EvolDir

January 1, 2016

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

Biosphere2 Arizona PhenotypeRCN Feb26-28

The Fifth Annual Summit of the Phenotype Ontology Research Coordination Network will be held at the University of Arizona's Biosphere2, about 40 miles north of Tucson, AZ, from February 26-28, 2016 (Friday through Sunday noon).

The theme of this meeting will be 'Complex data integration with phenotypes' with a focus on the integration of phenotype data with other data sets. We will summarize where our phenotype community is at with respect to integration with other data types, and we will highlight active projects. We will be looking to the future – what projects should be priorities for the future? Joining us this year will be folks from the newly funded 'FuturePhy' (futurephy.org), who are interested in how to integrate multiple data types, including phenotype, with phylogenetic trees.

We estimate that the costs for this meeting (transportation to meeting from airport, lodging, food) will be approximately $500, though we will be able to cover expenses for a small number of participants, particularly students and postdocs who have specific interests in using phenotypic data associated with environment in their research. Please contact one of us if you are interested in attending. It should be a great meeting!

Paula Mabee; pmabee@usd.edu Eva Huala; huala@acoma.stanford.edu Andy Deans; adeans@psu.edu Suzanna Lewis; suzi@berkeleybop.org

The Phenotype Ontology RCN (http://phenotypercn.org) was funded by the U.S. NSF to establish a network of scientists who are interested in comparing phenotypes across species and in developing the tools and methods needed to enable comparisons. In contrast to the many well-established efforts in the molecular community, the representation of phenotypic traits using ontologies is in its infancy. Phenotype ontologies, however, have the potential to integrate these data across all levels of the biological hierarchy and to the environment. This RCN is building a community that, because of its expertise, fosters communications across disciplines to enable co-development of interoperable community standards and best practices for phenotype.

"adeans@psu.edu" <adeans@psu.edu>

CambridgeU PathogenHostShifts Apr12

Meeting: Pathogen Host Shifts, Cambridge UK, 12^th April 2016

The meeting will cover the ecology, evolution, mechanisms, immunity and epidemiology underlying pathogen host shifts. The meeting aims to bring together a broad range of researchers working on this important topic, to discuss their work and develop collaborations. Full details can be found here < http://www.infectiousdisease.cam.ac.uk/events-and-training/pathogen-host-shifts-workshop >.

The meeting is sponsored by Cambridge Infectious Diseases, < http://www.infectiousdisease.cam.ac.uk/ > the Genetics Society < http://genetics.org.uk/ > and the British Ecological Society Parasite and Pathogens special interest group. < http://www.britishecologicalsociety.org/getting-involved/special-interest-groups/parasite-and-pathogen-ecology-and-evolution/ >

*Invited speakers include: *

Kate Jones, Biodiversity Modelling Research Group, UCL

Marco Vignuzzi, Pasteur Institute, Paris

Wendy Barclay < http://www.imperial.ac.uk/people/w.barclay >, Imperial

Santiago Elena,** Instituto de Biología Molecular y Celular de Plantas

Lucy Weinert < http://www.vet.cam.ac.uk/directory/lw461@cam.ac.uk >, University of Cambridge

Daniel Streicker, University of Glasgow

Ian Goodfellow, University of Cambridge

*Registration fees:*Â£8 students, Â£15 PIs and Postdocs- includes lunch and refreshments.

We will also be accepting abstracts for talks and posters - if you would like to submit an abstract please fill in the form on the event website. We particularly encourage submissions from female researchers to ensure a 50:50 sex ratio amongst speakers.

http://www.infectiousdisease.cam.ac.uk/events-and-training/pathogen-host-shifts-workshop
"bjl48@hermes.cam.ac.uk" <bjl48@hermes.cam.ac.uk>

FloridaStateU SoutheasternEcolEvol-SEEC Mar11-13

Dear colleagues,

We are excited to announce that registration is now open for the 2016 Southeastern Ecology and Evolution Conference (SEEC) at Florida State University on March 11-13, 2016.

SEEC is a regional conference created by and for early-career scientists in the fields of Evolution and Ecology. This is a great opportunity for undergraduates to present for the first time, for graduate students to practice for a larger meeting, or for anyone to present research in a low-key setting. On a budget? It's just $35 for early bird registration (until February 12). The first 40 student ASN members to register for SEEC 2016 will receive a $30 discount on their registration costs, making registration just $5!

Some of the great things in store this year: - Plenary speaker Joseph Travis - Alternative career panel lunch on Saturday

To register, visit our website at https://seec2016.wordpress.com/registration/register-here/ . If you're not ready to send in your abstract yet, let us know you're coming on Facebook.

Questions? Contact us at seec.host@gmail.com or on Facebook/twitter

– *SEEC planning committee* Florida State University website / https://seec2016.wordpress.com/ email / seec.host@gmail.com twitter / @seechost < https://twitter.com/SEECHOST > FB / SoutheasternEcologyEvolution < https://www.facebook.com/SoutheasternEcologyEvolution >

Helsinki SocialInsectEvolution Aug8-11

Dear colleagues,

The North-West European Section of the IUSSI and

The Centre of Excellence in Biological Interactions at the University of Helsinki are delighted to invite you to join us at the 6th European IUSSI Congress (/EURO-IUSSI/), to be held 8-11.8 2016 in Helsinki, Finland.

The conference website can be found at http://www.iussi2016.com/ As our plenary speakers, we are thrilled to have three speakers from the top of social insect research and beyond - Michel Chapuisat (Lausanne, CH), Elli Leadbeater (Royal Holloway, UK) and Ashleigh Griffin (Oxford, UK).

We have 12 symposia run in two parallel sessions, covering diverse topics in ecology, evolution, genetics and conservation of social insects, and open sessions for the talks falling outside the symposia. We aim for a balance of speakers from all career stages, making this an excellent venue for students to present their research in a friendly atmosphere. For the current list of symposia, see http://iussi2016.azurewebsites.net/2015/08/20/symposia/ The venue will be the University of Helsinki downtown campus, within easy reach from accommodation, restaurants and shopping. Social events include an opening event at the Natural History Museum, a reception by the Rector Magnificus of the University of Helsinki, and a conference dinner at Restaurant Uunisaari, located on an islet off the cost of Helsinki.

Registration and abstract submission will open 1^st Feb 2016.

Looking forward to seeing as many of you as possible in Helsinki next summer!

The organizing committee

University of Helsinki, Department of Biosciences Liselotte Sundström (chair) Perttu Seppä Heikki Helanterä Nick Bos Dalial Freitak Stafva Lindström

The scientific committee

With representatives from all European sections of the IUSSI Prof. Mark Brown, Royal Holloway University of London (NW European section) Prof Stefano Turillazzi, University of Florence (Italian section) Dr Alexandra Schrempf, University of Regensburg (Central European section) Dr Thibaud Monnin, CNRS (French speaking section)

Website

http://www.iussi2016.com/ https://www.facebook.com/events/632017803604014/ *Contact*

For all inquiries concerning scientific matters, please contact organizing committee at iussi2016-sci@helsinki.fi

For inquiries concerning practicalities, please contact congress office Next Travel Ltd at iussi2016@nexttravel.fi

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Heikki Helanterä, PhD Kone Foundation Researcher

Centre of Excellence in Biological Interactions Department of Biosciences University of Helsinki POB 65 / Viikinkaari 1 FI-00014 Univ. of Helsinki Finland

e-mail:heikki.helantera@helsinki.fi website:http://www.helsinki.fi/science/ants/Heikki.htm phone: +358-2941-57682

Heikki Helanterä <heikki.helantera@helsinki.fi>

Marseilles EvolBiol Sep20-23 DeadlineJan31

Dear AllÂ

The early dead line for the,Â20th Evolutionary Biology Meeting at Marseilles (September 20-23 2016),Â is January 31 2016

info:

http://sites.univ-provence.fr/evol-cgr/Â or http://aeeb.fr/?page_id=333 best regards Pierre

PONTAROTTI Pierre <pierre.pontarotti@univ-amu.fr>

Montpellier ComputEvolBiol Jun12-16

MCEB - Mathematical and Computational Evolutionary Biology 12-16 June 2016 - Hameau de l'Etoile, Montpellier, South of France.

Webpage: http://www.lirmm.fr/mceb2016/ Pre-registration deadline: February 25th Notification to applicants: March 15th Final list of attendees: April 15th

Scope: Mathematical and computational tools and concepts form an essential basis for modern evolutionary studies. The goal of the MCEB conference (at its 8th edition) is to bring together scientists with diverse backgrounds to present recent advances and discuss open problems in the field of mathematical and computational evolutionary biology. The theme of this year's edition will be “forecasting evolution”: while most analyses are designed to reconstruct the past in order to understand evolution, our modern society is in dire need of anticipating the future using sound scientific approaches. This is particularly true in the context of global warming and more generally global changes. New approaches that model future evolution are emerging, for example to predict epidemics, evolution of cancer, shifts in species/population distributions or species loss. Evolutionary biology is thus widening its focus, trying to predict future biological states and better define the range of applicability of these predictions. Making progress in this new research area will involve cross-disciplinary approaches, accurate statistical methods, and powerful computational techniques. Beyond this year's theme, general concepts, models, methods and algorithms will be presented and discusse, just as in the previous editions of MCEB. Keynote speakers will introduce a field of research and discuss their own work in this field. Afternoon will be for short presentations and posters, with plenty of time for discussions and outdoors.

Where and when: Hameau de l'Etoile, near Montpellier, in the South of France, 12-16 June 2016.

Cost: Conference fees including accommodation for four nights, meals, coffee breaks, buses, etc., will be between 300 and 550, all inclusive, and will vary depending on the room. PhD students and postdocs will benefit of the cheapest rooms.

Keynote speakers (to be completed): Jeffrey Jensen - http://jensenlab.epfl.ch/ Ecole Polytechnique FÃÂ©dÃÂ©rale de Lausanne, CH

Laura S. Kubatko - http://www.stat.osu.edu/~lkubatko/ Departments of Statistics and Evolution, Ecology, and Organismal Biology - The Ohio State University, USA

Amaury Lambert - http://www.proba.jussieu.fr/pageperso/amaury/index.htm Stochastics & Biology Group - Laboratoire de ProbabilitÃÂ©s & ModÃÂles AlÃÂ©atoires - UPMC - UniversitÃÂ© Paris 06, FR

Richard Neher - https://neherlab.wordpress.com/ Max Planck Institute for Developmental Biology - DE

Bruce Rannala - http://www.rannala.org/?page_id=111 UC Davis - University of California, USA

Isabel SanmartÃn Bastida - http://www.rjb.csic.es/jardinbotanico/jardin/contenido.php?Pag=386&tipocientifico&cod=98&len=en Real JardÃn BotÃÂnico (RJB-CSIC), Madrid, SP

Yun S. Song - http://www.eecs.berkeley.edu/~yss/ Departments of Mathematics and Biology - Universty of Pennsylvania, USA

For more information and register: http://www.lirmm.fr/mceb2016/ Please forward this announcement

Olivier Gascuel <olivier.gascuel@lirmm.fr>

Orlando PopEvolQuanGenet Jul13-17

Dear Colleague,

I'm writing to let you know about an exciting NEW meeting to be sponsored by the Genetics Society of America (GSA). After nearly 100 years of research in Population, Evolutionary, and Quantitative Genetics (PEQG), the time has finally come for a meeting to be focused specifically on PEQG. As with the many other periodic meetings sponsored and managed by the GSA, the plan is for PEQG to become the premier, regular gathering of graduate students, postdoctoral scholars, and established scientists in these central areas of genetics.

Held in conjunction with The Allied Genetics Conference (TAGC), or what GSA President Jasper Rine is referring to as the Totally Awesome Genetics Conference, PEQG will be part of a genetics conference which will unite, for the first time, most of the GSA-sponsored model organism meetings at one venue. This large meeting coincides with the 100th anniversary of the journal GENETICS. TAGC Logo

The meeting will be in Orlando, Florida from July 13-17 at the Orlando World Center Marriott, which provides a campus-like environment for unparalleled networking. In Orlando you will find inexpensive room rates and abundant domestic and international flights. Your meeting budget will stretch further here than at other venues.

Yes, we know Orlando is hot in the summer - outside. But inside, the AC will be working and if you want GREAT science and access to the leaders of the field, Orlando is the place for you.

Orlando was chosen to ensure that all submeetings can be under one roof, making accessible the best that each field has to offer, with the addition of a stellar line-up of featured speakers for the joint plenary sessions transcending all aspects of genetics. Check out the TAGC Website for details, and mark it on your calendar now!

