney2/Sean_Downey/Opportunities.html < http://terpconnect.umd.edu/%7Esdowney2/Sean_Downey/Opportunities.html > http://www.anth.umd.edu/content/graduate-admissions seanowney@gmail.com

UMinnesota ButterflyPlasticityTranscriptomics

Postdoc Position at the University of Minnesota

The Snell-Rood lab at the University of Minnesota is seeking a postdoc for an NSF-funded project investigating the costs and consequences of variable gene expression as a mechanism of developmental plasticity. More specifically, this project will contrast populations of cabbage white butterflies that vary in host plant niche breadth, testing for life history tradeoffs associated with epigenetic mechanisms of plasticity. The position is funded for up to 2.5 years with a somewhat flexible start date (between fall 2014 and spring 2015). Bioinformatics experience is essential. Familiarity with rearing and dissecting insects is desirable, but not necessary.

The University of Minnesota has state-of-the-art genomics and supercomputing facilities (http://www.bmgc.umn.edu/) and has recently invested in hiring a range of new faculty that address ecological and evolutionary questions using genomics (see http://www.cbs.umn.edu/explore/departments/eeb/graduate/graduate-program-faculty).

To apply, visit https://employment.umn.edu/applicants/jsp/shared/position/JobDetails_css.jsp?postingId=683817 . Please submit a cover letter, CV, and a 2-page research statement describing your research interests, background and your goals for your career and postdoc. Please also include the names and contact information for 2-3 references. Applications will be reviewed starting May 1st, 2014, and will be considered until the position is filled. For questions, please contact Emilie Snell-Rood (emilies@umn.edu) or visit the lab website: http://www.cbs.umn.edu/lab/emilies/ emilies@umn.edu

UNebraska PopulationBiol

POPULATION BIOLOGY POSTDOCTORAL RESEARCH FELLOWSHIP

THE UNIVERSITY OF NEBRASKA-LINCOLN is seeking applications for a 2-year postdoctoral position in the Population Biology Program of Excellence.

The goal of the Population Biology-POE Postdoctoral Fellowship is to stimulate synergistic interactions between faculty and postdoctoral scholars interested in the broad area of Population Biology. Qualified candidates are required to develop a single, coherent 2-year research project under the guidance of two or more faculty advisors, one of whom must be in the Ecology, Evolution & Behavior (EEB) section in the School of Biological Sciences (http://biosci.unl.edu/research-specializations). The second advisor may be in the School of Biological Sciences (including EEB), the Institute of Agriculture and Natural Resources (ianrhome.unl.edu/colleges), Mathematics (http://www.math.unl.edu) or in another UNL department. While in residence, the postdoctoral fellow will be expected to teach a graduate seminar on a topic of his/her choice (Year 1), and to help organize a local symposium (Year 2). Applications must include a CV, a 1-page description of previous or current research and a 2- 3 page description of proposed research as well as a brief description of possible seminar and symposium topics. In addition, the applicant must arrange for two recommendation letters from non-UNL faculty, and one from each of the proposed UNL faculty sponsors (a total of 4 letters) to be emailed to the address below. The expected salary will be $45,000. The position does not include research funds so it is anticipated that these needs, if modest, can be met through contributions from the faculty sponsors and should be addressed in the proposal.

Application materials should be emailed to: Dr. Gwen Bachman at: gbachman1@unl.edu. The subject line should read “Population Biology Post-doc application”. Applications should be received by 1 May 2014 in order to ensure full consideration. We strongly encourage applications from women and members of minority groups. The University of Nebraska is committed to a pluralistic campus community through affirmative action, equal opportunity, work-life balance, and dual careers. We assure responsible accommodation under the Americans with Disabilities Act.

Diana Pilson School of Biological Sciences 348 Manter Hall University of Nebraska Lincoln, NE 68588-0118

402-472-2347 (office) 402-472-2083 (fax)

dpilson@unl.edu

UOregon Bioinformatics MicrobialEcol

Postdoctoral Research Associate Institute of Ecology and Evolution Posting: 14066 Location: Eugene Closes: Open Until Filled

Position in Bioinformatics/Microbial Ecology

Jessica Green (http://pages.uoregon.edu/green/) and Brendan Bohannan (http://pages.uoregon.edu/-bohannanlab/) are currently seeking a bioinformatics postdoctoral researcher to explore fundamental questions in microbial ecology and evolution. Applicants should have a PhD with extensive training using bioinformatics to understand the ecology and/or evolution of complex biological communities, and strong writing skills. The ideal candidate will have experience developing and applying quantitative community and population ecological methods to the analysis of environmental sequence data and next-generation sequence data.

The successful candidate will play a key role in the Biology and Built Environment (BioBE) Center (http:/-/biobe.uoregon.edu/), funded by the Alfred P. Sloan Foundation. The BioBE Center is training a new generation of innovators to study the built environment microbiome - the diversity of indoor microbial life, their genetic elements and their interactions. The vision of this national research center is to understand buildings as complex ecosystems and to explore how architectural design mediates urban microbial ecology and evolution. For a description of partner projects see http://www.microbe.net/ . The position is available for 1 year with the possibility for renewal depending on performance. The start date is flexible. Please email questions regarding the position to Jessica Green (jlgreen@uoregon.edu).

To apply

A complete application will consist of the following materials:

(1) a brief cover letter explaining your background and career interests

(2) CV (including publications)

(3) names and contact information for three references

Submit materials to ie2jobs@uoregon.edu. Subject: Posting 14066

To ensure consideration, please submit applications by April 25, 2014, but position will remain open until filled.

Women and minorities encouraged to apply. We invite applications from qualified candidates who share our commitment to diversity. EO/AA/ADA institution committed to cultural diversity. http:/-/jobs.uoregon.edu/unclassified.php?id=4621 http://-jobs.uoregon.edu/unclassified.php?id=4620 Research Assistant Institute of Ecology and Evolution Posting: 14064 Location: Eugene Closes: Open Until Filled

The Institute of Ecology and Evolution at the University of Oregon currently has an opening for a full time Research Assistant to work in the area of microbial ecology. The successful candidate will play a key role in the Biology and Built Environment (BioBE) Center (http://biobe.uoregon.edu/), funded by the Alfred P. Sloan Foundation. The BioBE Center is training a new generation of innovators to study the built environment microbiome - the diversity of indoor microbial life, their genetic elements and their interactions. The vision of this national research center is to understand buildings as complex ecosystems and to explore how architectural design mediates urban microbial ecology and evolution. For a description of partner projects see http://www.microbe.net/ . The initial appointment is for one year, with the possibility of extension dependent on funding and satisfactory performance. The University of Oregon is located in Eugene, Oregon, recently rated in the top 10 “Best Places to Live” (livability.com).

Extensive experience using molecular techniques is required, including some combination of skills in DNA/RNA extraction, PCR, cloning, next-generation DNA sequencing, bioinformatics, and phylogenetic analysis. Ability to work in a team atmosphere is a must. A Master’s degree in biology is desirable, but individuals with a bachelor in biology or related field and extensive experience are also encouraged to apply. The successful candidate will be responsible for conducting laboratory research under the direction of Principle Investigators Jessica Green (pages.uoregon.edu/green) and Brendan Bohannan (http://pages.uoregon.edu/-bohannanlab/). Salary will be commensurate with education and experience. We invite applications from qualified candidates who share our commitment to diversity.

Please e-mail a cover letter and current CV with names and contact information of three references to: ie2jobs@uoregon.edu Subject: Posting 14064

Or mail to:

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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

UOtago NZ Molecular basis sexreversal fish

Postdoctoral Opportunity

Fixed term, Three years

The molecular basis of sex reversal in sequentially hermaphroditic fish We are currently seeking an outstanding postdoctoral researcher with interests in genetics, evolution, physiology and behavioural ecology to conduct research into the genetic basis of sex reversal in sequentially hermaphroditic fish.

Project Description: Most plants and animals irreversibly differentiate becoming either males or females. However, in some groups, notably fishes, individuals begin life as one sex and reverse sex sometime later in response to social cues (sequential hermaphrodism). Sex reversal in sequential hermaphrodites is complete, entailing radical restructuring of the gonad, alterations in morphology, and modifications to behaviour. The molecular basis of this stunning transformation is unknown, but is of intense interest, not only as a means to enhance our understanding of sex determination and differentiation, cellular commitment and tissue reengineering, but also as a spectacular example of phenotypic plasticity in response to environment. Using the ubiquitous NZ spotty, together with two distant tropical relatives, the bluehead and three-spotted wrasse, both leading models for sex reversal, we will undertake a series of experiments to determine the genetic pathway underlying this stunning transformation. We will couple in the field ecological manipulations to produce a time series of samples taken during the process of sex reversal, with state-of-the-art gene expression analyses and comparative genomic approaches, to identify both the primary trigger and subsequent genetic cascade that results in female-male sex reversal in fishes.

The project emerges from a new Marsden Grant headed by Professor Neil Gemmell and will be based in the Gemmell laboratory at the University of Otago.