Our PEQG meeting, really a meeting within a meeting, will present numerous opportunities for sharing research results and forming lasting collaborations. PEQG will provide graduate students with the opportunity to explore post-doctoral interests in other fields, and postdocs the opportunity to network with faculty from other institutions. This meeting will also launch the first James Crow Award competition for young investigators. With the promise of providing a breadth of perspective never before possible at any model-organism focused meeting, we hope to see you in Orlando this July. Michael Lynch Picture

Sincerely, Michael Lynch John Schimenti Signature

Population, Evolutionary and Quantitative Genetics Conference Chair TAGC 2016 Coordinating Committee GSA Past President

Genetics Society of America 9650 Rockville Pike, Bethesda, MD 20814 (301) 634-7300 - society@genetics-gsa.org www.genetics-gsa.org Michael Lynch <society@genetics-gsa.org>

SanAntonio Texas AdmixedPopulations May18-20

Conference Announcement: SMBE Satellite Meeting on the Genetics of Admixed Populations

May 18-20, 2016

San Antonio TX

Studies of admixed populations and the admixture process touch on topics central to evolutionary and molecular biology, including the dynamics of gene flow and hybridization, population expansions, and adaptation. Admixed populations have been leveraged to detect disease and phenotypic associations, elucidate mechanisms and timescales of speciation, and infer regions under selection. Acting as a natural experiment, admixed populations provide insight into unique adaptations of their parental populations, and evolutionary processes in related populations more generally. Admixture is also intimately linked with the recombination process, which shuffles segments of different ancestry, and is proven to vary in rate and location based on ancestry.

The primary goal of this satellite meeting is to emphasize the common theoretical and empirical underpinnings of the study of admixed human populations with the study of hybridization in other animals and even plants, opening up methods and study design from a specific organism to a wider audience. We hope to bridge theoretical and data-driven approaches, starting a discussion on the suitability of methods to various systems and open questions that may be better resolved using an interdisciplinary approach, as well as considering ethical concerns associated with these studies.

Workshop sessions include:

Admixture as a dynamic process Novel Methods to Untangle Admixture Empirical Studies of Population History Admixture as a Mechanism for and Against Speciation Admixture and Selection: Phenotypic and Medical Implications Panel Discussion: Ethical considerations and Sampling Schemes

For a full list of confirmed speakers and information on local arrangements, please visit: http://anthgen.org/-smbe2016 Registration and abstract submission will be available in early December

Please direct all questions to the conference organizers at smbe2016admix@gmail.com

Conference Organizers:

Amy Goldberg: agoldb@standford.edu Ellen Quillen: EQuillen@txbiomed.org Heather Norton: heather.norton@uc.edu Joanna Malukiewicz: jmalukie@gmail.com Anne Stone: acstone@asu.edu

Heather L. Norton Assistant Professor Department of Anthropology 446 Braunstein Hall PO Box 210380 University of Cincinnati Cincinnati, OH 45221-0380

Office: 513-556-3594

heather.norton@uc.edu

http://homepages.uc.edu/ ˜ nortonhr/MoCHA/-Home.html "nortonhr@ucmail.uc.edu"

Seville EvolEcol Feb2017

To Evoldir members:

Below you will find the annoucement of a Meeting we are organizing at Seville (Spain) in Feb. 2017 for those interested in the interface between Ecology and Evolution

http://www.aeet.org/MEDECOS_XIV_International_Conference__XIII_AEET_Meeting_363_p.htm

Dear colleagues,

The International Society for Mediterranean Ecology (ISOMED) together with The Spanish Society for Terrestrial Ecology (AEET), invites you to attend the forthcoming MEDECOS XIV International Conference - XIII AEET Meeting, that will be hold in Sevilla, Spain, from 31st January to 4th February 2017. This meeting is organized by the AEET andISOMED and hosted by the University of Sevilla and the Doñana Biological Station.

More information about the Congress will be soon available at http://www.aeet.org and http://www.incomme.org/upcoming-medecos-xiii .html

For questions and suggestions please send an email to info@aeet.org

SAVE THE DATE. THE ORGANIZING COMMITEE LOOKS FORWARD TO YOUR ATTENDANCE TO MEDECOS XIV -AEET XIII IN SEVILLA!!

Thank you very much for disseminate this announcement

Best Regards,

The Organizing Committee of MEDECOS XIV International Conference - XIII AEET Meeting

Dr. Juan Arroyo arroyo@us.es Departamento de Biologia Vegetal y Ecologia. Dept. of Plant Biology and Ecology Universidad de Sevilla Apartado 1095 - E41080 Sevilla, Spain phone: desk office: +34 954 557 058 lab: +34 955 420 845 fax: +34 954 557 059 Research group: http://grupo.us.es/grnm210/ https://www.researchgate.net/profile/Juan_Arroyo3/ Juan Arroyo <arroyo@us.es>

UBern EvolutionCooperation Feb24-26

Genetics and Development of Cooperation FUNDED PLACES AVAILABLE

Dates: February 24-26^th 2016

The Ecology and Evolution group at University of Bern will host a workshop in February 2016 on the genetics and development of cooperative behaviour.

The two-day meeting aims to bring together scientists working on a range of questions important to this area of research, including quantitative genetics, molecular genetics, transcriptomics, endocrinology, epigenetics, and maternal effects. As an integrative approach is becoming increasingly necessary to address these research questions, the ultimate goal of the meeting will be to discuss new perspectives and techniques on the genetics and development of cooperative behaviour. We would like participants to summarise and synthesise recent progress in these areas with what they feel are key emerging questions, conceptual issues, potential problems, and future directions for research.

We plan for the workshop to be largely discussion-based, but will include lectures and posters as a foundation for discussion. The meeting will be a small-scale, intensive workshop where all participants are encouraged to take an active role, with particular emphasis on the inclusion of early-career researchers. The venue will be an organic farm/eco-retreat near the city of Bern.

Invited speakers include:

Jason Wolf University of Bath

Marta Soares CIBIO

Anna Lindholm University of Zurich

Ursula Paredes University of Oxford

With more to be confirmed.

We are excited to offer a limited number of fully-funded places for interested participants at any level of their academic career. For more information on how to apply, please contact organisers Maddalena Vierbuchen (susanna.vierbuchen@iee.unibe.ch) and Claudia Kasper (claudia.kasper@iee.unibe.ch).

Maddalena Vierbuchen PhD Student Behavioural Ecology Institute of Ecology and Evolution University of Bern Wohlenstrasse 50a CH-3032 Hinterkappelen Switzerland

susanna.vierbuchen@iee.unibe.ch

UDebrecen Hungary EvolutionOfMechanisms Jan28-31 Deadline

Evolution of Mechanisms, January 28-31, 2016, University of Debrecen, Hungary

Please be reminded that the registration deadline for our symposium “The evolution of mechanisms: a workshop on the integration of life history evolution and physiology” is January 03, 2016.

Symposium summary:

In the past decades research in behavior and life history has been dominated by two different approaches: molecular biologists and physiologists investigated the fine-scaled mechanisms of how life history and behavioral processes are regulated, while theoretical and organismal biology provided an explanation for the adaptive value of such traits and the evolutionary forces that shape them. While both approaches have been extremely successful, the proximate-ultimate dichotomy is not warranted anymore: our next challenge is to integrate these approaches and to understand the evolution of the genetic, endocrine mechanisms and signaling pathways that ultimately lead to a bewildering diversity of life-forms.

In order to advance the discussion between these traditionally distinct areas, we organize a workshop where we invite theoreticians and empiricists working in the fields of physiology, molecular biology and evolutionary ecology to discuss the current state of the art and to articulate a research agenda for the future, where they identify the key challenges and approaches to study the evolution of the integrated phenotype and physiological underpinnings of life history evolution. Instead of the dominantly unidirectional information flow of conference symposia, we organize this meeting to promote discussion and debate about ideas, concepts of how we can understand the evolution of mechanisms that provide the raw material for natural selection.

Participants are invited to give contributed talks that advance the goal of the meeting. Additional poster presentations will also be welcome.

Invited speakers:

Thomas Flatt (University of Lausanne): The mechanisms underpinning life history evolution

David Gems (UCL): Role of insulin/IGF-1 signaling in the evolution of life histories and ageing

Laura Lavine (Washington State University): Endocrine signaling and the development of the weapons of sexual selection: insights from beetles

Pat Monaghan (University of Glasgow): Environmental effects that shape individual life histories: mechanisms, trade-offs and time scales

Contact: evolmech2016@gmail.com

For further details and registration visit: http://zoology.unideb.hu/meetings/XIII/?lang=en Hope to see you there,

the organizers:

Ãdám Lendvai, Zoltán Németh, Jácint Tökölyi, Zoltán Barta

Zoltan Nemeth <znemeth05@gmail.com>

GradStudentPositions

BangorU PollenMetabarcoding

3.5 year, NERC ENVISION Doctoral Training Program PhD Studentship (Â£14,057pa) - Pollen forecast 2020: using DNA metabarcoding to assess aerial pollen mixtures and identify linkages to hay fever (Lead supervisor: Simon Creer).

The School of Biological Sciences is currently advertising for PhD opportunities to be hosted in the Molecular Ecology & Fisheries Genetics Laboratory (MEFGL), at Bangor University (http://mefgl.bangor.ac.uk/) to commence in September 2016. The PhDs are part of the NERC ENVISION Doctoral Training Programme (http://www.envision-dtp.org/), a PhD consortium partnership between Bangor, Nottingham and Lancaster Universities, alongside numerous environmental bodies, aimed at equipping the next generation of Environmental Biologists with advanced skills.

Project rationale: Approximately 20% of people display allergic reactions to combinations of tree and grass pollen causing symptoms ranging from discomfort (e.g. hay fever) to respiratory complications (e.g. asthma), with associated costs to society and health services.

Identifying pollen from different species of tree can be achieved using labour-intensive microscopy. Nevertheless, since most grass pollens look the same, an outstanding challenge is to understand which species of grass contribute to the allergic response. Aims: This studentship has three components. The first aims to use different combinations of molecular genetic tools to see how effectively we can assess aerial tree pollen mixtures. Secondly, to use modelling approaches to compare and contrast the aerial transit of tree and grass pollens and finally, to use a molecular ecology/environmental epidemiology approach to identify which species of grass pollen are most closely associated with hay fever symptons. The PhD will form a distinct, but highly complementary component within a larger Â£1.2M NERC funded study (now recruiting PDRA http://-

mefgl.bangor.ac.uk/news/3“25077) and provides an opportunity to work with an interdisciplinary team of molecular ecologists, aerobiological modellers and environmental epidemiologists from a range of UK Universities and the UK Met Office. Co-supervision will be provided by Natasha DeVere, Gareth Griffith (Aberystwyth), Carsten SkjÃth (Worcester) and Nick Osborne (Exeter/Sydney).

Training will be provided in the main areas of molecular ecology, genomics, taxonomy, bioinformatics, modelling; multidisciplinarity skills; science communication and environmental epidemiology complemented by a host of additional opportunities for postgraduate development. Fieldwork will occur within the UK, with opportunities for travel/collaborations in Europe and Australia.

Applicants should hold a minimum of a UK Honours Degree at 2:1 level or equivalent in subjects such as Environmental or Natural Sciences, with a strong motivation to study biodiversity-environment interactions. The ENVISION link is here: http://www.envision-dtp.org/portal/projects/-002712/pollen-forecast-2020 –using-dna-metabarcoding-to-assess-aerial-pollen-mixtures-and-identify -linkages-to-hay-fever and in the meantime, informal enquiries should be sent to Dr S. Creer, email s.creer@bangor.ac.uk; http://mefgl.bangor.ac.uk/staff/-si.php; @spideycreer or members of the broader team where appropriate and we will be able to assist with your enquiries.

Closing date for applications: 13th of January 2016 with interviews predicted to take place on the 20th January 2016. Many thanks and look forward to hearing from you. Si Creer

Simon Creer

Senior Lecturer Molecular Ecology and Fisheries Genetics Laboratory School of Biological Sciences Environment Centre Wales Bangor University Gwynedd LL57 2UW

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Rhif Elusen Gofrestredig 1141565 - Registered Charity No. 1141565

Simon Creer <s.creer@bangor.ac.uk>

BiK-F Germany EvolutionaryGenetics

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

The Department of “Evolution and Climate” at Senckenberg and the Research field 6 of the working group of Prof. Dr. Axel Janke jointly invites applications for a

PhD Position in Evolutionary Genetics Ref. #6.5

We are looking for a dedicated PhD student with strong interest and proven skills in evolutionary genetics to study speciation in mammals at the genomic level. Experience in analyzing genomic data is an advantage and good English skills are a prerequisite. The applicant should be able to work in an international, interdisciplinary group for expanding the work to species distribution modeling, paternal inference and/or conservation genetics.