The Ideal Candidate: Applications are invited from postdoctoral candidates who have experience in molecular biology, evolutionary and population genetics/genomics, and bioinformatics. The successful candidate will likely be skilled in molecular genetic techniques and in the analysis of genetic data and associated statistics. They will be highly self-motivated and be able to work alongside a wide variety of people. In addition they will have a strong commitment to research excellence with a track record of high research productivity based on international, peer-reviewed publications commensurate for their career stage.

How to Apply: Interested applicants are encouraged to make informal enquiries to Professor Neil Gemmell. Please send your Curriculum Vitae, a sample of your written scientific work and the names of three referees with a covering letter to:

Professor Neil J. Gemmell e-mail: neil.gemmell@otago.ac.nz

Formal Applications must be made at: https://otago.taleo.net/careersection/2/jobdetail.ftl?lang=en&job=1400626 Salary Level and Range: Postdoctoral Fellow ($72,046), Fixed term until January 2017

Reference Number: 1400626

Closing Date: Thursday, 17 April 2014

Professor Neil J. Gemmell Head of Department Department of Anatomy University of Otago, PO Box 913 Dunedin 9054 New Zealand

Phone: +64 3 479 6824 Fax: +64 3 479 7254 e-mail: neil.gemmell@otago.ac.nz Web: http://gemmell-lab.otago.ac.nz/ Allan Wilson Centre for Molecular Ecology and Evolution: http://www.allanwilsoncentre.ac.nz/ Gravida - National Centre for Growth and Development: http://www.gravida.org.nz/ Neil Gemmell <neil.gemmell@otago.ac.nz>

UOxford PlantEvolutionFellowships

Independent Research Fellowships in Oxford UK

The Department of Plant Sciences at the University of

Oxford is keen to hear from early career researchers who feel they have what it takes to secure a fellowship from one of the UK or international research sponsors and become an Independent Research Fellow in the Department. Fellowship opportunities include: * BBSRC David Phillips Fellowship * Royal Society University Research Fellowship * NERC Fellowship * ERC Starting Grants.

These schemes enable the best early career researchers to establish themselves as independent research fellows with their own research groups. The fellowships are prestigious and competitive. Sponsors' eligibility criteria apply. We can support the best candidates to apply for fellowships. We are also keen to hear from fellows who may wish to transfer a current fellowship to the Department.

See www.plants.ox.ac.uk *We particularly welcome enquiries by Friday 4 April, 2014.*

Dmitry Filatov <dmitry.filatov@plants.ox.ac.uk>

UPennNCStateU HoneyBeeBreedingSociogenomics

Postdoctoral position in honey bee sociogenomics and breeding

A postdotoral researcher position is available for a US Department of Agriculture funded project that seeks to use artificial selection and sociogenomic approaches to study and ultimately improve honey bee traits associated with queen reproductive quality. This project is a close collaboration between the Linksvayer lab (http://linksvayer.bio.upenn.edu/) in the Department of Biology at the University of Pennsylvania and the Tarpy lab (http://entomology.ncsu.edu/apiculture) in the Department of Entomology at North Carolina State University.

We seek enthusiastic, talented, and driven individuals to carry out the funded research project as well as to conduct related original research. We are especially interested in candidates with experience in one or more of the following: honey bee in vitro rearing or other organismal honey bee research, artificial selection and instrumental insemination, RNA or genome sequencing, evolutionary genetics, and bioinformatics. The project will present opportunities to work at both universities to gain expertise in these and other approaches.

The start date is flexible but can begin right away. Applications will be considered as they are received until the position is filled. Funding is available for multiple years, contingent on satisfactory progress. To apply, send your CV, a short statement of research interests, contact information for three references, and optionally a representative paper or manuscript to Tim Linksvayer at tlinks@sas.upenn.edu. Please contact Tim Linksvayer or David Tarpy (drtarpy@ncsu.edu) for further information.

Timothy Linksvayer Assistant Professor Department of Biology, University of Pennsylvania 225 Leidy Laboratories, 433 South University Avenue Philadelphia PA 19104-6018 tlinks@sas.upenn.edu phone +1 215 573 2657 http://www.bio.upenn.edu/faculty/linksvayer/
Tim Linksvayer <tlinks@sas.upenn.edu>

USaoPaulo GWU BiodiversityInformatics

Postdoctoral Fellow in Biodiversity Informatics

The University of São Paulo (Department of Botany) and The George Washington University (Computational Biology Institute) seek candidates for a postdoctoral fellowship in biodiversity informatics for up to three years. The successful candidate would split time between the two host institutions working on applications of next-gen sequencing approaches to biodiversity science through effective informatics. We seek a candidate with a PhD in bioinformatics, evolutionary biology, biodiversity science, or a related field (or anticipate a PhD by a targeted start date of September 1, 2014). The candidate should have a strong background in bioinformatics, evolutionary methodology, and project management skills. The candidate will work directly with Drs. Lúcia Lohmann (São Paulo), Amy Zanne, and Keith Crandall (Washington DC) and the bioGENESIS working group http://www.biogenesis-diversitas.org to provide an evolutionary framework for biodiversity science. Our specific project is to use next-generation DNA sequencing approaches to characterize forest and associated soil communities and their diversity across ecosystems using novel informatic approaches. Interested candidates should send their CV and letter of interest by April 22, 2014 to cbi@gwu.edu. For questions concerning this opportunity, please contact Lúcia Lohmann llohmann@usp.br, Amy Zanne azanne@gwu.edu or Keith Crandall kcrandall@gwu.edu.

Keith Crandall, PhD Director - Computational Biology Institute George Washington University 45085 University Drive Innovation Hall Suite 305 Ashburn, VA 20147-2766 w: (571) 553-0107 c: (202) 769-8411 kcrandall@gwu.edu

Keith Crandall <kcrandall@gwu.edu>

USydney EvolutionOfVirulence

POSTDOCTORAL RESEARCH ASSOCIATE - EVOLUTION OF VIRULENCE IN VIRAL PATHOGENS FACULTY OF SCIENCE, SCHOOL OF BIOLOGICAL SCIENCES, UNIVERSITY OF SYDNEY, AUSTRALIA REFERENCE NO. 2580/1113

- Further develop your research profile on an Australian Research Council Discovery Grant project - Virology, bioinformatics and evolutionary biology - Full-time, fixed term 3 years; remuneration package: up to $99K p.a.

The University of Sydney is Australia's first University with an outstanding global reputation for academic and research excellence. It employs over 7500 permanent staff supporting over 49,000 students. The University's School of Biological Sciences has over 30 academic staff members who are active in teaching, research, and have outstanding international reputations.

Applications are sought for a Postdoctoral Research Associate positions to participate in a new research programme investigating the evolution of virulence in viral pathogens, using caliciviruses of rabbits as a model system. The project is funded by an Australian Research Council Discovery Grant held by Professor Edward C. Holmes (NHMRC Australia Fellow).

Rabbit Haemorrhagic disease virus (RHDV) is a calicivirus that is used widely in Australia and New Zealand to control overabundant rabbits, a major environmental and economic pest. It is an example of an emerging disease that likely evolved from a non-virulent predecessor via mutation into an extremely virulent virus. However, the nature of these mutations remains unknown. The first part of the project will involve sequencing of large numbers of non-pathogenic and pathogenic calicivirus sequences for genetic analysis, aimed at identifying the likely âgenetic switches' responsible for the acquisition of virulence and tissue tropism. The second part of the project will involve the design and development of recombinant viral genomes in order to deactivate the proposed genetic switches, and the subsequent testing of these viruses in the rabbit host.

This is an outstanding opportunity to further develop your research career in a specialised field under the guidance and mentoring of highly regarded research academics. As this is a collaborative project with CSIRO Ecosystem Sciences in Canberra, you will be largely based in Canberra for the laboratory work.

To succeed you will have: - a PhD and a record of published research as sole author or in collaboration on a related subject area (e.g. virology, molecular evolution, biocontrol)

- strong demonstrated skills in molecular biology and virology with a good understanding of the key aspects of virus biology

- demonstrated experience in planning, conducting and interpreting next-generation sequencing data and analyses

- experience in Bioinformatic analysis (i.e. computational biology) of gene and genome sequences

- keen interest in phylogenetic analysis, bioinformatics and evolutionary biology

- willingness to work with laboratory animals for research purposes

- demonstrated ability to conduct research/scholarly activities under limited supervision either independently or as a member of a team, and to facilitate collaborations with other research groups

- good written and verbal communication skills, experience in research record keeping, preparation of research papers and seminars.

The position is full-time fixed term for three years subject to the completion of a satisfactory probation period for new appointees. Membership of a University approved superannuation scheme is a condition of employment for new appointees.

Remuneration package: up to $99K including base salary up to level A step 7, leave loading and up to 17% superannuation. Some support towards relocation and visa sponsorship will be available for the successful appointee if required.

All applications must be submitted via the University of Sydney careers website. Visit sydney.edu.au/recruitment and search by the reference number for more information and to apply. Previous applicants need not apply.

CLOSING DATE: 21 April 2014 (11:30pm Sydney time)

The University is an equal opportunity employer committed to equity, diversity and social inclusion. Applications from equity target groups and women are encouraged. The University of Sydney has also established a scheme to increase the number of Aboriginal and Torres Strait Islander staff employed across the institution. Applications from people of Aboriginal and Torres Strait Islander descent are encouraged.

PROFESSOR EDWARD C. HOLMES NHMRC Australia Fellow

THE UNIVERSITY OF SYDNEY Marie Bashir Institute for Infectious Diseases & Biosecurity, Charles Perkins Centre, School of Biological Sciences and Sydney Medical School, Macleay Building A12 | The University of Sydney | Sydney | NSW | 2006 | Australia T +61 2 9351 5591 F +61 2 9351 3890 E edward.holmes@sydney.edu.au

Edward Holmes <edward.holmes@sydney.edu.au>

UVirginia EcologicalGenomics

The Department of Biology at the University of Virginia invites applications for a postdoctoral Research Associate position in the Blackman laboratory. A collaborative project between Dr. Stacey Harmer at UC Davis and the Blackman lab will utilize investigate solar tracking by developing sunflower heads as an experimental system for investigating how and why internal and environmental signals are integrated to regulate plant growth. Funded by a grant from the NSF Plant Genome Research Program, the postdoc will take a central role in developing and implementing studies of the genetics of natural variation. Responsibilities will include association mapping of circadian and growth traits, characterization of candidate genes, and implementation of functional studies.

The postdoc will work closely with the PI, lab personnel, the Harmer lab, and other collaborators to design and lead research in the lab and field. The position also will also involve significant time devoted to data management and dissemination, mentoring graduate and undergraduate students, and coordinating data analysis efforts with collaborators at UVA and elsewhere.

The ideal candidate will demonstrate the ability to integrate across biological disciplines, identify and troubleshoot promising new methodologies independently, and use the appointment to develop and pursue novel, exciting questions. Demonstrated expertise in quantitative and developmental genetics is essential. Specific experience in at least two of the following areas is also required, and experience with more than two of these areas is preferred: 1) Analysis of association and QTL mapping data 2) transgene construction and plant transformation in tissue culture, 3) programming, database development, and analysis of NextGen genomic or transcriptomic datasets, and 4) morphometrics.

The completion of a Ph.D. degree in Biology or related field by appointment start date is required. Preferred appointment start date is April 2014.

This is a one-year appointment; however, appointment may be renewed for an additional two, one-year increments, contingent upon available funding and satisfactory performance.

To apply, please submit a candidate profile through Jobs@UVA (https://jobs.virginia.edu) and electronically attach: curriculum vitae with list of publications, a cover letter that summarizes their research interests and professional goals, and contact information for three (3) references; search on posting number 0613701.

Review of applications will begin March 8, 2014; however, the position will remain open until filled.

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

Richard Haverstrom rkh6j@virginia.edu

The University will perform background checks on all new hires prior to making a final offer of employment.

The University of Virginia is an affirmative action/equal opportunity employer committed to diversity, equity, and inclusiveness. Women, Minorities, Veterans and Persons with Disabilities are encouraged to apply.

bkb2f@virginia.edu

Umea ModellingEcologicalSpeciation

Postdoctoral Scholarship (2 years) for Modelling of Ecological Speciation - Umeå University

The Department of Ecology and Environmental Science (EMG) www.emg.umu.se and Integrated science Lab (Icelab) www.org.umu.se/icelab is offering a postdoctoral scholarship within the project 'Speciation in action'.

Project description This project is focused on the interplay between ecology and evolution. The goal of the project is to understand the flip side of ecological speciation. As speciation is occurring in the focal species, the food web can be modified as the focal species changes its mechanisms of predator avoidance or its diet. The postdoc will be involved in building a general theoretical model that includes the within-species diversification, the impacts on the food web, and the feedback between the two. Collaboration with the empirically oriented research group of Professor Göran Englund is possible if the successful candidate is interested to model diversification in Scandinavian whitefish populations.

Requirements To qualify for the scholarship you should have a PhD degree in evolutionary biology, or equivalent, not more than 3 years old. Knowledge of population genetics and modelling of ecological and evolutionary dynamics is highly desirable. In-depth knowledge of an empirical system fitting the project description would also be an asset. From the successful candidate, we expect a documented capability of cooperative scientific research work and skills in writing scientific publications in English. International applicants are encouraged to apply.

The fellow will be based at Icelab and the Department of Ecology and Environmental Science in Umeå, and is financed through a personal scholarship from the Kempe Foundations.

Application The application should include a short description of your research interests and why you are interested in the scholarship, a CV, a publication list, copies of exam certificates (official copies are not necessary for the application, but may be required at the time of hire), and contact information of 3 reference persons. The application should be written in English and should be submitted electronically (ideally in a single pdf).

For more information, please contact Dr. Xavier Thibert-Plante, e-mail xavier.thibert.plante@emg.umu.se.

Union information is available from SACO, +46-(0)90-786 53 65, SEKO civil, +46-(0)90-786 52 96 and ST, +46-(0)90-786 54 31.

Your complete application marked with reference Kempe-2014, should be sent to xavier.thibert.plante@emg.umu.se (with reference number on the subject line). Review of the application starts now and continues until the fellowship is awarded.

Umeå University is dedicated to providing creative environments for learning and work. We offer a wide variety of courses and programmes, world leading research, and excellent innovation and collaboration opportunities. More than 4 400 employees and 34 000 students have already chosen Umeå University. We welcome your application!

http://xavier.thibert-plante.com Xavier Thibert-Plante, Ph.D. Email: xavier@thibert-plante.com Website: http://www.xavier.thibert-plante.com xavier@thibert-plante.com

WorkshopsCourses

Aix-en-Provence France Meta-analysis May13-15

The Center for synthesis and analysis of biodiversity (CESAB), Aix en Provence, France, is pleased to announce a training course on meta-analysis organized May 13-15, 2014.

http://cesab.org/index.php?option=com_content&view=article&id=86:announcement-for-a-meta-analysis-training-workshop&catid=41:actualites&Itemid=347&lang=fr

Deadline for registration is almost up: March 10, 2014. Selection of applicants: March 15, 2014.

bruno.fady@avignon.inra.fr

Barcelona GeometricMorphometrics Aug4-8

Introduction (August) and Phylogeny (September), Barcelona, Spain Soledad De Esteban Trivigno <soledad.esteban@transmittingscience.org>

Dear colleagues,

Registration is open for the following courses:

"INTRODUCTION TO GEOMETRIC MORPHOMETRICS- 5th edition", August 4-8, 2014; 38 hours on-site. Instructors: Dr. Chris Klingenberg (University of Manchester, UK) and Dr. Jesús Marugán (UAM, Spain). www.transmittingscience.org/courses/gm/introduction-to-gm/ "GEOMETRIC MORPHOMETRICS AND PHYLOGENY- 5th edition"; September 8-12, 38 hours on-site. Instructor: Dr. Chris Klingenberg (University of Manchester, UK). http://www.transmittingscience.org/courses/gm/gm-and-phylogeny/ PLACE: Facilities of the Centre of Restauració i Interpretació Paleontologica, Els Hostalets de Pierola, Barcelona (Spain).

Organized by: Transmitting Science, the Institut Catalá de Paleontologia Miquel Crusafont and the Council of Hostalets de Pierola.

Please feel free to distribute this information between your colleagues if you consider it appropriate.

With best regards

Soledad De Esteban Trivigno, PhD. Course Director Transmitting Science < http://www.transmittingscience.org/ >

Soledad De Esteban Trivigno <soledad.esteban@transmittingscience.org>

Florida EvolutionaryGenomics

Dear colleagues -

Are any of you interested in learning RNAseq, 2b-RAD, qPCR or meta-barcoding in the beautiful Florida Keys this summer?

Back by popular demand, we are pleased to announce that in June-July 2014 we will teach a series of week-long workshops on Methods in Ecological and Evolutionary Genomics at the Mote Tropical Research Laboratory, Florida Keys. We sending out a survey to determine which courses will gather the most interest since we can only offer three (~1 week long) courses.

1. tag-based RNA-seq 2. 2b-RAD 3. quantitative PCR 4. Meta-barcoding with amplicon sequencing

If you are interested in participating in these workshops, please respond to this survey

http://www.surveymonkey.com/s/5ftx7rs

See the links below for examples of manuscripts produced from previous workshops, with workshop participants as co-authors:

http://www.plosone.org/article/-info%3Adoi%2F10.1371%2Fjournal.pone.0026914#pone-0026914-g005 http://onlinelibrary.wiley.com/doi/-10.1111/1755-0998.12218/full Keep in mind that each workshop will be roughly $1,500 (depends on reagents, to be finalized), which includes accommodation but not food and transportation.

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

matz@utexas.edu

HCMR Crete MicrobialDiversity May27-Jun6

Micro B3 Summer School in Crete 2014: from sampling to analyzing microbial diversity & function

This summer school is organized as a two-week interactive training *from Tuesday 27 May to Friday 6 June 2014* at the HCMR on Crete, Greece. Every day a high-level lecturer will share expertise with the students, focusing on standards & methods, with theory in the morning and interactive practical work in the afternoon.