Your tasks: - Study speciation in mammals at the genomic level - Labwork - Produce and analyze mammalian genome data - Population genetic analyses - Teaching

Your profile: - Fulfill the requirements to enroll as a PhD student at Goethe University - Experience in producing and analyzing genomic data - Very good English skills - Highly motivated, able to work independently

Salary and benefits are in accordance with a public service position in Germany (TV-H E13, 50%). The contract shall start March 1st, 2016 and will be initially limited until February 28th, 2019. The Senckenberg Research Institute supports equal opportunity of men and women and therefore strongly invites women to apply. Equally qualified handicapped applicants will be given preference. The place of employment will be Frankfurt am Main, Germany. The employer is the Senckenberg Gesellschaft für Naturforschung.

Please send your application before January 17th, 2016 preferably by e-mail (attachment in a single pdf document), mentioning the reference of this position (Ref.

#6.5) and including a cover letter detailing your research interests and experience, a detailed CV, and a copy of your credentials to the address below:

Dr. Tobias Schneck c/o Senckenberg Gesellschaft für Naturforschung Senckenberganlage 25 60325 Frankfurt am Main recruiting@senckenberg.de

For scientific enquiries please contact Prof. Dr. Axel Janke axel.janke@senckenberg.de, phone +49 (0)69/7542-1842

In addition, please indicate in your application how our advertisement came to your attention.

For further information and to answer your questions please contact me by email. Thank your very much!

Mit freundlichen Grüßen /Best Regards

Isabell Bast Personalsachbearbeiterin

SENCKENBERG Gesellschaft für Naturforschung Zentralabteilung Verwaltung (ZAV) - Gruppe Personal & Soziales Senckenberganlage 25 60325 Frankfurt/Main

Telefon/Phone: 0049 (0)69 / 7542 -

Leiterin Personal & Soziales - 1458 Loke, Uta

Stellv. Leiterin Personal & Soziales - 1319 Elsen, Carina

Team Personalbeschaffung (Recruiting) - 1313 di Biase, Maria - 1313 Bast, Isabell - 1478 Gajcevic, Isabel

Fax: 0049 (0)69 / 7542-1467 Mail: recruiting@senckenberg.de Homepage: www.senckenberg.de SENCKENBERG Gesellschaft für Naturforschung (Rechtsfähiger Verein gemäß Â§22 BGB) Senckenberganlage 25 60325 Frankfurt am Main Direktorium: Prof. Dr. Dr. h.c. Volker Mosbrugger, Prof. Dr. Andreas Mulch, Hon. Prof. Dr. h.c. (STU) Rolf Pfrengle, Prof. Dr. Katrin Böhning-Gaese, Prof. Dr. Uwe Fritz, PD Dr. Ingrid Kröncke Präsidentin: Dr. h. c. Beate Heraeus Aufsichtsbehörde: Magistrat der Stadt Frankfurt am Main (Ordnungsamt) P Before printing, think about the environment

recruiting <recruiting@senckenberg.de>

CharlesUPrague PlantPollination

A Ph.D. studentship *Plant-pollinator interactions along an Afrotropical altitudinal gradient*

We are seeking a highly motivated Ph.D. student to join a project assessing studies of plant-pollinator relationships between selected flowering plants and their pollinators on Mt. Cameroon. The research is focused on changes of general characteristics of pollination networks along the altitude, as well as on case studies of selected pollination systems. The student will process already collected data and material, as well as actively participate on field sampling (at least two times during the study) of data and their subsequent processing in collaboration with international specialists. The length of the study is 4 years.

The successful applicant will be supervised by Dr. Stepan Janecek and Dr. Robert Tropek (www.insect-communities.cz) as a part of the multidisciplinary team at the Faculty of Science, Charles University of Prague with a close collaboration with the Institute of Entomology and Institute of Botany, Czech Academy of Sciences.

Offered - attractive scientific topic in an established international team - standard university scholarship (up to 114,000 CZK annually according to discharging of the study responsibilities) and a part time employment (132,000 CZK annually), it sufficiently covers living expenses in the Czech Republic

Required - enthusiasm in nature and ecological science - ability to lead a field research in challenging conditions of tropical environments - fluency in English - a MSc degree in biology or related fields (in early summer 2016 at the latest)

Desirable (but not necessary) - previous experience of collaboration in scientific projects evidenced by a (co)authorship of research papers or conference contributions - previous experience with botany and/or pollination biology - basic knowledge of French

All applicants will send a structured CV, contacts of three referees, and a cover letter stating their previous work, qualification and motivation to both emails of Robert Tropek (robert.tropek@gmail.com) and Stepan JaneÄek (janecek.stepan@centrum.cz). Any questions should be sent to the same emails as well. Review of applications will begin on 5th January 2016 and will continue until the position has been filled.

Selected applicants will be interviewed through Skype in half January 2016. The position is available from early summer 2016.

Robert Tropek <robert.tropek@gmail.com>

CityUNewYork ComparativePopGenetics

The Hickerson lab at the City University of New York (CUNY) has an opening for a PhD student who is interested in developing models that link biogeographic history, community ecology and comparative population genomics. Our group is focusing on developing and implementing methods for understanding the evolutionary and demographic histories of species assemblages and ecosystems given environmental, spatial, and aggregate population genomic data. The statistical models we develop are broadly applicable to a variety of regions and members of our group have worked with a diverse set of taxa and ecosystems.

?The ideal candidate will have a strong interest and aptitude in quantitative biology, modeling, and programming as well as an interest in evolutionary genetics and biogeography. The lab welcomes qualified applicants with diverse backgrounds, including biology, anthropology, mathematics, physics, computer science, and related fields.

To offset teaching requirements, the PhD candidate will be supported by two five-year grants funded by NSF and NASA (1. DEB-1253710 - CAREER: Dynamic models of isolation and admixture for community-scale population genomic inference & 2. DEB-1343578 - Dimensions US-BIOTA-Sao Paulo: A multidisciplinary framework for biodiversity prediction in the Brazilian Atlantic forest hotspot - http://www.afbiota.org/?).

Our lab is located in Manhattan and locally we have tight collaborations with the lab groups of Ana Carnaval (CUNY), Kyle McDonald (CUNY), Frank Burbrink (AMNH), and Brian Smith (AMNH), as well as international collaborations with Konrad Lohse (U. of Edinburgh, UK), Graham Stone (U. of Edinburgh, UK) and Brent Emerson (Canary Islands, Spain). CUNY has a large and thriving community of faculty, students, and post-docs studying ecology, evolution, and behavior and we benefit from the academic environment in New York City that allows us to have close ties to the AMNH, the New York Botanical Gardens as well as other local universities, including Columbia, Fordham, Rockefeller, NYU and Stony Brook.

The positions would start in the Fall of 2016. Contact mhickerson 'at' ccny cuny.edu if there is interest. Note that applications for Fall 2016 to the CUNY EEB subprogram must be received before January 1rst of 2016.

For more information visit: http://hickerlab.wordpress.com/ Michael J Hickerson Associate Professor City College of New York - Biology Department; 160 Convent Ave New York, NY 10031 lab 212-650-3457

Chair, Ecology Evolution, and Behavior subprograms (EEB) City University of New York and the Graduate Center 365 Fifth Avenue New York, NY 10016-4309

Research Associate - Division of Invertebrate Zoology American Museum of Natural History http://hickerlab.wordpress.com/ "mhickerson@ccny.cuny.edu" <mhickerson@ccny.cuny.edu>

ColoradoStateU EvolutionaryEcology

PH.D. ASSISTANTSHIP IN AVIAN EVOLUTIONARY ECOLOGY. We seek a self-motivated and creative doctoral student to conduct research on the evolutionary ecology and population genomics of the Island Scrub-Jay. Fieldwork will start in spring 2016 and the student will enroll at Colorado State University (CSU) in the 2016 fall semester. This dissertation research will be part of multi-investigator project involving CSU, the Smithsonian Institution, and The Nature Conservancy. The student will be co-advised by Drs. Cameron Ghalambor and Chris Funk at CSU and by Dr. Scott Sillett at the Smithsonian, and be supported by both teaching and research assistantships.

A key project objective is to understand population structure, dispersal, and adaptation to inform conservation management of the jay and the California Channel Islands. The student will have freedom to develop a thesis topic, so long as the dissertation overlaps sufficiently with this objective. We welcome applications from prospective students with a record of academic excellence, molecular lab experience, and extensive training in the observation, capture, and handling of wild birds. Ideal candidates will have a Master's degree (or extensive undergraduate research experience), at least one first-authored publication, and graduate or advanced undergraduate coursework in statistics and population/evolutionary genetics. The successful applicant will need to meet the entrance requirements for doctoral candidates in CSU's Graduate Degree Program in Ecology (http://ecology.colostate.edu/).

To apply, email your CV (including names, phone numbers, and email addresses of three references) and a one-page statement of research interests to issj.student2016@pobox.com. We anticipate selecting a Ph.D. candidate by early March 2016.

"Chris.Funk@colostate.edu"
<Chris.Funk@colostate.edu>

ColoradoStateU PopulationGenomics

PH.D. ASSISTANTSHIP IN AMPHIBIAN POPULATION GENOMICS. A self-motivated and creative doctoral student is sought to join the Funk Lab (http://wp.natsci.colostate.edu/funklab/) to conduct research on the population/conservation genomics and evolutionary ecology of Columbia spotted frogs (Rana luteiventris) and Oregon spotted frogs (R. pretiosa). Research will start in late spring/early summer 2016 and the student will enroll at Colorado State University (CSU) in the 2016 fall semester. The student will be supported by both teaching and research assistantships.

A key project objective is to understand population structure and local adaptation to inform conservation and management of Great Basin Columbia spotted frogs and Oregon spotted frogs. The student will have freedom to develop a thesis topic, so long as the dissertation overlaps sufficiently with this objective. Applications are welcome from prospective students with a record of academic excellence; a strong interest in amphibian genomics, evolution, ecology, and conservation; and molecular lab experience. Ideal candidates will have a strong background in population genetics, amphibian field experience, at least one first-authored publication, and advanced coursework in statistics, bioinformatics, and genetic data analysis. The successful applicant will need to meet the entrance requirements for doctoral candidates in CSU's Graduate Degree Program in Ecology (http://ecology.colostate.edu/).

To apply, email your CV (including names, phone numbers, and email addresses of three references) and a one-page statement of research interests to Dr. W. Chris Funk at Chris.Funk@colostate.edu. Please specify "Spotted frog genomics PhD position" in the subject line of your email. A Ph.D. candidate will be selected by March 2016.

"Chris.Funk@colostate.edu"
<Chris.Funk@colostate.edu>

DurhamU EvolutionaryEcology

A competitive four year PhD studentship opportunity in evolutionary and ecological genetics is available at Durham University, UK.

Title: The fitness consequences of inbreeding in wild flax.

Supervisory team: Dr Adrian Brennan, Durham University, UK, with the co-supervision of Prof Rus Hoelzel, Durham University, UK, and Dr Kirsten Wolff, Newcastle University, UK.

Project description: This project aims to improve our understanding of inbreeding and its relationship with fitness, a fundamental aspect of evolution. We will use wild flax as a model to study this important relationship, thereby raising the possibility of rapidly translating results into sustainably enhancing agricultural production via genetic improvement of crops. Our research in wild flax will allow for the comparison of natural populations exhibiting different levels of selfing, thereby revealing the extent to which natural selfing leads to purging and the development of a genome more resistant to inbreeding depression. We will use new genotyping by sequencing technologies to obtain an unprecedented genome-wide perspective on inbreeding and its evolution, allowing the identification of relevant genes, and therefore the consideration of molecular mechanisms. Inbreeding is widely understood to reduce fitness through both the expression of recessive deleterious alleles in homozygotes, and through over-dominant allelic interactions. Even naturally highly inbreeding organisms cannot completely purge their genetic load by selection because of faster drift at reduced effective population size. For many crops, including flax, elite lines have been intensively inbred to optimize the stable expression of desirable traits. However, these same lines then suffer inbreeding depression. Studies of flax have found up to 91 % heterotic increases in F1 seed yield following controlled crosses. However, the agronomic potential of heterosis has only been fully realized in hybrid varieties of maize so far. Only recently have genotyping technologies advanced to a stage where it is possible to test the long-held hypothesis that heterozygosity positively correlates with fitness using genome-wide data for many individuals of non-model organisms. Initial results are encouraging but more research is needed in organisms showing a wider range of mating systems and population structures to better understand the fitness consequences and genetic basis of inbreeding. The student will be trained in next generation sequencing technologies, and integrate studies of wild and glass-house populations to test key hypotheses about inbreeding and fitness.

Eligibility and Funding: For a UK-based applicant who is successful in competition with other PhD projects, the studentship will provide tuition fees, research funds and a maintenance allowance. A successful European economic area applicant will be provided tuition fees and research funds only.

Application details: If interested in applying, please contact Dr Adrian Brennan, a.c.brennan@durham.ac.uk , with a CV and a covering letter. The deadline for applications is 29th January 2016.