The summer school focuses on *preparing* and *planning* integrated *sampling work* and *data flows*, taking into account some legal aspects, with a focus on *bioinformatic* and *oceanographic tools*. The group will perform data and sample management based on the use of enrichments for analyses during the course, on existing (OSD) data sets and the OSD Handbook. Trainees will learn how to decide on using methods and standards to address their research questions in the fields of plankton diversity, ecology and function, including biotechnological applications.

A small boat trip will be planned, log sheets & standardized sampling methods tested on board and in the lab, and samples prepared for sequencing. Also the group will learn about Access and Benefit Sharing aspects, documentation and archiving. Finally, the use of selected datasets for ecological modelling will be explored.

The number of participants is limited to 25 and the application period will close on *15 March 2014*.

Information: http://www.microb3.eu/events/-workshops/micro-b3-summer-school-crete Katerina Vasileiadou Institute of Marine Biology, Biotechnology and Aquaculture Hellenic Centre for Marine Research (HCMR) P.O. Box 2214 71003 Heraklion Crete Greece

Tel: +30 2810 337742 Fax: +30 2810 337870 email: kvasileiadou@hcmr.gr

Hellenic Center for Marine Research

Katerina Vasileiadou <kvasileiadou@hcmr.gr>

Helsinki DynamicsInfectiousDisease Aug17-24

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

Hinxton Cambridge HumanGenomeAnalysis Jul23-29

Human Genome Analysis, Genetic Analysis of Multifactorial Diseases Venue: Wellcome Trust Genome Campus, Hinxton, Cambridge, UK When: 23 - 29 July 2014 Application deadline: 11 April 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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Italy PopBiolGenetics May30-Jun1

UZI Spring School 2014 in "Population Biology and Population Genetics"

Organized by _Unione Zoologica Italiana_ - UZI

Dates

May 30-31, June 1, 2014

Teaching staff

Guido Barbujani -/Università di Ferrara/

Giacomo Bernardi -/University of California at Santa Cruz/

LuigiBoitani –/Università di Roma la Sapienza/

Michael Bruford -/Cardiff University/

Gisella Caccone -/Yale University/

Gary Carvalho -/Bangor University/

Claudio Ciofi -/Università di Firenze/

Scott Edwards - /Harvard University/

Diego Fontaneto -/CNR Pallanza/

Tomaso Patarnello -/Università di Padova/

Program

- Genetics and global biodiversity policy (M. Bruford)
- Global climate change and fish genomics (G. Bernardi)

- Population biology, population genetics and speciation in animals with asexual reproduction (D. Fontaneto)

- Bridging the gap between population genetics and phylogenetics: an overview of theory and examples (S. Edwards)

- Evolutionary genetics and conservation of giant Galapagos tortoises//(G. Caccone)

- The vagaries of island living: population ecology and genetics of Komodo dragons (C. Ciofi)

- Genetic structuring in an open world: detection and significance in marine fishes (G. Carvalho)

- The genetics and genomics of Lessepsian bioinvasions (G. Bernardi)

- Living in the cold, fish adaptation and evolution in the Southern Ocean (T. Patarnello)

- Management of large carnivores in Europe: a different dimension of the population concept(L. Boitani)

- Phylogeography and conservation of African mammals (M. Bruford)

- We, the Africans: fifteen things to remember about human genome diversity/ /(G. Barbujani)//

Webpage

http://www.uzionlus.it/ Application Deadline: April 28, 2014

Location

The school will be held at the /Istituto Veneto di Scienze, Lettere ed Arti/, hosted in /Franchetti Palace/, one of the most beautiful historical palaces on the Canal Grande(web site: http://-www.istitutoveneto.it/index.html)

*_Who can apply_*

The course is designed for PhD students, post-doctoral and young tenure-track researchers. Maximum number of participants is 30. Preference will be given on the basis of personal motivation, and CV. Application form is available at http://www.uzionlus.it/-and must be sent to segreteriauzi@unimore.it < https://webmail.unipd.it/squirrelmail/src/-compose.php?send_to=segreteriauzi%40unimore.it > by April 28

Costsandfacilities

The fee is of 150 euro and includes:

- double-room accommodation for 2 nights at Istituto Artigianelli (http://www.donorione-venezia.it/)

- 1 welcome dinner

- 1 lunch

- 4 coffee breaks

School Director: Tomaso Patarnello (tomaso.patarnello@unipd.it)

Tomaso Patarnello <tomaso.patarnello@unipd.it>

MathVillage Turkey QuantEvolutionaryBiol Sep14-21

*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

Murat Turul

PhD Student @ Barton Group Evolutionary Genetics, IST-Austria

muratugrul@gmail.com

Milan MicrobialEcology Jul12-25

*_FACILIS 2014_*

This year, the University of Milan will host an international short course of the EU-US Taskforce on Biotechnology Research, working group of Environmental Biotechnology. The event builds on the success of the four previous courses in training early-career scientists in state-of-the-art theoretical and practical aspects of environmental biotechnology. This year's short course is entitled "FACILIS 2014, Microbially-driven facilitation systems in environmental biotechnology". The two-week long, hands-on experimental programme includes field trips and daily lectures in environmental microbiology and microbial biotechnology. The central concept focuses on the identification of microbial strains that can be harnessed for environmental purposes such as contaminant degradation or for beneficial plant-microbe interactions. Course experiments will include community analyses by PCR fingerprinting, barcoding, pyrosequencing and metagenomics, and tests on bacterial isolates such as growth on biphenyl, search for degradation-related genes, plant growth promotion, strain genetic labelling and /in vivo/ colonisation.

Twenty four young scientists will be invited to participate – 12 from each side of the Atlantic. Applications will be accepted from students working in the USA or one of the EU Member States or Associated Countries at the time of application, or from students having a citizenship of one of those countries. The course will be held from 12-25 July 2014 in Milan, Italy.

Registration is open until 15 April 2014. Complete information on the venue, speakers and course programme, as well as on how to apply for registration, is available on the course website http://www.facilis2014.unimi.it Bessem Chouaia, PhD. Department of Food, Environmental and Nutritional Sciences (DeFENS) University of Milan via Celoria 2, 20133 Milano, ITALY Tel: +39-0250319146; Fax: +39-0250319238 E-mail: bessem.chouaia@unimi.it

bessem <bessem.chouaia@unimi.it>

NESCentAcademy Macroevolution Jul22-29

Title: Paleobiological and phylogenetic approaches to macroevolution Dates: July 22-29, 2014 Application review begins: May 1, 2014 Website: academy.nescent.org Where: National Evolutionary Synthesis Center (NESCent), Durham, NC

As part of the NESCent Academy, we are pleased to open applications for 'Paleobiological and phylogenetic approaches to macroevolution'. This course will teach participants to use fossil and phylogenetic data to analyze macroevolutionary patterns using traditional paleobiological stratigraphic methods, phylogenetic comparative methods and combined fossil and tree approaches. By the end of the course participants will be able to use online paleobiological databases to download fossil occurrence data and estimate speciation and extinction rates while controlling for sampling bia; will understand the basics of building phylogenies of fossil and extant species and use such phylogenies to estimate speciation and extinction rates; and finally, will understand how to use models of evolution to calculate phenotypic disparity using stratigraphic and phylogenetic approaches as well as estimate ancestral states and the tempo and mode of trait evolution. This cross-disciplinary course is designed to train a new generation of researchers capable of implementing both fossil and tree-methods, paving the way towards a new synthetic approach to study macroevolution.

Instructors: * Roger Benson: Dept. of Earth Sciences, University of Oxford * Samantha Hopkins: Clark Honors College and the Department of Geological Sciences, University of Oregon * Gene Hunt: Dept. of Paleobiology, National Museum of Natural History, The Smithsonian Institution * Samantha Price: Dept. Evolution & Ecology, University of California Davis * Daniel Rabosky: Dept. of Ecology and Evolutionary Biology, University of Michigan * Lars Schmitz: Keck Science Department, Claremont McKenna, Pitzer, and Scripps Colleges * Graham Slater: Dept. of Paleobiology, National Museum of Natural History, The Smithsonian Institution

Areas to be covered include: * introduction to paleobiological data and the use of online paleobiological databases * introduction to phylogenetic data * stratigraphic and phylogenetic approaches to analyzing lineage diversification * estimating disparity using fossils and phylogenies * analyzing patterns of trait evolution using fossils and phylogenies

Questions? Email academy@nescent.org

karen.cranston@gmail.com @kcranstn

Karen Cranston <karen.cranston@gmail.com>

NESCentAcademy NGS Phylogenetics Phylogeography Jul14-19

Title: Next-generation sequencing for phylogenetics and phylogeography Dates: July 14-19, 2014 Application review begins: May 1, 2014 Website: http://academy.nescent.org Where: National Evolutionary Synthesis Center (NESCent), Durham, NC

The fields of phylogenetics and phylogeography are on the cusp of a revolution, enabled by the rapid expansion of genomic resources and explosion of new genome sequencing technologies. Researchers are now able to obtain large phylogenomic data sets for any system rapidly and economically. In this course, students will receive an overview of recent technological advances, learn about data collection using emerging phylogenomic approaches, and analyze data sets using the most recent methods. This couse will provide tools for many critical efforts in the field including assembling the Tree of Life, delimiting species, and understanding the processes driving speciation. The intended audience is graduate students, postdoctoral researchers, and faculty who wish to gain training in this area.

Instructors: * Alan Lemmon: http://www.evotutor.org/LemmonLab/People-Dr.Lemmon.html, http://www.anchoredphylogeny.com * Emily Moriarty Lemmon: http://www.bio.fsu.edu/chorusfrog/, http://www.anchoredphylogeny.com * Cecile Ane: http://www.stat.wisc.edu/ ˜ ane/ * Jeremy Brown: http://www.phyleaux1.lsu.edu * Frank Burbrink: http://csivc.csi.cuny.edu/Frank.Burbrink/files/ * Seth Bybee: http://lifesciences.byu.edu/ ˜ sb38 * David Weisrock: http://sweb.uky.edu/ ˜ dweis2/The_Weisrock_Lab/Front_Page.html * Paul Fransden: http://rci.rutgers.edu/˜insects/grads.htm Areas to be covered include:

* emerging sequencing technologies * targeted high-throughput sequencing approaches, such as anchored phylogenomics, transcriptome sequencing, reduced-representation library sequencing/RAD sequencing, and high-throughput amplicon sequencing * data analysis, including phylogenetic and phylogeographic analysis, and species delimitation.

Questions? Email academy@nescent.org

karen.cranston@gmail.com @kcranstn

Karen Cranston <karen.cranston@gmail.com>

NESCentAcademy PhylogeneticAnalysisUsingRevBayes Aug25-31

Title: Phylogenetic Analysis Using RevBayes Dates: August 25-31, 2014 Application review begins: May 1, 2014 Website: academy.nescent.org Where: National Evolutionary Synthesis Center (NESCent), Durham, NC

Phylogenies have become central to virtually all areas of research in evolutionary biology, ecology, molecular biology and epidemiology. The development of a Bayesian statistical framework for phylogeny estimation is one of the most significant developments in this area of study over the past decade and has facilitated the development of models that better capture biological complexity. Moreover, by integrating over parameter values, Bayesian inference provides a natural way to accommodate uncertainty in both estimates of phylogeny (and other model parameters) and inferences based on those phylogenies.

Advances in theory have been accompanied by advances in software implementing new phylogenetic models. This course is built around the use of the new, open-source program RevBayes (http://sourceforge.net/projects/revbayes/) and is organized and staffed by the developers. RevBayes has as a central idea that phylogenetic models, like any statistical model, are composed of smaller parts that can be decomposed and put back together in a modular fashion. This comes from considering phylogenetic models as probabilistic graphical models, which lends flexibility and enhances the capabilities of the program. RevBayes implements an R-like language (complete with control statements, user-defined functions, and loops) that enables the user to build up phylogenetic models from simple parts (random variables, transformations, models, and constants of different sorts).

Fundamentally, this course will begin by covering the basics of probability theory, graphical models, and phylogenetics. Then, building on these concepts, we will provide lectures on statistical methods for phylogenetic inference, macroevolution, and epidemiology. Each component of the course will include hands-on tutorials for conducting analyses in RevBayes. Additionally, open-labs are scheduled for participants interested in applying these methods to their own data or working with the developers to create new models in the RevBayes language.

Instructors: * Bastien Boussau, LBBE, Lyon, France * Tracy Heath, UC Berkeley & U Kansas * Sebastian Höhna, Stockholm University * John Huelsenbeck, UC Berkeley * Michael Landis, UC Berkeley * Brian Moore, UC Davis * Fredrik Ronquist, NRM Stockholm * Tanja Stadler, ETH Zürich

Questions? Email academy@nescent.org

karen.cranston@gmail.com @kcranstn

Karen Cranston <karen.cranston@gmail.com>

NIMBioS Knoxville EvolutionaryQuantGenet Aug4-9

The National Institute for Mathematical and Biological Synthesis (NIMBioS) is now accepting applications for its Tutorial, “Evolutionary Quantitative Genetics,” to be held August 4-9, 2014, at NIMBioS.

*Objectives: *Quantitative genetic theory has been applied to a wide range of phenomena including the evolution of differences between the sexes, sexual preferences, life history traits, plasticity of traits, as well as the evolution of body size and other morphological measurements. This tutorial is for evolutionary biologists interested in how quantitative genetics theory can be tested with data. Participants – graduate students, postdocs, and junior faculty – will learn how to use R to build and test evolutionary models. There is a need for evolutionary biologists to understand the field of evolutionary quantitative genetics because of the ability to collect large amounts of data by computer, the development of statistical methods for changes of traits on evolutionary trees and for changes in a single species through time, and the realization that quantitative characters will not soon be fully explained by genomics.

*Location: *NIMBioS at the University of Tennessee, Knoxville

*Co-Organizers: *Stevan J. Arnold, Integrative Biology, Oregon State Univ. and Joe Felsenstein, Genome Sciences, Univ. of Washington, Seattle

*Co-Sponsors: *National Evolutionary Synthesis Center (NESCent) and the American Society of Naturalists

For more information about the tutorial and a link to the online application form, go to http://www.nimbios.org/tutorials/TT_eqg There are no fees associated with this tutorial. Tutorial participation in the tutorial is by application only. Individuals with a strong interest in the topic, including post-docs and graduate students, are encouraged to apply, and successful applicants will be notified within two weeks of the application deadline.

*Food and Lodging: *Breakfast and lunch will be provided at NIMBioS each day of the tutorial, as well as coffee and mid-morning and mid-afternoon snacks. NIMBioS is not covering other expenses for participants, but a block of rooms will be reserved at a nearby hotel. More information will be available on our website soon about lodging, room rates, and how participants can make reservations.

Application deadline: May 1, 2014

The National Institute for Mathematical and Biological Synthesis (NIMBioS) (http://www.nimbios.org) brings together researchers from around the world to collaborate across disciplinary boundaries to investigate solutions to basic and applied problems in the life sciences. NIMBioS is sponsored by the National Science Foundation, the U.S. Department of Homeland Security, and the U.S. Department of Agriculture with additional support from The University of Tennessee, Knoxville.

Catherine Crawley, Ph.D. Communications Manager National Institute for Mathematical and Biological Synthesis (NIMBioS) University of Tennessee 1122 Volunteer Blvd, Ste. 106 Knoxville, TN 37996 e ccrawley@nimbios.org t +1 865 974 9350 f +1 865 974 9461 http://www.nimbios.org http://www.facebook.com/nimbios http://twitter.com/nimbios Catherine Crawley <ccrawley@nimbios.org>

Roscoff France MarineEvolGenomics May25-Jun7

>From May 25th - June 7th, 2014 10th Summer Course on Marine Evolutionary & Ecological Genomics at the Station Biologique de Roscoff, Roscoff, France.

First announcement

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

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>

SCENE Scotland Morphometrics May12-15 DeadlineExtended

Course outline and details;

A geometric morphometric course will be taking place at the Scottish Center for Ecology and the Natural Environment (SCENE), from the 12th-15th May, 2014. Details of SCENE can be found using the link below http://www.gla.ac.uk/researchinstitutes/bahcm/-researchfacilitiesgroups/scene/ Prof. Chris Kligenberg will be delivering the course, Chris is a professor at Manchester University and designed/wrote the software morphoJ (http://www.flywings.org.uk/-MorphoJ_page.htm) and specialises in geometric morphometrics and analysing evolutionary data sets based on shape change. The software is used a lot in in plant biology, evolutionary biology, functional morphology palaeontology, etc. and can really be applied to many different fields. It allows comparison of shapes, images, structures in either two or three dimensions. This type of analysis is well suited to analysing evolutionary and functional morphology data, population dynamics, anything that can be compared using shape or physical characteristics.

The course will take participants through the complete process involved with preparing and analysing shape data. There will be a background explaining the history and principles behind geometric morphometrics. It will cover the basics of data acquisition and the most productive method to digitise landmarks using software TPSdig and TPSutil as well as others. Cover in detail how to extract and visualise shape changes from your images. Identify where variation is in your samples using Principle Component Analysis, how to export, for example PC scores to be analysed further in, for example, R. Compare the amount of variation between groups using Discriminant Function and Canonical Variance Analysis). How covariation, using regression, can be used to size correct data i.e. to remove the effect of allometry or unwanted shape variation. Modularity, Partial Least Squares and mapping shape change with phylogeny (to compare across species/families) will also be covered before a final overview of how these different types of analysis can be used to answer hypothesis.

The course is delivered to participants by working through exercises and examples which specifically give good insight as to how you might answer or formulate questions about your own data so is both lecture style and practical.

The course is 4 days long (Monday 12th - Thursday 15th May, 2014, 9:30 - 18:30 (approx. 8 teaching hours). There are 20-24 spaces on the course (to be confirmed) which costs Â£375 (stand alone) or with meals, refreshments and accommodation (arrival Sunday 11th in the pm and departure Friday 16th in the am) Â£575 when booked before April 12th, Â£450.00 and Â£650.00 respectively when booked after this date. This reduced fee deadline has been extended from February 28th due to a lot of late interest from people.