"a.c.brennan@durham.ac.uk"
<a.c.brennan@durham.ac.uk>

Edinburgh PlantEvolution

I am advertising a PhD project titled "Genetic variation at range margins in monkeyflowers". This project will use common garden experiments and genomic approaches to study adaptive genetic variation in the North American model plant species Mimulus guttatus. Please see the link below for more details.

Alex Twyford

http://www.geos.ed.ac.uk/postgraduate/PhD/-getDocument?SerialNo=1136 Alex Twyford <atwyford@staffmail.ed.ac.uk>

ETH Zurich BiodiversityModeling

ETHZurich.BiodiversityModeling

The group of Landscape Ecology at ETH Zurich (www.ethz.ch< http://www.ethz.ch >) and WSL Birmensdorf (www.wsl.ch< http://www.wsl.ch >) under the supervision of Prof. Loïc Pellissier is invites applications for a PhD position in biodiversity modelling.

The successful candidate will develop mechanistic models including speciation and extinction to explore how landscape dynamic history shaped extant biodiversity patterns. Ultimately the model will inform on ecosystem responses to global changes. The new approach will be applied to several ecosystems with an emphasis on tropical marine reef fishes. The PhD position will be embedded within the group's core research interests focused on three main themes: 1) Developing spatial models of biodiversity. 2) Understanding the effect of history on extant biodiversity patterns. 3) Monitoring and forecasting biodiversity and ecosystem responses to global changes.

Applicants must hold a Master degree in ecology, evolutionary biology, bioinformatics or another relevant discipline. Significant experience in programming (e.g. in R, Julia, C++) is expected. Experience in Geographic Information System (GIS) would be an advantage. Strong oral and written communication skills in English are required. The expected starting date is February 2016 with a funding for three years.

The chair of Landscape Ecology is shared between ETH Zürich and the Swiss Federal Institute for Forest, Snow and Landscape Research (WSL). This project is part of an international research collaboration with the teams of Prof. Fabien Leprieur in Montpellier, France and Dr. Laurent Vigliola (IRD, Nouméa).

Please provide a maximum two-page cover letter that explains your motivation, research experience and interest, a CV including publications, and a list of three professional references. Application review will begin in January 1, and continue until the position is filled.

Please address your application online following this link:

https://apply.refline.ch/845721/4273/pub/-1/index.html "loic.pellissier@usys.ethz.ch" <loic.pellissier@usys.ethz.ch>

ETHZurich EcologyEvolutionModeling

PhD position: Modeling ecology/evolution of a plant pathogen, ETH Zurich

The project

will explore population dynamics of Zymoseptoria tritici, an important fungal pathogen of wheat, using eco-evolutionary modeling and field/lab experimentation.

Plant diseases often cause serious yield losses in agriculture. Current chemical and genetic technologies used to manage plant diseases are highly vulnerable to pathogen evolution and are not sustainable. Pathogen evolution is facilitated by the genetic uniformity underlying modern agroecosystems. Thus, there is an urgent need to develop new, efficient and sustainable ways to control plant diseases.

This PhD project intends to make an important contribution towards achieving this goal. The first phase aims at comprehensive characterization of both epidemic and evolutionary factors of the pathogen by combining eco-evolutionary modeling, field/lab experiments and genome sequence analyses. In the second phase the models will be used to predict the rate of pathogen adaptation to disease control and propose optimal spatio-temporal patterns for applications of fungicides and resistant host varieties that can disrupt pathogen adaptation.

Working conditions

Plant Pathology group at the Institute of Integrative Biology, ETH Zurich offers a creative, collaborative research environment and excellent infrastructure (www.path.ethz.ch). Salary is approximately 48000 Swiss francs per year. Zurich is a vibrant, international and green city.

The PhD project is funded for three years by the Ambizione grant from the Swiss National Foundation with a possibility of extension for the fourth year.

Unique training in mathematical modeling, bioinformatics and field/lab experiments increases chances to find a job in academia, industry or governmental agencies.

Requirements

—Master's/diploma in a quantitative discipline (e.g. physics, mathematics or computer science), biology or agricultural/environmental sciences.

—Strong interest in mathematical/computational modeling in population biology

—Desire to link the models with real-world field experiments and spend about 40% of time doing experimental work

—Excellent communication skills in English

—Programming skills, experience in mathematical modeling or bioinformatics are important, but optional plus points

Application

For more details, please contact Dr. Alexey Mikaberidze by email. Please apply as early as possible, at latest February 1st, 2016. Project start: April 1st, 2016. To apply, please send Dr. Alexey Mikaberidze as a single pdf file

—a motivation letter that describes how your scientific interests and qualifications fit this project (1 page) —a CV —a copy of the MSc certificate —arrange 2-3 letters of recommendation to be sent by referees directly to Dr. Alexey Mikaberidze via email

Alexey Mikaberidze <alexey.mikaberidze@env.ethz.ch>

Europe MEME EvolBiol

Erasmus+ Master Program in Evolutionary Biology (MEME)

MEME is a two-year research oriented master program for talented and motivated students who are interested in understanding evolution in all its facets. It intends to provide an optimal preparation for subsequent doctoral studies and eventually a career in academic research.

The MEME program addresses the driving forces of evolution at all levels of organismal organization (from cells and individuals to populations and ecosystems), and allows students to study all kinds of organisms (microorganisms, plants, animals) in all kinds of habitats (marine as well as terrestrial) with a diversity of approaches (field, lab, theory). The focus of the program is not only on how evolution shaped life on our planet in the past, but also on how understanding the principles underlying evolution can provide new insights and help to cope with present-day challenges in a variety of fields, including ecology, epidemiology, physiology, immunology, genetics/genomics, bioinformatics, economics and the social sciences.

To offer a program of such broad scope, four European universities (University of Groningen, Netherlands; University of Montpellier, France; Ludwig Maximilians University of Munich, Germany; Uppsala University, Sweden), have joined forces with Harvard University (USA). Together, this consortium has put together an attractive multidisciplinary program that meets highest standards. All students have to study at (at least) two partner universities, and they will receive a double degree from two partner universities they have attended.

Being financed by the European Community, MEME has to satisfy the high quality standards imposed the prestigious Erasmus+ Program. A limited number of full scholarships is available for European and non-European students and these will be awarded in a selective procedure. Details on the program and the selection procedure can be found on www.evobio.eu . Starting date: 15 August 2016

Application deadline: 1 February 2016

Please alert your students to this great opportunity!

More information and how to apply - please see www.evobio.eu Questions about the contents of the program: Franjo Weissing (f.j.weissing@rug.nl)

Questions about the requirements and the application procedure: Irma Knevel (i.c.knevel@rug.nl)

"m.c.w.g.giesbers@rug.nl" <m.c.w.g.giesbers@rug.nl>

Halle Germany HoneybeeResistance

Halle_Germany.HoneybeeResistance

PhD project in the Molecular Ecology group at Martin-Luther-University, Halle-Wittenberg, Germany.

The aim of the project is to find genetic basis of the honey bee Apis mellifera resistance to Varroa destructor. This will be done by using the latest methods in genomics, transcriptomics and proteomics. Thus representing a unique opportunity to gain experience in an area which is of high demand in the research field. The group has excellent laboratory facilities with all state of the art equipments including a next generation sequencing platform.

The PhD position is funded for three years in which time the PhD student is expected to finish her/his degree.

The chosen PhD student is expected to work independently within the project framework. The skills should reflect the project description. The candidate will be familiar with standard molecular methods in the lab as well as bioinformatics and running scripts. Willingness to learn new methods is a must as well as ability to adapt to ever-changing circumstances. Some travelling to France or India might be included. Excellent command of English in both writing and speaking is essential. Knowledge of German is beneficial but not must.

Information of the research group can be obtained from Dr. Jarkko Routtu, tel: 0049 (0) 345 55 26382, email: jarkko.routtu(at)zoologie.uni-halle.de

http://www.mol-ecol.uni-halle.de/staff/routtu-j/ http://www.mol-ecol.uni-halle.de/research/genomics/-varroa_resistance/ Application deadline before 15. January 2016, subject line referring to "PhD resistance", together with your letter of motivation, CV, publication list, names of two referees in a single pdf file.

Jarkko Routtu <jarkko.routtu@zoologie.uni-halle.de>

Heidelberg Phyloinformatics

Dear Community,

One PhD scholarship is available in my group at the Heidelberg Institute for Theoretical Studies (HITS gGmbH) in Heidelberg, Germany

The Scientific Computing group (www.exelixis-lab.org), the home of RAxML, at the Heidelberg Institute for Theoretical Studies (HITS gGmbH) is soliciting applications for a PhD positions in the broader area of Phyloinformatics.

HITS gGmbH is a private non-profit research institute carrying out multidisciplinary research in the computational sciences. It receives its base funding from the HITS Stiftung. PhD students will be inscribed at the computer science department of the Karlsruhe Institute of Technology (KIT), which is among the top 5 CS departments in Germany.

Applicants shall have a background and MasterÂs degree in bioinformatics or computer science and excellent C/C++ programming skills. Expertise in the area of high performance computing will be a plus.

Our research mainly focuses on:

-Computational Molecular Phylogenetics -Large scale evolutionary biology data analyses -Supercomputing -Quantifying Biodiversity -Next and 3 rd Generation Sequence Data Analysis

Secondary research interests include, but are not limited to:

-Emerging parallel architectures (GPU, Xeon PHI) -Discrete algorithms on trees and sequences -Population Genetics

The starting date is flexible. To apply, please enter your application via the following link: (https://application.h-its.org/intern/register.php?id=ua6d971)

Applications must be submitted by December 31st, 2015.

Please note that applications not submitted via the online system will not be considered.

Please contact Alexandros Stamatakis (Alexandros dot Stamatakis at h-its dot org) if you have any further questions.

Also have a look at my supervision strategy:

http://sco.h-its.org/exelixis/jobs.html 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

HumboldtU ParasiteHostPopulationGenomics

The Group "Ecology and Evolution of Molecular Parasite-Host Interactions" of Juniorprofessor Emanuel Heitlinger at the Humboldt University and the Leibniz Institute for Zoo and Wildlife research, Berlin, Germany, invites applications for a:

PhD position in population genomics of parasite-host interaction

The position is offered for 3 years at the German 65% TV-L E13 pay scale.

Research topic: We are establishing the house mouse hybrid zone (HMHZ) close to Berlin as a system to study host-parasite interactions. In the HMHZ two subspecies of the house mouse (Mus musculus domesticus and Mus musculus musculus) meet and hybridize. We investigate parasite specialization vs. generalism and recombination between strains of unicellular parasites of the genus Eimeria. Eimeria spp. occur at high prevalence (around 30%) and differ in specificity for the mouse subspecies.

Requirements/Qualification of the PhD student: - Excellent degree (Master or equivalent) in (molecular) evolutionary biology or computational biology/bioinformatics - Good communication skills in English - Some background in statistics and data analysis is required. - Experience in programming (R/Perl/Python/C) is an advantage, interest in it is required. - Experience in genomics applications and next-generation sequencing analysis is an advantage. - Background in evolutionary theory and population genetics is an advantage.

The Heitlinger group works on ecology and evolution of parasite-host interactions using tools from genomics and transcriptomics. The PhD candidate will focus on genome evolution of Eimeria spp. in two closely related subspecies of the house mouse. Phenotypic aspects (immunology) of the same host individuals are investigated in an ongoing project of another PhD student. A third PhD project in the Heitlinger group is focused on gene expression of both host and parsitized cells. The candidate is expected to closely collaborate with both PhD students working on these ongoing projects and will be directly supervised by Emanuel Heitlinger on genomics data analysis.

The Heitlinger group provides a multidisciplinary working environment. Methods range from field studies, experiments "at the bench" to computational analyses. The group is located at the Department of Molecular Parasitology of the Humboldt University and has access to laboratories and resources at the Leibniz Institute for Zoo and wildlife research. This provides a diverse working environment allowing interaction with researchers working on topics ranging from conservation ecology to genetic manipulation of parasite biochemical pathways.

The student has the opportunity to apply for an association with the structured graduate training program GRK2046 "Parasite Infections: >From Experimental Models to Natural Systems" integrating his project in the Berlin community of parasitologists and providing additional resources.