I have attended this this course so if you have any questions as to what is covered then please email me or my telephone number is at the bottom of the email.

Oliver Hooker <o.hooker.1@research.gla.ac.uk>

Samara SouthAfrica DNAmetabarcoding Nov3-7

Dear Colleagues,

This year we are pleased to organise for this year a second session of the DNA metabarcoding spring school. It will hold in South Africa and will focus on diet analysis. Please find enclosed below all the information about this new session

Best regards

Eric Coissac

Dr Eric Coissac Associate professor Laboratoire d'Ecologie Alpine UMR CNRS-UJF 5553 / UMR CNRS 5553 Université J. Fourier Domaine de Saint Martin d'Hères 2233, rue de la piscine Bât. D Biologgie BP 53, 38041 Grenoble Cedex 9 France

The fourth DNA metabarcoding spring school in South Africa

3-7 NOVEMBER 2014 (ARRIVAL ON 2 NOVEMBER, DEPARTURE ON 8 NOVEMBER)

The fourth metabarcoding spring school is dedicated to DNA-based diet analysis.

Organizer: Jointly organized by Laboratoire d'Ecologie Alpine, Grenoble, France and the Centre for African Conservation Ecology, Nelson Mandela Metropolitan University, Port Elizabeth, South Africa (within a PROTEA project: collaboration between South Africa and France)

Place: Samara Private Game Reserve (http://www.samara.co.za)

Course fee: There is no course fee, but participants are required to pay their own transport and accommodation.

Maximum number of participants: For practical reasons, the number of participants is limited to 20. If more than 20 students, post-docs, or scientists apply to the school, we will prioritize the candidates according to their research project and their country of origin (we will promote candidates from Africa).

Course application: To apply to this school, please send an e-mail to diet2014@metabarcoding.org including a one-page CV and a one-page application letter describing how DNA metabarcoding fits in your research plans and the stage you are currently at when you inquire about the course registration. The application deadline is 4 May 2014.

Confirmed course presenters:

- Aurélie BONIN, Laboratoire d'Ecologie Alpine, Grenoble, France - Frédéric BOYER, Laboratoire d'Ecologie Alpine, Grenoble, France - Eric COISSAC, Laboratoire d'Ecologie Alpine, Grenoble, France - Graham KERLEY, Nelson Mandela Metropolitan University, Port Elizabeth, South Africa - Marietjie LANDMAN, Nelson Mandela Metropolitan University, Port Elizabeth, South Africa - Delphine RIOUX, Laboratoire d'Ecologie Alpine, Grenoble, France - Pierre TABERLET, Laboratoire d'Ecologie Alpine, Grenoble, France Prerequisites: You will need a laptop throughout the course. Make sure you have administrator privileges and that you have preinstalled VirtualBox (a free software available on the following web site:https://www.virtualbox.org) on the computer. No programming experience is required but basic knowledge of R and Unix will be helpful.

Description: The DNA metabarcoding spring school is now in its fourth edition. DNA metabarcoding is a rapidly evolving technique for assessing biodiversity from environmental DNA. Its range of applications is wide and covers, as examples, biodiversity monitoring, animal diet assessment and paleo-ecology. DNA metabarcoding relies on up-to-date molecular techniques such as PCR and next generation sequencing, and requires bioinformatic and biostatistic competencies to be able to analyse the results. This is intrinsically a technique at the interface of several disciplines that requires a broad range of skills in addition to the classical ecology knowledge related to the specific research topic. Each participant will have to present a 12 minute talk on their work and the relevance of DNA metabarcoding to their work to other participants in order to stimulate discussions with other participants and with the presenters.

Travel and accommodation: Travel and accommodation is for the participants' account. The travel between Port Elizabeth airport and the Samara reserve will be organized on Sunday 2 November 2014 in the afternoon (departure from Port Elizabeth at 15.30). Return will be on Saturday 8 November (arrival in Port Elizabeth airport at 11.00). The cost of the accommodation (including all meals) at Samara is 6000 ZAR, corresponding to about 410 EUR or 560 USD. The transfer from Port Elizabeth to Samara is estimated to be about 700 ZAR corresponding to about 50 EUR or 65 USD. Payments must be paid directly to the service providers by the successful applicants within 2 weeks of notification of acceptance for the school (more information will be given to successful applicants after 4 May 2014).

We are looking for funds to partially support accommodation costs for participants from Africa, but there is as yet no such supporting funds available.

Content: The school will comprise of a series of lectures and practicals introducing different aspects of DNA metabarcoding, with a focus on diet analysis. Participants will be trained in sample identification and collection in the field, followed by extraction techniques. The

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Toulouse EvolutionEconomics May22-23

Call for papers in evolutionary biology Poster session at the "2nd Toulouse Economics and Biology workshop" (May 22-23, 2014, Toulouse, France)

Confirmed speakers: Erol Akcay (Biology, University of Pennsylvania) Sam Bowles (Economics, Santa Fe Institute) David Cesarini (Economics, New York University) Andy Gardner (Biology, University of St Andrews) Michael Hochberg (Biology, Institut des Sciences de l'Evolution - Montpellier) Hillard Kaplan (Anthropology, University of New Mexico) Laurent Lehmann (Biology, University of Lausanne) Olof Leimar (Biology, Stockholm University) Bobbi Low (Biology, University of Michigan) Georg Nöldeke (Economics, University of Basel)

Submissions (abstract + C.V.) to the poster session should be sent to econbio_poster@iast.fr no later than March 15, 2014. A limited number of travel grants will be available. When submitting, please specify whether you are applying for a travel grant.

For more information, please visit: http://www.iast.fr/event/2nd-toulouse-economics-and-biology-workshop

Ingela Alger <ingela.alger@gmail.com>

UCM Madrid EvolutionaryBiol Autumn2014

Dear EvolDir members:

The Master in Evolutionary Biology at Complutense University of Madrid (Spain) is about to open its application period for the new course, starting in autumn 2014.

The Master is an official postgraduate program directed to students seeking a comprehensive introduction to the major questions in evolutionary biology. To complete the program, students have to complete 60 ECTS credits. All students take four compulsory courses (The genetic basis of evolution, Natural selection and adaptation, Phylogenetic systematics, Patterns and processes in macroevolution, each 6 ECTS) and produce a Master's Thesis (12 ECTS). The program is completed with four more 6-credit courses, to be chosen among the following: Molecular phylogenies, Phylogeography and its applications, Animal phylogeny, Evolution and phylogeny of plants, Life-history evolution, Mechanisms of speciation in plants, Principles of experimental design, Data analysis in ecology and evolution, and Methods in evolutionary biology.

Information about the Master: www.ucm.es/biologia-evolutiva Prospective students will have three different deadlines to submit applications:

- Early application: 20 March - 10 April 2014. This early application is designed for students who need an admission letter in order to apply for travel grants or studentships, or for those who need to apply for permits to study at Complutense University. Foreign students have to apply for this permit to secure admission in the program.

- Ordinary application: 10 to 27 June 2014.

- Late application: 4-11 September 2014. This will be opened only if there are vacancies.

Further information about the documents required to complete applications is available at the University website: www.ucm.es/biologia-evolutiva Best regards,

Javier Pérez-Tris Master coordinator

Javier Perez-Tris <jperez@bio.ucm.es>

UNordland NGS of NonmodelOrganisms Jun10-20

PhD course: High throughput sequencing of non-model organisms

Faculty of Biosciences and Aquaculture, University of Nordland, 10 - 20 June 2014

High throughput sequencing technologies are being applied to a wide range of important topics in biology. However, the analyses of non-model organisms, for which little previous sequence information is available, pose specific problems. This course will address the specific strengths and weaknesses of alternative HTS technologies, the computational resources needed for HTS, and how to analyze non-model species using HTS. The course consists of a practical training module on the Ion Torrent PGM, HTS bioinformatics training, and lecturing/seminars of HTS approaches specifically targeting non-model organisms.

Detailed course description

ECTS Credits: 5 Level of course: PhD level Type of course: Elective PhD in Marine Biosciences Duration: Ten days summer course 10-20 June, 2014 Study start: 10 June, 2014 Year of study: 2014 Study place: Bodø Faculty responsible: Faculty of Biosciences and Aquaculture Language of instruction: English Course responsible person: Truls Moum E-mail address: tmo@uin.no

Costs: Tuition fee 2 500 NOK. Students not affiliated with UiN need to arrange for lodging (contact Truls Moum for options). Students will have the option to analyze own samples during the course, at the expense of some of the materials used (contact Truls Moum for further information). Other course materials and sundry expenses will be covered.

Course contents: Practical module and bioinformatics: Prepare and run fragment library on the Ion Torrent PGM, mapping and query of PGM data Basic computational resources and skills needed for HTS Sampling a representative set of unlinked loci in non-model species. Reduced Representation Libraries (RRL) and Restriction site Associated DNA (RAD) sequencing Enriching specific genomic targets for resequencing RNA-Seq, transcriptomics of non-model species, de novo transcriptome assembly tools Advances in de novo genome assembly Population genomics of non-model species Participants' presentations of own projects

Learning outcomes:

On successful completion of the course the student should have the following learning outcomes

Knowledge

The student should:

- have a general understanding of the power and limitations of high- throughput sequencing technologies - understand the specific strengths and weaknesses of alternative high- throughput sequencing technologies - understand the principles of de novo genome and transcriptome assembly - understand how to assess transcript prevalence from RNA-seq data

Skills

The student should:

- be able to make use of basic computational resources - know how to transfer large data sets between computers - be able to execute scripts and run extended analyses - be able to map short-read sequence data to sequenced genomes and query the mapping for variation

General competence

The student should:

- be able to address biological questions in non-model species using short sequence reads - be able to choose the most suitable sequencing technologies and analytical tools to be used to address the problem at hand - be able to convey essential topics, exchange experiences, and keep updated within the field of high- throughput sequencing

Offered as a free-standing course: The course is offered to PhD students at UiN and PhD students unaffiliated with UiN.

Prerequisites: All PhD students at Faculty of Biosciences and Aquaculture, UiN, and PhD students unaffiliated with UiN are eligible.

Recommended previous knowledge: Basic computer skills and some knowledge of molecular biology and genomics.

Mode of delivery: Face-to-face teaching.

Learning activities and teaching methods: Lectures, lab exercises, individual presentations, and feedback.

Assessment methods and criteria: Individual oral presentations. Pass/not pass.

Work placement: Campus UiN.

Recommended or required reading: Literature list

Apply now

Please send in the complete application form no later than 29 May 2014. The form you can download here: http://www.uin.no/omuin/fakulteter/fba/phdakvakultur/courses/Documents/application%20form%20High%20throughput%20sequencing%20of%20non-model%20organisms.pdf We can accommodate a maximum of 12 students.

Jeanett Kreutzmann <Jeanett.Kreutzmann@uin.no>

UTrento Italy CogEvo Jul7-9

Dear Colleagues,

I am pleased to inform you that the registration for the workshop on Cognition and Evolution (CogEvo 2014) is now open. The workshop will take place at the Center for Mind/Brain Sciences, at the University of Trento (Italy), in Rovereto from July 7-9, 2014. The theme for this year's workshop is "Foundations of Social Cognition".

Invited speakers:

GERGELY CSIBRA, Central European University, Hungary PIERFRANCESCO FERRARI, University of Parma, Italy KILEY HAMLIN, University of British Columbia, Canada PER JENSEN, Linköping University, Sweden TETSURO MATSUZAWA, Kyoto University, Japan RUI F. OLIVEIRA, University of Lisbon, Portugal KRISTIN SHUTTS, University of Wisconsin-Madison, USA CHARLES T. SNOWDON, University of Wisconsin-Madison, USA

Organizers:

SANG AH LEE, University of Trento, Italy LUCIA REGOLIN, University of Padua, Italy ANNA VALERIA SOVRANO, University of Trento, Italy ELIZABETH SPELKE, Harvard University, USA GIORGIO VALLORTIGARA, University of Trento, Italy

The goal of this workshop is to provide a unique forum for researchers from a range of perspectives who are interested in cognition, neuroscience and evolution, to come together to discuss their research and develop new directions and collaborations.

The workshop distinguishes itself from larger conferences by hosting a small number of speakers (all invited) with no concurrent talks. In addition to the individual talks, there will be a poster session for young researchers to present their work. The best five poster abstracts will each be awarded 200 euros. Deadline for poster submissions is May 23.

For more details on the workshop, please visit: http://events.unitn.it/en/cimec-cogevo2014 Information: comunicazione-rovereto@unitn.it

Giorgio Vallortigara, Ph.D., FSB Professor of Neuroscience Center for Mind/Brain Sciences - Director University of Trento Corso Bettini 31, I-38068 Rovereto, Italy Italy E-mail: giorgio.vallortigara@unitn.it Phone: +39 0464-808676 Fax +39 0464 808654 Mobile: +39 347 1417478 Personal webpage: http://www.unitn.it/en/cimec/11761/giorgio-vallortigara www.cambridge.org/9781107005358 www.cambridge.org/9780521183048 "Vallortigara, Giorgio" <giorgio.vallortigara@unitn.it>

UWisconsin Madison EvolQuantGenet May19-23

COURSE ANNOUNCEMENT

EVOLUTIONARY QUANTITATIVE GENETICS Local/Date: University of Wisconsin-Madison, May 19-23, 2014 Instructor: Dr. Bruce Walsh (University of Arizona)

Dr. Bruce Walsh (Department of Ecology and Evolutionary Biology, University of Arizona; jbwalsh@u.arizona.edu) will be teaching an intensive course on ^{3}Evolutionary Quantitative Genetics^2 at the University of Wisconsin-Madison, May 19-23, 2014.

The course will be held at the Microbial Sciences Building, room 1420 (see interactive map at www.wisc.edu), 1550 Linden Dr., University of Wisconsin-Madison, WI

53706.

Topics covered in the course include:

1. Background: Basic stats, population genetics

General introduction, Basic stat machinery Basic linear algebra Basic linear models Introduction to Quantitative Genetics

2. Basic Quantitative Genetics

Covariance between relatives Estimation of basic genetic parameters: basics Estimation of basic genetic parameters: mixed models Inbreeding and heterosis

3. Evolutionary response in quantitative traits

Univariate response: changes in mean Univariate response: changes in additive variance Multivariate response: changes in the mean Multivariate response: changes in G

4. Estimating the fitness of traits

Fitness estimation I: Univariate Fitness estimation II: Multivariate Tests of neutral trait divergence Mixed models: the animal model

5. Mixed Models and their extensions

Repeatability models, maternal effects Associative effects Response in natural populations Random regressions

The lectures will be held 8:30-12 AM and 1:30-5 PM, with a 30 min coffee break in each period. Participants are expected to have some knowledge of basic statistics and genetics, and some very basic exposure to R. Course reading material will be provided to participants, mostly based on Lynch & Walsh: Genetics and Analysis of Quantitative Traits, and Walsh & Lynch: Evolution and Selection of Quantitative Traits (http://nitro.biosci.arizona.edu/zbook/NewVolume_2/newvol2.html)

REGISTRATION INFORMATION

The fees for the course are as follows:

- The course is gratis for U. of Wisconsin (UW) faculty, students and staff. However, ALL UW participants must register via the site: https://events.uwex.uwc.edu/cos/getdemo.ei?id(004&s=_6XG0UKRP9 UW students wishing to take the course for credit (1 cr, ANSCI 875), please refer to the Summer 2014 timetable, and also complete registration via the standard channels.

- Outside participants will be assessed the fees indicated below covering instruction cost and coffee breaks. Participants will have a 1.5-hour lunch break and there are several nearby campus cafeterias and Unions where food is available.

MS/PhD students from universities: $250

Academic and research staff from other public institutions: $500

Private industry staff: $700

The on-line registration for non-UW participants is: https://events.uwex.uwc.edu/cos/getdemo.ei?id(004&s=_6XG0U80SU If on-line registration is not an option for you, a form for fax/mail registration is available upon request to grosa@wisc.edu

ACCOMMODATION

Participants will be responsible for their own lodging arrangements. Some lodging possibilities on campus are:

1) Wisconsin Union Hotel, 1308 W Dayton Street, Madison, WI 53715 Phone (608) 263-2600 (http://www.union.wisc.edu/wuhotel.htm)

2) Memorial Union Guest Rooms, 800 Langdon Street, Madison, WI 53715 Phone (608) 263-2600 (https://www.union.wisc.edu/muguestrooms-roomsrates.htm)

Additional lodging possibilities on or near campus are:

a) https://kb.wisc.edu/vip/page.php?id92 (These are called ^{3}Short-course dorms^2. Very basic, dorm-type accommodations. They are fairly full at that time of the year)

b) http://lowellirm.uwex.edu/irmnet/default.ASPX (This is a very convenient, cost-effective, place to stay). Reservations can be made by toll-free call (866) 301-1753 or email lowell@ecc.uwex.edu)

c) http://www.inntowner.com/ (10-15 minutes walk to the Microbial Sciences Building)

d) http://doubletree3.hilton.com/en/hotels/wisconsin/doubletree-by-hilton-hotel -madison-MSNDTDT/index.html (20-25 minutes walk)

MISCELLANEOUS INFORMATION

Information about the University of Wisconsin and the City of Madison is available in: www.wisc.edu

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UlosAndesBogota Phylogenetics Jul8-11

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 y una motivación persuasiva para hacer el curso. Las aplicaciones deben ser enviadas por email a bogota.phylogenetics.course@gmail.com antes del 1 mayo, 2014. Las aplicaciones pueden ser escritas en inglés o español; sin embargo todos los estudiantes deben tener un nivel básico de inglés científico. Preguntas pueden ser dirigidas a liam.revell@umb.edu.

– Liam J. Revell, Assistant Professor of Biology University of Massachusetts Boston

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mcmaster.ca/~brian/evoldir.html

Vienna NGS for PopGenetExperimentalEvol

Practical Course on Next Generation Sequencing for Population Genetics and Experimental Evolution

1st announcement:

The Vienna Graduate School of Population Genetics is organising a next generation sequencing (NGS) course from October 19 to 26 at the Vetmeduni Vienna, Austria.