Please send your application as single pdf-file by January 31, 2016 to emanuel.heitlinger@hu-berlin.de.

emanuelheitlinger@gmail.com emanuelheitlinger@gmail.com

IGB Berlin HostParasiteCoevol ChineseCandidates

Open PhD position for Chinese candidates

WolinskaÂs Lab is seeking an outstanding PhD Candidate for applying to a PhD program to undertake his/her PhD in at the Leibniz Institute of Freshwater Ecology and Inland Fisheries (IGB) located in Berlin, Germany (affiliated with the Free University Berlin). The candidate will apply for a PhD stipend with China Scholarship Council. The application deadline (i.e. first step) is 04.01.2016. For application procedure, see link below (page 5-7):

http://www.fu-berlin.de/en/sites/china/media/FUB-CSC-Programm-2016-Broschuere_22092015.pdf PhD Project description

Project title: Role of parasitic chytrids in regulating cyanobacterial blooms

Project description: Parasitic fungi of the order Chytridiales (i.e. Chytrids) are able to infect a wide number of phytoplankton species. Although overlooked for a long time, chytrids are an important factor driving the dynamics of phytoplankton. For example, Chytrids seem to be involved in the decline of toxic cyanobacteria blooms, by inducing direct mortality of parasitized cells and indirectly by the mechanistic fragmentation which weakens the resistance to grazing. On the other hand, selection on host populations exerted by Chytrids is also thought to be responsible for maintaining high host diversity in nature. The candidate will use a novel host-parasite system (based on a cyanobacterial host and its chytrid parasite) for advancing in the field of parasitism in phytoplankton. The scope of the project will address different questions related to the physiology, molecular genetics and genomics (including next-generation-sequencing) of the interactions and their ecological and evolutionary implications.

Language requirements: excellent English skills (fluent conversation and good writing skills)

Academic requirements: Master degree in biology or bioinformatics. Solid background in ecology, evolution and/or molecular biology.

Information of research group leader: We are a group of evolutionary ecologists who study how rapid evolutionary changes are being influenced by environmental challenges. We have a long-standing experience working with the Cladoceran model system: Daphnia and its microparasites. Recently, we also employ a Cyanobacteria-Chytrid system to explore a number of ecological and evolutionary questions.

http://www.igb-berlin.de/staff-a2/show/573.html
Justyna Wolinska

Leibniz-Institute of Freshwater Ecology and Inland Fisheries (IGB) Department II (Ecosystem Research) Mueggelseedamm 301 12587 Berlin, Germany

Group Leader at the IGB & Professor for Aquatic Evolutionary Ecology at the Free University of Berlin

Phone: +49 (0)30 64181 686 Fax: +49 (0)30 64181 682
email: wolinska@igb-berlin.de

http://www.igb-berlin.de/staff-a2/show/573.html
Justyna Wolinska <wolinska@igb-berlin.de>

ImperialCollege EcolEvolution

PhD Studentship advertised at Imperial College London, Silwood Park campus, UK

On: Trans-generational fitness consequences of chronic stress induced by global change

Supervisors: Dr Julia Schroeder (Imperial College London) and Prof Terry Burke (University of Sheffield)

Application deadline: 10 January 2016.

Project description: Human-induced global changes impose chronic environmental stress on ever more natural populations. The physiological symptoms of chronic stress are changes in hormone levels that can lead to stunted growth and increased risk of infection. Furthermore, the physiological mechanisms invoked by stressed are similar to those in ageing individuals. Recent studies suggest that chronic stress can lead to faster senescence (measured in telomere shortening rates), not only in affected individuals but also in their offspring. What are the trans-generational fitness consequences of a chronic stress response, and how is it adaptive? Stress could 'prime' offspring to enable them to endure stressful conditions in the future, by a 'life-fast die-young' trade-off. This projects tests the hypothesis that chronic stress primes the next generation. To test this, we make opportunistic use of an exceptionally well suited long-term 'natural experiment' in wild passerines and supplement statistical analyses on existing long-term data with focused experiments on captive birds.

The aim of this study is to quantify the fitness consequences of chronic stress to gain a better understanding of the long-term fitness costs and benefits of chronic stress in a wild population the consequences for population viability. The student will utilise a unique long-term study of a wild passerine population. The precise direction and emphasis of the project will be determined by collaboration between the student and the supervisors. Next to the traditional academic skills, the student will also learn and improve key skills such as state-of-the-art statistical modelling, data management, experimental design and field work. The student can expect to receive exceptional training in state-of-the-art analytical methodology, as well as benefitting from a well established and rewarding field project.

Imperial College London is a world leading university; it has been Ranked 3rd in Europe and 8th in the world by the Time Higher Education Rankings 2015-16. The student will be based at the Silwood Park campus < http://www.imperial.ac.uk/visit/campuses/silwood-park/ > which has a large graduate student community, with internationally renowned researchers.

The funding for this post is covered by an SSCP DTP-NERC studentship, and covers home fees and a stipend for 3.5 years. Applicants, who must be residents of the EU OR have been 'ordinarily resident' in the UK for 3 years prior to the start of the studentship, must have an outstanding honours degree, a masters degree, or equivalent, in a relevant subject, should complete an online application, upload a supporting statement explaining why they want to pursue this PhD (maximum 1 page), their CV, and 2 references, at: http://www.imperial.ac.uk/grantham/education/science-and-solutions-for-a-changing-planet-dtp/ Any enquiries about the project should be directed to:

Dr Julia Schroeder julia.schroeder@imperial.ac.uk

Julia Schroeder

Imperial College London, Silwood Park Campus Buckhurst Road, SL5 7PY Ascot, Berks, UK julia.schroeder@imperial.ac.uk +44 (0) 20 7594 9086 https://sites.google.com/site/evolbehavecol/home-1 and:

Group Leader Evolutionary Biology Max Planck Institute for Ornithology Seewiesen, Germany jschroeder@orn.mpg.de +44 (0) 74 9254 9908

julia.schroeder@imperial.ac.uk

ImperialCollege eDNA

PhD Studentship (to start October 2016)

Assessing ecosystems diversity and function using environmental DNA

Supervision: Professor Vincent Savolainen, Imperial College London, Life Sciences Department, in collaboration Thomson Ecology (Thomson Ecology are leading Ecological Consultants, which expertise is in all ecosystems, providing the full range of services within ecology from survey, through data management to consultancy and public inquiry).

Funded by NERC's Doctoral Training Programme 'Science and Solutions for a Changing Planet'

Environmental DNA (eDNA) has been used predominantly in conservation biology for monitoring the absence/presence of one particular individual focal species of conservation concern (e.g. the great crested newt). However, the methodology has the potential to revolutionise the entire field of ecosystem assessment.

eDNA is being advocated increasingly in this role, as, in theory, it simply requires a sample of water or soil to be sequenced to give a comprehensive picture of the species which are present, levels of abundance, an ecosystem's biodiversity and, by extension, ecosystem functioning and services. It has the potential to supersede current biomonitoring approaches, although there are several knowledge gaps for this approach. Here, we propose to resolve some of the issues. Specifically the PhD thesis will comprise four main parts:

(i) Using focal species of interest for biomonitoring in the UK, such as crayfish, water vole and otter, the student will firstly investigate the applicability of the eDNA technique for determining absence/presence of these species. The student will develop a standard sampling protocol for the reliable detection of the chosen species.

(ii) For the same species, the student will model how eDNA detection correlates with animal density. Preliminary work in Savolainen lab demonstrated that detection of crayfish eDNA from lotic environments was feasible, albeit only from high density populations. Savolainen also found that crayfish and newt densities also correlated significantly with their eDNA concentrations under controlled settings. These findings will be tested using more sensitive techniques that qPCR (e.g. droplet digital PCR). The objective here will be to determine whether the eDNA technique can usefully be employed to indicate relative abundance from site to site or year to year.

(iii) It is unclear how the use of the eDNA technique compares to traditional biomonitoring techniques that are in widespread use. Therefore, the student will compare the performance of eDNA over traditional bioassessment metrics in freshwater, marine and/or terrestrial ecosystems. The study will make use of traditional assessments undertaken by CASE partner Thomson Ecology in these ecosystems, with the same samples being tested using eDNA-derived metrics (concentrations, phylogeny-based, etc). The objective here will be to determine whether the eDNA is as effective a technique as conventional methods.

(iv) In support of (iii) above, testing of traditional vs eDNA techniques will also be done in experimental, controlled conditions e.g. in large glasshouses or water-filled tanks. The aim will be to calibrate species diversity estimates. This work has the potential to revisit current estimates of species diversity, while providing new tools for monitoring function or biodiversity more efficiently than has ever been performed in the past.

It is expected that the student will published the results of the PhD in high-profile scientific journals

Any enquiries, please contact v.savolainen@imperial.ac.uk

In addition to NERC's stipend, the student will receive a top up paid by Thomson Ecology.

Savolainen Lab: http://www3.imperial.ac.uk/-savolainenlab SSCP DTP: https://-www.imperial.ac.uk/grantham/education/science-and-solutions-for-a-changing-planet-dtp/ To apply

Send a cover letter, full CV and letters from 2 referees to v.savolainen@imperial.ac.uk

Make sure you provide evidence of academic quality (e.g. academic awards), research potential (e.g. final year project score, publications), communication skills (e.g. engagement in outreach activities, written news articles), and leadership outside degree requirements (e.g. organised events/activities, managed clubs/societies).

Eligibility: you must be UK citizen or resident

Deadline 18 January 2016

Prof. Vincent Savolainen Deputy Head, Department of Life Sciences Imperial College London, Silwood Park Campus Buckhurst Road, SL5 7PY Ascot, Berks, UK Tel: +44 (0)20 7594 2374 Fax: +44 (0)20 7594 2339 v.savolainen@imperial.ac.uk skype vincent.savolainen1 www3.imperial.ac.uk/people/v.savolainen

"v.savolainen@imperial.ac.uk"
<v.savolainen@imperial.ac.uk>

ImperialCollege Evolution

Masters + PhD Studentship (October 2016 start)

Evolution of species under environmental stress: ecological genomics in island palms

Building on our decade-long evolutionary research on Lord Howe Island (LHI, pictured), the student will use this emerging model system to disentangle the genomic underpinning of stress tolerance in plants. Uniquely, we have identified a pair of closely related palm species that have evolved on the minute LHI by adapting to different soil types. One of the species, Howea forsteriana, evolved on calcareous soils deposited by the sea one million year ago, which lead to water, salt and metal stresses whilst affecting flowering phenologies. The student will look at the underlying genomics of the species split. S/he will attempt to validate candidate genes by (i) rescuing wild-type phenotypes in Arabidopsis mutants by introducing orthologous palm genes; and (ii) attempting to transfer Howea genes into oil palms, the latter having a generation time much more tractable for such functional confirmation experiments. This research is highly interdisciplinary and will help identify genes of interest for agriculture (oil palm, coconuts, crops) and horticulture, thereby contributing to ensure food security under global change. The student will start with a 1-year MRes followed by 3-year PhD at the Silwood Park Campus (Savolainen Lab, in collaboration with Dr Colin Turnbull), combining genomics, statistics, fieldwork and greenhouse experiments.

The studentship is funded by BBSRC's doctoral training programme to Imperial College London.

Contact: v.savolainen@imperial.ac.uk

How to apply Initial applications should include a full CV, names and addresses and contact details of two academic referees, a personal statement (500 words max) and a covering letter. In the covering letter, applicants should indicate the projects in which they are interested (here include the title above 'Evolution of species under environmental stress: ecological genomics in island palms')

Completed applications should be submitted to the DTP Team via email- dtp@imperial.ac.uk (cc v.savolainen@imperial.ac.uk) by 6 pm on the 22nd January 2016.

Please note only shortlisted applicants will be contacted by Vincent Savolainen, we anticipate interviews will take place until the end of February

Eligibility: you bust be UK resident or citizen

Funding Notes The studentship covers: (i) an annual tax-free stipend at the standard Research Council rate (Â£16,057 for 2015-2016, to be confirmed for 2016-2017 but typically increases annually in line with inflation), (ii) contribution towards research costs, and (iii) tuition fees at the UK/EU rate.

Prof. Vincent Savolainen Deputy Head, Department of Life Sciences Imperial College London, Silwood Park Campus Buckhurst Road, SL5 7PY Ascot, Berks, UK Tel: +44 (0)20 7594 2374 Fax: +44 (0)20 7594 2339 v.savolainen@imperial.ac.uk skype vincent.savolainen1 www3.imperial.ac.uk/people/v.savolainen

"v.savolainen@imperial.ac.uk"
<v.savolainen@imperial.ac.uk>

KansasStateU EvolGenetics

The KSU interdepartmental genetics program is offering competitive PhD fellowships to begin in Fall 2016. After an initial rotation, students may choose a home lab in one of many departments across the colleges of agriculture and sciences. Please note the 15 December deadline. Applicants are encouraged to contact one or more potential mentors prior to submitting an applicaiton. In addition to the genetics program, KSU houses the Ecological Genomics Institute and the Arthropod Genomics Institute, providing excellent resources for genetics-oriented research in ecology and evolution, agriculture, and vector biology. Please refer to http://www.k-state.edu/genetics/ for additional information and instructions.

Kansas State University Interdepartmental Genetics Program

PhD applicants are encouraged to apply for a KSU Genetics Doctoral Fellowship Program. This Fellowship is open to both US and international applicants.

This competitive Fellowship requires that all application materials are received by December 15, 2015 and requires additional material to be included in your application - consult the Applications page for details.

The KSU Genetics Doctoral Fellowship Program provides students with an opportunity to experience research in up to 3 Genetics faculty labs before choosing a PhD mentor. Each Fellow is supported with a Graduate Research Assistantship 12 month stipend ($29,400 for the 2015-16 year) plus tuition and benefits yearly. This level of support is guaranteed to the Fellows for 5 years as long as they continue to make progress towards their PhD and maintain a 3.4 GPA.

Rotations: KSU Genetics Fellows are required to perform at least 2 laboratory rotations under different advisors, and are encouraged to rotate in a third lab. Rotations should be approximately 8 weeks long, and will give Fellows an opportunity to experience difference research topics, methods, and styles of different research groups before choosing a permanent PhD advisor and home laboratory by the end of their first year. During the rotations, Fellows will gain research experience relevant to each lab's focus, and will also be expected to attend regular journal club and/or laboratory meetings of the host lab.

Greg Ragland Assistant Professor Department of Entomology Kansas State University 123 W. Waters Hall 1603 Old Claflin Pl Manhattan KS 66506-4004 PHONE: (785) 532-6139 http://raglandlab.wordpress.com
"gragland@ksu.edu" <gragland@ksu.edu>

KansasStateU EvolutionBacterialPathogens

PhD or MS opportunities in the Platt lab at Kansas State University. The Platt lab studies the forces driving the evolution of bacterial pathogens as well as the disease ecology consequences of these dynamics. Current projects focus on the evolution and ecology of plasmids, cooperation, and virulence. Our approach integrates theoretical and quantitative ecology and evolution with microbial genetics using the plant pathogen Agrobacterium tumefaciens. Please visit www.platt-lab.com for more information about our work and current projects.

Our lab is in KSU's Division of Biology (http://www.k-state.edu/biology/), an active research group that houses the Ecological Genomics Institute (http://www.k-state.edu/biology/interdisciplinary/egi.html) and the Konza Prairie Biological Station (http://www.k-state.edu/biology/interdisciplinary/konza.html). For information about graduate studies at KSU's Division of Biology please visit: http://www.k-state.edu/biology/grad/index.html Kansas State University is in Manhattan, Kansas in the beautiful Flint Hills region of Kansas. The town offers excellent schools, parks, and a college town atmosphere. The surrounding area features many outdoor opportunities including the nearby Tuttle Creek State Park and Konza Prairie, a tall grass prairie reserve and LTER site.

If interested please email Tom Platt (tgplatt@ksu.edu) a statement of your research interests and experiences, your CV, and a brief statement of why you want to pursue graduate studies.

Tom Platt <tgplatt@ksu.edu>

KielU ComputationalEvolutionaryGenomics

The Genomic Microbiology Group of Prof. Tal Dagan in the Institute of Microbiology at Kiel University, Germany, invites applications for a:

PhD position in computational evolutionary genomics

The position is offered for 3 years at the German 65% TV-L E13 pay scale, with a possibility for an extension.

Research topic: Reconstructing evolutionary history of microbial genomes from metagenomic data The advance in sequencing technology now allows a deeper than ever sampling of the genomic space of unknown communities using metagenomics. This enables the extraction of further information on genetic heterogeneity within the community members that can be used for a functional and evolutionary reconstruction. The project is aimed to characterize the evolutionary history of symbiotic bacterial communities residing in deep-sea mussels. The focus will be on quantifying genetic heterogeneity and the detection of mobile genetic elements like plasmids, phages and transposons. These analyses will provide insights into the co-evolutionary dynamics of symbiotic communities and their host.

Requirements/Qualification - Excellent degree (Master or equivalent) in Computational Biology/Bioinformatics or alternatively in Microbiology or Molecular Biology with a strong focus on bioinformatics - Experience in programming and scripting. Hands-on experience in genomics applications and next-generation sequencing analysis is an advantage. - Background in statistics and data analysis. - Good communication skills in English - Ability to progress independently and a creative approach to problem-solving - Background in evolutionary theory and population genetics is an advantage

Research Group The PhD candidate will work in the Genomic Microbiology group led by Prof. Tal Dagan (http://www.mikrobio.uni-kiel.de/de/ag-dagan) that is focused on microbial genome evolution. The group is international and multidisciplinary with both computational and experimental working scientists. The student will be co-supervised by Dr. Anne Kupczok that has a strong background in population genomics and bioinformatics.

Research environment Kiel University (http://www.uni-kiel.de/) has a strong focus on life sciences (http://www.kls.uni-kiel.de/) and is maintaining an active bioinformatics network (http://www.bioinf.uni-kiel.de/). Together with the Max Planck institute for Evolutionary Biology in Plön, the Kiel area is a center for evolutionary research. The PhD position is funded by the Collaborative Research Centre 1182 "Origin and Function of Metaorganisms". Everyday life in Kiel is strongly influenced by the large proportion of students and the vicinity to the Baltic Sea. The Kiel area is a center for aquatic sport including sailing, windsurfing and kiting.

Applicants should upload curriculum vitae with a list of publications, a motivation statement and contact addresses of two referees to https://bewperle.uni-kiel.de/ifam/ .Please abstain from sending application portraits.

The University strives for a high proportion of women in research and teaching. Applications from qualified female scientists are therefore particularly encouraged.

Applications from candidates with migration background are welcome.

Disabled persons will be given preference in filling vacancies within the existing legal provisions if equally qualified.

Application deadline: 17.01.2016 or until the position is filled. Interviews will take place during January-February 2016. The position is available from January 2016 and the starting date is flexible.

For enquiries regarding the position and research topic please contact Anne Kupczok akupczok@ifam.uni-kiel.de

"akupczok@ifam.uni-kiel.de" <akupczok@ifam.uni-kiel.de>

KielU ExperimentalEvolutionaryGenomics

The Genomic Microbiology Group of Prof. Tal Dagan in the Institute of Microbiology at Kiel University, Germany, invites applications for a:

PhD position in experimental evolutionary genomics

The position is offered for 3 years at the German 65% TV-L E13 pay scale, with a possibility for an extension.

Research topic: Evolutionary genomics of microbial communities associated with domesticated plants. Plants are colonized by a wide diversity of microbes including both eukaryotic and prokaryotic species. Experimental data of phyllosphere microbes have showed evidence that the plant-associated microbiota may play a role in plant temperature and disease resistance. The project aims to identify and characterize the impact of host domestication on the associated microbial community. This will proceed through a functional and evolutionary comparison of microbial communities associated with wild and domesticated wheat species. The focus will be on quantifying genetic diversity and the detection of mobile genetic elements like plasmids, phages and transposons. These analyses will provide insights into the co-evolutionary dynamics of symbiotic communities and their host.

Requirements/Qualification - Excellent degree (Master or equivalent) in Microbiology or Molecular Biology. Experience in genomics applications and next-generation sequencing analysis is an advantage. - Knowledge and experience in molecular microbiology techniques. Any of following expertise is an advantage: DNA and RNA extraction for sequencing projects, work with environmental samples, isolation of microbial strains, plasmid engineering and generation of knockout mutant strains. - Background in statistics and data analysis is an advantage. - Good communication skills in English. - Ability to progress independently and a creative approach to problem-solving - Background in evolutionary theory and population genetics are an advantage

Research Group The PhD candidate will work in the Genomic Microbiology group led by Prof. Tal Dagan (http://www.mikrobio.uni-kiel.de/de/ag-dagan) that is focused on microbial genome evolution. The group is international and multidisciplinary with both computational and experimental working scientists.

Research environment Kiel University (http://www.uni-kiel.de/) has a strong focus on life sciences (http://-www.kls.uni-kiel.de/) and is maintaining an active bioinformatics network (http://www.bioinf.uni-kiel.de/). Together with the Max Planck institute for Evolutionary Biology in Plön, the Kiel area is a center for evolutionary research. The PhD position is funded by the Collaborative Research Centre 1182 “Origin and Function of Metaorganisms”. Everyday life in Kiel is strongly influenced by the large proportion of students and the vicinity to the Baltic Sea. The Kiel area is a center for aquatic sport including sailing, windsurfing and kiting.

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Disabled persons will be given preference in filling vacancies within the existing legal provisions if equally qualified.

Application deadline: 17.01.2016 or until the position is filled. Interviews will take place during January-February 2016. The position is available from January 2016 and the starting date is flexible.

For enquiries regarding the position and research topic please contact Tal Dagan tdagan@ifam.uni-kiel.de

“akupczok@ifam.uni-kiel.de” <akupczok@ifam.uni-kiel.de>

LMU Munich Paleobiology

Dear EvolDir readers,

we would like to announce that application to our Master Program Geobiology and Paleobiology (MGAP), starting in the winter semester 2016/17 is now open for international students and kindly ask to forward the attached message to interested students.

With kind regards, Oliver Voigt

Applications invited for the Master’s program “Geobiology and Paleobiology” (MGAP) at the Ludwig-Maximilians-Universität (LMU) Munich (Germany)

The Master's program "Geobiology and Paleobiology" (MGAP) is a consecutive, research-focussed, two-year Master of Science program at the Faculty of Geosciences of the Ludwig-Maximilians-Universität (LMU) Munich, in collaboration with researchers of the Bavarian Natural History Collections and the GeoBio-Center @ LMU. MGAP aims to provide students with a comprehensive introduction into the interdisciplinary research fields of geobiology and paleobiology to prepare them for careers in science and beyond.

The MGAP program is based on interdisciplinary, research-oriented courses in geo- and biosciences that address patterns and processes of evolutionary and environmental geobiology and paleobiology. The module-based curriculum provides an integrative approach facilitated by experts in different areas of expertise. Students will learn and acquire routines with a wide range of scientific methods such as modern techniques in molecular biology, fieldwork, collection management, comparative morphology, phylogeny, bioinformatics, statistics and (paleo-) biodiversity assessments. Students will learn independent scientific work in individual and intensively supervised research projects at early stages of the curriculum.

MGAP in brief

- International Master's program in Geobiology and Paleobiology (Master of Science, M.Sc.) at the LMU Munich
- 2 years, 4 semesters, start in October (winter semester)
- All courses taught in English
- Course total: 120 credit points (ECTS)

More information is available on the program's website: < http://www.mgap.geo.uni-muenchen.de >

For the winter semester 2016-2017 (courses start mid-October), application dates are as follows:

1) January 31, 2016 for non-EU international students (and EU students from outside of Germany. but application is also possible later), applications are possible now: <http://www.mgap.geo.uni- muenchen.de/admission>

2) February 15 to May 31, 2016 for EU students (including German students).

All applications have to be submitted via an online submission portal:

< https://www.efv.verwaltung.uni-muenchen.de/-mageopal> Oliver Voigt <oliver.voigt@lmu.de>

MaxPlanck FishBehaviour

The mechanisms and evolution of social influence

Jordan Lab

The production, perception, and cognitive processing of social cues can have far reaching effects on the social structure and behaviour of individuals within animal groups. Studying how the nature, frequency, and fine-scale detail of these interactions leads to emergent properties at the level of the collective is essential for understanding social and collective behaviour generally.

An aspect of social interaction that is commonly overlooked in studies of collective systems is that interacting nodes within social networks are not of equal status - a hierarchy exists that affects the nature and frequency of interactions among individuals, and ultimately the influence an individual will have in its social network. This hierarchy may be based on size, sex, familiarity, or reputation, and has the potential to influence numerous aspects of sociality and collective behaviour.

In this project, we seek to understand how relationships among group members can mediate the flow of information within natural groups of either Lake Tanganyikan cichlid fish or colonial spiders in Central America. We aim to characterise social influence at numerous levels - from behavioural interactions in the lab to studies of massive populations in the field, examining the neurobiological basis of social influence and socio-cognitive abilities that facilitate social interactions.

We seek students who wish to employ multidisciplinary approaches to explore their own research questions around this central theme. In our department, students have access to cutting edge digital tracking of animal behaviour and leading molecular techniques, which can be combined with in-depth lab and field experiments examining the adaptive significance and mechanisms of social influence.

Collective Animal Behaviour

Couzin Lab

Abstract Understanding collective action in biological processes is a central challenge, essential for achieving progress in a variety of fields including the coordinated communication among cells, or animals, to the dynamics of information exchange among sophisticated organisms, and the emergence of complex societies. Consequently the study of collective behaviour naturally spans scales, from how neural circuits control individual behaviour in a social context, to the analogous issue of determining the structure and function of the communication network among organisms that gives rise to emergent group, and population-level, behaviour.