Recent technological advances in sequencing have greatly changed the scope of biological questions addressable in experimental evolution systems. In particular, in addition to the study of phenotypes it is now possible to study molecular data genome-wide. Even population genetic analysis have become within reach for moderate research budgets by pooling individuals before sequencing. However, the analysis of massive amounts of data generated in course of a single experiment, especially time series data, require new statistical skills to be maximally informative.

Unfortunately, many research groups aiming to use the new sequencing technologies are facing enormous practical and conceptual difficulties handling the data. The planned course aims to facilitate the use of new sequencing technologies by providing users a hands-on introduction to available tools and techniques and explaining the concepts underlying them. The demand for such training is large and growing and this course is in particular aimed for evolutionary groups that usually do not have access to in house training for next generation sequencing.

Teaching Faculty (Names in bold indicate the organizers of the course): Eszter Ari, Eötvös Loránd University, Hungary Andrea Betancourt, Vetmeduni Vienna, Austria Simon Boitard, INRA Tolouse, France *Jonathan Bollback, Institute of Science and Technology Austria* Sinead Collins, University of Edinburgh, UK Santiago Elena, Instituto de Biologia Molecular y Celular Plantas, Valencia, Spain Angela Hancock, University of Vienna, Austria Darren Kessner, University of California Los Angeles, USA Robert Kofler, Vetmeduni Vienna, Austria *Carolin Kosiol, Vetmeduni Vienna, Austria* *Ville Mustonen, Sanger Institute, UK* Magnus Nordborg, Gregor Mendel Institute, Austria Mark Robinson, University of Zürich, Switzerland *Christian Schlötterer, Vetmeduni Vienna, Austria*

Draft Schedule: Day 0 (Sunday October 19th 2014) Arrival

Day 1 (Monday October 20th 2014) am: Introduction to Next Generation Sequencing Technologies, Introduction to UNIX pm: Assessing the Quality of the Data, Mapping Reads

Day 2 (Tuesday October 21st 2014) am: Population Genetics pm: Experimental Design Evening Presentation Open practical session: Teaching Assistants (TAs) - Free for analysis of trainees own data

Day 3 (Wednesday October 22nd 2014) am: Pooled Sequencing pm: Pooled Sequencing

Day 4 (Thursday October 23rd 2014) am: RNASeq pm: De Novo Assembly

Day 5 (Friday October 24th 2014) am: GWAS pm: GWAS Evening presentation Open practical session: Teaching Assistants (TAs) - Free for analysis of trainee's own data

Day 6 (Saturday October 25th 2014) am: Time Series Analysis pm: Time Series Analysis Final discussion session, trainee feedback, additional issues raised during the course

Day 7 (Sunday October 26th 2014) Departure

Application details and other information can be found here: http://www.popgen-vienna.at/training/-ngs-course-2014.html – Dr. Julia Hosp Vienna Graduate School of Population Genetics Coordinator www.popgen-vienna.at c/o Institut für Populationsgenetik Vetmeduni Vienna Veterinärplatz 1 A-1210 Vienna

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

julia.hosp@gmail.com

WestVirginia WildlifeParasites Jul28-31

Third Annual International Workshop on Malaria and Related Haemosporidian Parasites of Wildlife

Monday July 28th - Thursday July 31st, 2014 National Conservation Training Center, Shepherdstown, West Virginia

Sponsored by the NSF Research Coordination Network for Haemosporida of Terrestrial Vertebrates1

Dear Colleagues,

The NSF-sponsored Research Coordination Network for Haemosporida of Terrestrial Vertebrates (MalariaRCN) is pleased to announce our third annual workshop on the malaria parasites and closely related haemosporidians of natural populations of vertebrates. The four day workshop will include both field and laboratory exercises as well as lectures and discussions led by RCN members2.

Topics to be covered throughout the workshop include vertebrate and invertebrate field capture techniques, blood sampling and preparation of blood smears, sample vouchering and preservation, parasite taxonomy, light microscopy for parasite identification and parasite and cell counts, sequence data analysis, and databasing. Discussion topics will include, but are not limited to, the basic biology, phylogenetics and systematics of Haemosporida, community ecology of parasites, coevolution and the evolution of virulence, and conservation and disease.

All food, lodging and workshop events will take place at the US Fish & Wildlife Service's National Conservation Training Center in Shepherdstown, West Virginia, a site easily accessible through Washington, D.C. area airports. The workshop will commence on Monday morning, July 28th, and continue through until the evening of Thursday, July 31st.

The workshop is geared towards graduate students, postdoctoral researchers, and other investigators new to the field of wildlife haemosporidians. We will be accepting applications in early 2014 and encourage individuals from outside the United States, particularly from developing countries. Applications will be available in early February 2014 through the RCN website. Workshop cost, accommodations, meals, and transportation from the Washington Dulles International Airport will be covered by the RCN grant for workshop participants. In addition, applications for travel funds will be considered. Additional information on the workshop including an overview of the four days of events will be made available on the RCN website (we encourage you to register on the RCN website and become a member of the Malaria Research Coordination Network). In the meantime, further information can be obtained from the workshop organizers (email: MalariaRCNWorkshop@gmail.com). Applications should also be sent to this e-mail address. Applications will be considered until April 15th and decisions on participation made in early May 2014.

1 The Research Coordination Network for Haemosporida of Terrestrial Vertebrates ("Malaria RCN"), sponsored by the U. S. National Science Foundation and funded through 2015 at the University of Missouri-St. Louis, was established to promote communication among researchers working on the ecology and evolution of haemosporidian parasites of vertebrate wildlife populations. Please visit the website for the network (www.malariarcn.org) for more information.

2 Workshop organizers and instructors include Robert Ricklefs (University of Missouri - St. Louis), Staffan Bensch (Lund University), Gediminas Valkiunas (Nature Research Center, Vilnius), Carter Atkinson (USGS), Susan Perkins (American Museum of Natural History), Robert Fleischer (Smithsonian Conservation Biology Institute), and Ellen Martinsen (Smithsonian Conservation Biology Institute). Other members of this RCN include Patricia Parker (University of Missouri - St. Louis), Ravinder Sehgal (San Francisco State University), Tom Smith (University of California, Los Angeles), and Robert Adlard (Queensland Museum).

**The workshop is likely to be of interest to evolutionary biologists as it will center around the systematics of a very successful and diverse group of parasites of natural vertebrate populations and include laboratory exercises involving phylogenetic analysis of parasite lineages and readings and discussions on the evolutionary history of the parasites including cospeciation of hosts and parasites as well as the evolution of virulence.

ellensarah.martinsen@gmail.com

WoodsHole MolEvol Jul27-Aug6

Workshop on Molecular Evolution at the Marine Biological Laboratory at Woods Hole

Directors: David Hillis < http://www.biosci.utexas.edu/IB/faculty/hillis.htm >, University of Texas, Austin; and Mitchell L. Sogin < http://jbpc.mbl.edu/labs-msogin.html >, MBL

Course Dates: July 27 V August 6, 2014

Online Application Form Deadline: April 7, 2014 at http://ws2.mbl.edu/studentapp/studentapp.asp?courseID=MOLE The Workshop on Molecular Evolution at Woods Hole presents a series of lectures, discussions, and bioinformatic exercises that span contemporary topics in molecular evolution. Since its inception in 1988, the workshop has encouraged the exchange of ideas between leading theoreticians, software developers and workshop participants. The workshop serves graduate students, postdoctoral students and established faculty from around the world. The 2012 Workshop will use computer packages including AWTY, BEAST, BEST, Clustal W/X, FASTA, FigTree, GARLI, MIGRATE, LAMARC, MAFFT, MP-EST, MrBayes, PAML, PAUP*, PHYLIP, STEM, STEM-hy, and SeaView to address the topics:

* Phylogenetic analysis: theoretical, mathematical and statistical bases; sampling properties of sequence data; Maximum likelihood theory and practice; Bayesian analysis; hypothesis testing * Population genetics analysis using coalescence theory; maximum likelihood and Bayesian estimation of population genetic parameters * Databases and sequence matching: database searching: protein sequence versus protein structure; homology; mathematical, statistical, and theoretical aspects of sequence database searches; multiple alignment * Molecular evolution integrated at organism and higher levels: population biology; biogeography; ecology; systematics and conservation * Molecular evolution and development: gene duplication and divergence; gene family organization; coordinated expression in evolution * Comparative genomics: genome content; genome structure; genome evolution * Molecular evolution integrated at lower levels: biochemistry; cell biology; physiology; relationship of genotype to phenotype

Students, postdocs, faculty, and others working on molecular evolution are all welcome to apply.

“Hillis, David” <dhillis@austin.utexas.edu>

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ambridge DiseaseGeneticAnalysis Jul23-29

Human Genome Analysis, Genetic Analysis of Multifactorial Diseases Venue: Wellcome Trust Genome Campus, Hinxton, Cambridge, UK When: 23 - 29 July 2014 Application deadline: 11 April 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

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.