We seek multiple PhD candidates to join our highly international, collaborative and interdisciplinary research group to investigating the behaviour and evolution of collective animal behaviour in the lab and/or field. We are interested in both invertebrates (e.g. locusts) and vertebrates (e.g. fish, birds) and those applicants who wish to apply and/or develop modern technologies (e.g. in automated tracking, virtual reality, GPS, drone-based imaging, machine learning, neurobiology, genetics, computational modelling) to understand how animals sense their world and make decisions in the face of uncertainty and risk.

Given the broad nature of this search it will be extremely helpful if applicants can clearly state what excites them about collective animal behaviour, and what they may want to work on. Our positions are fully funded for 4 years to allow students time to develop their own ideas and to follow ambitious and creative research directions.

Collective behaviours and social structure in animal populations

Farine Lab

How do collective behaviours and social structure emerge in animal populations? Seemingly simple mechanisms can often be amplified to produce remarkable group-level behaviours or population-level patterns. For example, highly cohesive collective movement patterns can emerge when animals respond to the movement cues of nearby neighbours. Similarly, groups of animals can solve complex problems, such as sensing their environment or finding cryptic new food sources, by eavesdropping on information being generated by nearby individuals. While natural selection acts on the behavioural phenotypes of (often selfish) individuals, collective behaviours are a group-level, or sometimes population-level, property that themselves can shape selection, and therefore form part of a complex evolutionary process. To understand how collective behaviours evolve or social structure emerges, one must understand (1) the mapping between individual phenotypes and collective behaviour, (2) the link between collective behaviour, the environment (both social and physical), and individual fitness, and (3) how selection arising from ecological or social conditions drives the expression of the phenotypes that are linked with collective behaviour or particular decisions that lead to consistent social structure.

We are seeking one or more PhD students to join an exciting new group investigating the ecology and evolution of social and collective animal

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

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MaxPlanckInst 6 HumanHistory

6 PhD positions at the Max Planck Institute for the Science of Human History

The Archaeogenetics department at the Max Planck Institute for the Science of Human History in Jena, Germany, is offering up to 6 PhD positions beginning in summer 2016. The overarching research topic at the institute is the use of novel scientific approaches from high throughput sequencing of ancient DNA from human populations and their pathogens to explore research questions related to human history & demography, gene-culture coevolution, and adaptation to infectious disease. The main foci are the relationship between humans and pathogens through time, human population dynamics on a (pre)-historical time-scale, and in tandem with microbial evolution. The institute hosts a multi-disciplinary research team and is looking for students from a variety of backgrounds including, but not restricted to, molecular biology, bioinformatics, microbiology, chemistry, biochemistry, mathematics, physics, computer science, anthropology and archaeology. Students holding a Master's degree (or equivalent) with a proven record of success in their discipline and a genuine interest in examining questions related to human history are encouraged to apply. Deadline for applications is the 10th of February 2016. Please apply online at https://s-lotus.gwdg.de/mpg/mjws/ag_phd_2016.nsf/registration. For detailed information on the application procedure please visit our website: http://www.shh.mpg.de/phd_archeogenetics Karin Groten <groten@shh.mpg.de>

McGillU MathematicalGenetics

Graduate student and postdoc positions in mathematical and population genetics are available in Simon Gravel's group at McGill University in Montreal, Canada. The project aims at creating mathematical models of historical human migrations, family histories, and high-throughput genomic data. Students will be involved in conceptual methods development, implementation, and applications to exciting datasets. This is a unique opportunity to be involved in work that is relevant and interesting from a mathematical, medical, and historical perspectives.

We welcome applications from qualified candidates from diverse backgrounds, including biology, anthropology, mathematics, physics, and computer science. Programming experience and a demonstrated interest in mathematics, statistics, or related fields is required.

The position offers an exceptional opportunity to develop theoretical and computational ideas and apply them to cutting-edge data in a supportive and thriving research environment.

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

Simon gravel <gravellab@gmail.com>

MonashU 2 EvolSessileInverts

2 PhD positions available: the ecology and/or evolutionary biology of sessile marine invertebrates

Two fully-funded PhD stipends are available to students interested in working on the evolutionary ecology of sessile marine invertebrates in Professor Dustin Marshall's group (www.meeg.org). The specifics of the project will be a joint collaboration between student and supervisor.

The stipends include all course fees plus ~$26,288 AUD per annum tax-free (the equivalent of approx. $33,000 before tax) with no teaching requirements for 3.5 years (the length of a Ph.D. in Australia).

I can guarantee funding of project costs and research support including the costs of attending at least one conference per year.

Project start dates can be any time in 2016.

Interested students should send their CVs, a brief statement of their interests and the contact details of two referees to dustin.marshall@monash.edu

To be eligible, applicants must have completed at least one year of post-graduate research in ecology or evolution.

Preference will be given to those with strong quantitative skills and publications in international journals.

Applications close January 31^st, 2016.

Henry Wootton Marine Evolutionary Ecology Group Marshall Lab Research Assistant Location: 17/104 School of Biological Sciences Monash University, Clayton Victoria 3800 Phone: +61 3 9905 5655 Email: henry.wootton@monash.edu Web: http://meeg.org/ Henry Wootton <henry.wootton@monash.edu>

NorthernArizonaU ConiferAdaptation

NArizU.Epigenetics.Conifers.GlobalChange

PhD opportunity N.Ariz.U.: Evolutionary ecology /Epigenetics/Global Change Impacts/Conifers

We anticipate filling two Ph.D. positions to work on a NSF Macrosystems Biology project at Northern Arizona University, Collaborative research: Blending ecology and evolution using emerging technologies to determine species distributions with a non-native pathogen in a rapidly changing climate, to start in either June or August 2016. This project is a multi-university collaboration examining the interacting evolutionary and ecological responses of southwestern white pine (SWWP; Pinus strobiformis) to climate change and an invasive pathogen from local to regional scales.

A PhD positon in evolutionary ecology with emphasis on epigenetics will be based in the Department of Biological Sciences under the supervision of Dr. Amy Whipple with collaborators in the School of Forestry. This graduate student would develop a project examining aspects of epigenetic inheritance and modification in determining the traits of SWWP related to phenology, drought, climate, or disease.

Three years of research assistantship funding (stipend + tuition and health insurance) are available for each position; with additional funding through teaching assistantships or possibly fellowships. Start date is June 1, 2016 or August 22, 2016. For more information contact Amy Whipple, amy.whipple@nau.edu (928) 714-0409. Strong candidates may qualify for the NAU Presidential Fellowship Program (http://nau.edu/GradCol/-Financing/Presidential-Fellowship-Program/) as well.

To apply, submit graduate application to the NAU Biology Department and a rÃÂ©sumÃÂ© and cover letter to either Amy Whipple. Review of applications will begin immediately.

Amy Vaughn Whipple <Amy.Whipple@nau.edu>

NTU Singapore HumanEvolutionaryGenomics

The Gallego Romero lab (http://www.ntu.edu.sg/-home/igr) at Nanyang Technological University in Singapore is seeking a self-motivated, creative and enthusiastic PhD student to work on any of a number of projects aimed at deciphering the role of gene regulation in human evolution, be that at the inter-species or inter-population level. The lab combines the flexibility of induced pluripotent stem cells (iPSCs) with genomic approaches to address questions about the mechanisms of evolutionary adaptation in humans that are intractable by any other means. The lab also has a long-standing interest in human population genetics and local adaptive change, especially in non-European populations.

Possible research topics include, but are not limited to: - the contribution of developmental differences in gene expression to uniquely human traits - mechanisms of local adaptation in human populations - aetiology of heart disease in humans and the great apes

All projects in the lab incorporate aspects of iPSC culture and experimental manipulation, genomics, and bioinformatics in equal parts. It is expected that students will be involved in both the tissue culture and data analysis aspects, and will contribute intellectually to the development of the project. Previous experience with iPSC culture and/or genomic and transcriptomic data is greatly preferred.

How to apply: Interested candidates should email a CV (including names, phone numbers, and email addresses of three references) and a one-page statement of research interests to Irene Gallego Romero (igr@ntu.edu.sg) with the subject line “PhD application”. Additionally, candidates should submit a formal application for admission (http://goo.gl/YZK7SA) in either the School of Biological Sciences’ (http://goo.gl/khrM0g) or the LKC School of Medicine’s (http://goo.gl/spmrZW) PhD programmes. Deadline for applications through the online portal is January 31st for an August 2016 start.

Eligibility: The position is open to all applicants that meet NTU admission criteria, but note that the monthly stipend varies according to nationality.

Funding: Funding includes tuition and associated costs for four years, and a competitive monthly stipend of S$2,700 for Singapore Citizens, S$2,200 for Singapore Permanent Residents and S$2,000 for international students, which will be increased by S$500 upon passing the Ph.D. Qualifying Examination/Confirmation. Students are also eligible for on-campus housing during the first year of their studies.

International students are encouraged to apply for a SINGA scholarship (http://www.a-star.edu.sg/singa-award/Homepage.aspx), which includes one-time settlement and airfare allowances.

igr@ntu.edu.sg

NUI Galway PlantHeterosis

PhD Studentship Position on Genetics/Epigenetics of Heterosis in Plants

Plant & AgriBiosciences Research Centre (PABC), NUI Galway, Ireland.

Prof. Charles Spillane, Genetics & Biotechnology Lab, Plant and AgriBiosciences Research Centre, National University of Ireland Galway, University Road, Galway H91 REW4, Ireland. www.spillanelab.org

Ref No: NUIG Heterosis 15

Application Deadline: 1700 January 18th 2016

The Genetics & Biotechnology lab of Professor Charles Spillane in the Plant and AgriBiosciences Research Centre at the National University of Ireland Galway is inviting applicants for a Science Foundation Ireland (SFI) funded PhD position within the lab to work on genetics and epigenetics of heterosis (hybrid vigour) in plants. The PhD research will use the model plant Arabidopsis thaliana, and involve work on quantitative and evolutionary genetics, epigenetics, molecular genetics, microscopy, genomics and bioinformatics. The successful applicant will work closely with other research team members working on a Science Foundation Ireland (SFI) funded program on this topic within the lab. We are seeking highly motivated applicants who are eager to develop a long-term career in plant genetics and epigenetics research, including in translational research to crop and agricultural applications. The successful applicant will have significant and proven prior practical experience of Arabidopsis molecular genetics/genomics research in advanced research lab/institute settings. It is desirable that in addition to significant wet lab skills, successful applicants would also have skills in programming using Python, R; in quantitative genetics (e.g. GWAS studies); and phenomics approaches for measurement of plant growth. The successful applicant will be paid a tax-free stipend of 16,000 euro per annum and have their PhD fees covered.

Applicants should send an e-mail outlining in less than 200 words your research interest and motivations in relation to this position, including; (a) your C.V. (list grades, interests, experimental skills, etc) & (b) contact details and e-mail + phone contacts for 3 referees to [charles.spillane@nuigalway.ie].

Websites:

www.spillanelab.org www.plantagbiosciences.org

Please note that only applications that put NUIG Heterosis 15 in the subject line of the email application will be considered.

The deadline for applications is 1700 Monday 18th January 2016

Prof. Charles Spillane, Genetics & Biotechnology Lab, Plant and AgriBiosciences Research Centre, National University of Ireland Galway, University Road, Galway H91 REW4, Ireland.

National University of Ireland, Galway is an equal opportunities employer.

“Spillane, Charles” <charles.spillane@nuigalway.ie>

PennsylvaniaState EvolutionaryGenomics

The Assis lab (http://www.personal.psu.edu/rua15/index.html) at Penn State is recruiting a highly motivated Ph.D. student to work on a NSF-funded project examining the role of natural selection in the evolution of novel duplicate gene functions.

The project involves developing and applying computational and statistical approaches for examining the types and strengths of natural selection acting on duplicate gene functions. In particular, the project will incorporate sequence-based analyses and mathematical modeling of gene expression evolution. The major objective of this project will be to elucidate the role of natural selection in the functional evolution of duplicate genes, and to study differences in selective forces acting on duplicates in populations of different sizes, over evolutionary time, and with varying levels of functional divergence.

Note that our lab is solely computational. While prior knowledge of a programming language is not necessary, candidates should have strong quantitative skills and the drive to learn how to program.

If you are interested in joining the lab, please email Raquel Assis (rassis@psu.edu) a current CV and description of your research interests.

In addition, candidates must submit a formal application to one of the following three Ph.D. programs: Biology (http://bio.psu.edu/graduate-portal/join-our-program), Bioinformatics and Genomics (http://www.huck.psu.edu/education/bioinformatics-and-genomics/apply), or Molecular, Cellular, and Integrative Biosciences (http://www.huck.psu.edu/education/molecular-cellular-and-integrative-biosciences/education/molecular-cellular-and-integrative-biosciences/about/for-prospective-students/apply). Application deadlines for Fall 2016 admission to these programs are in December and January.

CAMPUS SECURITY CRIME STATISTICS: For more about safety at Penn State, and to review the Annual Security Report which contains information about crime statistics and other safety and security matters, please go to http://www.police.psu.edu/cler , which will also provide you with detail on how to request a hard copy of the Annual Security Report.

Penn State is an equal opportunity, affirmative action employer, and is committed to providing employment opportunities to minorities, women, veterans, disabled individuals, and other protected groups.

rassis7@gmail.com

SamNobleMuseum UOklahoma Ornithology

Potential PhD positions in in avian genomics, Sam Noble Oklahoma Museum of Natural History and Department of Biology, University of Oklahoma Matthew J. Miller (http://mj-miller.net)

I anticipate adding 2V3 PhD students to my lab over the next 21 months. I am particularly interested in recruiting 1-2 students for all 2016. Students should be willing to take a creative leadership role in one of three principal research areas in our group: i) comparative genomics of secondary contact in Mesoamerican lowland birds, ii) comparative genomics of hybridization in Great Plains birds, or the iii) ecology of emerging vector-borne diseases in Panama.

A student working on secondary contact in Mesoamerican birds should expect to spend considerable time during the first two years of the project leading collecting expeditions in multiple locations in Mexico and Central America in collaboration with local and regional partners. Thus, the ideal student will have previous Latin American ornithological field experience collecting museum voucher specimens, as well as the ability to understand and speak Spanish. Students from Latin America are particularly welcome. However, all potential students with strong field, lab, or collections ornithological skills are encouraged to contact me. This student will ultimately perform comparative genomic analyses using datasets that she/he developed using massively-parallel sequencing resources at the University of Oklahoma, so NGS experience is a plus.

A student working on the hybridization in Great Plains birds should be motivated to lead collecting expeditions in Oklahoma and adjacent states, and should have familiarity with population genomics theory and NGS library techniques (or be able to demonstrate an aptitude for learning these skills). This student will combine distributional records and genomic data from historical and contemporary museum specimens to illuminate how hybrid zones and bird distributional dynamics in the face of climate change.

Pending NIH and collaborator funding, opportunities to work on the ecological dynamics of vector-borne diseases in Panama may also exist in our lab. A student joining our group in disease ecology will be expected to work closely with Panamanian collaborators (especially Dr. Jose Loaiza, INDICASAT-AIP, https://www.researchgate.net/profile/Jose_Loaiza), on mosquito and vertebrate interactions. Specific research projects will be guided by secured and pending funding, but typically will involve a combination of mosquito genomics, screening bird blood for viral presence, and modeling invertebrate and vertebrate dynamics across a landscape land-use gradient.

My research group is based in the bird collection of the Sam Noble Oklahoma Museum of Natural History. SNOMNH (http://samnoblemuseum.ou.edu/collections-and-research/ornithology) is a world-class university natural history museum; as such, students should be motivated to participate in collection growth and curation as part of their research program. The museum has a modern genetic laboratory shared with Dr. Cameron Siler (http://cameronsiler.com), SNOMNH Curator of Herpetology. Genomic library preparation, sequencing, and data analysis will be conducted in the under-construction genomics core lab at the on-campus Stephenson Research Center (http://-srtc.ou.edu/index.php). Resources in this lab will include Illumina Mi-Seq and Hi-Seq platforms, as well as supercomputing resources for analytics.

The SNOMNH and the University of Oklahoma have exceptional resources for ornithology students. Additional faculty with ornithological expertise include Eli Bridge (http://faculty-staff.ou.edu/B/Eli.S.Bridge-1), Jeff Kelly (http://www.animalmigration.org), and Michael Patten (http://www.biosurvey.ou.edu/patten/-Patten%20CV.pdf). Additional research opportunities are available in collaboration with the Sutton Avian Research Center (http://www.suttoncenter.org). Also, the biology department is making a strategic commitment to Geographical Ecology (http://ge.ou.edu), which would encompass our groups research interests, and will provide world-class collaborative resources in ecological modeling of species distributions and interactions.

Graduate students in my group receive degrees in either Biology or the EEB program which is affiliated with the Biology department. Students are supported by Teaching Assistantships with a base salary of 17,000

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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

StellenboschU LizardAdaptation

A PhD studentship is available in the Botany and Zoology department at Stellenbosch University in the Western Cape of South Africa. The project is funded by the South African National Research Foundation and focuses on the evolutionary responses of lizards to climate change. The student will be supervised by Susana Clusella-Trullas (Stellenbosch University), Michael Logan (Stellenbosch University), and Jeffrey Streicher (Natural History Museum, London).

Global climate is changing rapidly and the degree to which natural populations respond to temperature variation is essential for predicting the impacts of climate change on biodiversity. Individuals can adjust to temperature variation through behaviour, acclimation responses and/or evolutionary mechanisms. While much work has focused on behavioural compensation and plastic responses, less emphasis has been placed on evolutionary adaptation. Furthermore, the links between behaviour and evolutionary adaptation have rarely been addressed, although theory predicts that behaviour could either inhibit or promote evolutionary processes. This project will combine physiological ecology and genetics to examine the evolutionary paths by which populations adapt to climate variability. This project should generate a powerful predictive framework for how climate change drives evolutionary adaptation, and how this is mediated by behaviour in terrestrial ectotherms.

In addition to collecting measurements of locomotor performance and metabolic rates in the lab, the student will conduct an ethological field study. Further, the student will travel to the Natural History Museum in London to receive training in high-throughput DNA sequencing techniques. Ideal applicants will have an exemplary academic record and prior research experience. All project running costs have been secured and successful candidates will receive a bursary for 3 years starting in 2016. For more information, or to apply, please send a CV and academic transcripts to Susana Clusella-Trullas: sct333@sun.ac.za. Review of applications will begin from the 20th of January 2016 onwards and short-listed candidates will be contacted to set up interviews by phone or skype.

Michael Logan <mike.logan1983@gmail.com>

StockholmSweden EvolGenetics

CSC Scholarships for Chinese students, PhD position in Evolutionary genetics and genomics

There is an excellent opportunity for Chinese students to apply for a CSC-stipend for 4 years PhD studies, at the Royal Institute of Technology and Science for life laboratory in Stockholm, Sweden. There are several PhD positions funded, so there are good chances to get this stipend.

Because of the broad aims of this study, students with different backgrounds are welcome to apply; we are looking for molecular biologists, bioinformaticians as well as students with experience of phylogeographic analyses.

The project concerns studies of the evolutionary history of the domestic dog, exploiting the new generation of very powerful DNA sequencing technology.

We perform massive phylogeographical studies to identify the geographical and cultural context of wolf domestication, and genome sequencing and bioinformatics to identify which genes were under selection in the domestication of wolf and further evolution of the dog.

Our previous studies have indicated South China to be the origin of the domestic dog, and we now intensify the studies, based on a unique, very dense, sample collection of dogs and wolves from South China. The studies are performed in collaboration with Kunming Institute of Zoology, Chinese Academy of Sciences.

Royal Institute of Technology (KTH) is the largest and oldest technical university in Sweden, ranking top 50 internationally in the engineering and technology subject. See https://www.kth.se/en/om/fakta Science for Life Laboratory, SciLifeLab, is the largest platform in northern Europe for molecular biosciences with focus on health and environmental research. See https://www.scilifelab.se/about-us/ Information about the research group, see http://www.kth.se/en/bio/research/genetech/evolutionary-biology-and-forensics-1.314219 Requirements for applicants: Open for Chinese students. Equivalent to a Swedish Master's degree required when you start your PhD studies at KTH (Master's degree or at least two years of study in combined $B!H(BMaster+PhD$B!I(B programs at recognized Chinese universities)

Deadline for consideration: December 31st, 2015

For full information about the application process, please send an email to Dr. Peter Savolainen, email: savo@kth.se, with CV.

Peter Savolainen <savo@biotech.kth.se>

TempleU EvolutionaryBiol

Ph.D. Positions in Evolutionary Computational Genomics at Temple University

Ph.D. positions are currently available in the Department of Biology at Temple University (Philadelphia, PA, USA) in the broad area of evolutionary computational genomics. The department has built up a group of ten core faculty members in this area (see http://igem.temple.edu/people/core) as part of two new research centers: the Center for Computational Genetics and Genomics (http://ccgg.temple.edu/) and the Institute for Genomics and Evolutionary Medicine (http://igem.temple.edu/).

In particular, the following research groups are seeking new students

- Jody Hey: population genetics

- Rob Kulathinal: speciation genomics

- Sudhir Kumar: molecular evolution and phylomedicine

- David Liberles: protein evolution and comparative genomics

- Sergei Kosakovsky Pond: evolutionary modeling and scientific software development

The ideal student will be either a biologist with a strong quantitative background/orientation, or a computational/quantitative scientist with a strong interest in genomics or other biological areas. Students with interdisciplinary backgrounds are especially welcome to apply.

Before applying, you are encouraged to contact one or several of us by email, indicating your research interests, including an up-to-date CV, and suggesting which research groups you would be interested in joining.

daliberles@temple.edu

David A Liberles <tuf77157@temple.edu>

TGAC Norwich WheatComparativeGenomics

Dear Evoldir'ers

Last chance to apply for this comparative genomics PhD focussing on alternative splicing in hexaploid wheat.

http://www.tgac.ac.uk/studentships/dtp-studentships/revealing-the-alternative-splicing-landscape-of-wheat-through-comparative-transcriptomics/ Alternative splicing (AS) is a mechanism that enables multiple distinct mRNAs to be formed from a single gene. Recent studies suggest that over 60 per cent of intron-containing genes in plants undergo AS, generating a vast repertoire of transcript isoforms.

While the importance of AS in contributing to protein diversity in plant and animal genomes is now well established few studies have examined AS in polyploid species. Polyploidy is the possession of more than two complete sets of chromosomes and is especially common in plants. Bread wheat (Triticum aestivum) is an allohexaploid (AABBDD) with the three subgenomes A, B and D derived from three diploid species within tribe Triticeae. Differential regulation of AS between the subgenomes may allow more regulatory flexibility in duplicated genes, AS has therefore potentially played an important role in the evolution and adaptation of cultivated crops to different environmental conditions and niches. This proposal aims to investigate the immediate and long-term effects of polyploidy on AS, examine the importance of AS in the evolution of duplicated genes and its potential role in domestication.

The successful student will apply the latest computational approaches and sequencing technologies to identify how much variation in AS exists in synthetic wheat hybrid lines and between wheat and its progenitor species. This will provide for the first time a detailed view of the role AS has played in the evolution and adaptation of wheat and its relationship to hybridisation and polyploidy. The student will have access to a high-performance computing environment and the opportunity to learn about gene regulation, transcriptomics, genome analysis, transcript assembly, bioinformatics and software development.

Best, Mark

Dr Mark McMullan Postdoctoral Research Associate The Genome Analysis Centre Norwich Research Park twitter: mcmullan0 Skype: mark.mcmullan

"Mark.McMullan@tgac.ac.uk"
<Mark.McMullan@tgac.ac.uk>

UAntwerp EvolutionaryPsychology

PhD-student position in evolutionary biology/psychology

We are currently seeking for a motivated candidate to work in the field of evolutionary psychology, focusing on the biological relevance of asymmetry and masculinity in human sexual selection. More details can be found at https://www.uantwerpen.be/en/jobs/vacancies/ap/2015bapfwetex311/ Kind regards

Stefan Van Dongen

Faculty of Science/Department of Biology Groenenborger Campus - building V - V324b Groenenborgerlaan 171 - 2020 Antwerp Stefan.vandongen@uantwerpen.be

StatUA Statistics Center, University of Antwerp (http://www.uantwerpen.be/statua)

"It is the mark of a truly intelligent person to be moved by statistics" George Bernard Shaw

P +32 3 265 33 36

Van Dongen Stefan <stefan.vandongen@uantwerpen.be>

UAuckland MathematicalPhylogenetics

A PhD Scholarship in Mathematical Phylogenetics is available at the University of Auckland, New Zealand.

Background. Inferring the evolutionary history of all life on Earth has long been a fascinating problem in biology. Traditionally, evolutionary (phylogenetic) trees are used to represent ancestral relationships between organisms. However, recent investigations into horizontal gene transfer and hybridization, which are processes that result in mosaic patterns of relationships, challenge the model of a phylogenetic tree. Indeed, it is now widely acknowledged that graphs with cycles, called phylogenetic networks, are better suited to represent evolutionary histories. Phylogenetic networks pose many interesting mathematical challenges and have become a vivid area of research since the beginning of the 21st century.

Project. This PhD project is an exciting opportunity to develop combinatorial and algorithmic approaches to analyze and reconstruct phylogenetic networks. For example, a better understanding of the mathematics that underlies the space of all phylogenetic networks is fundamental to the reconstruction of phylogenetic networks from biological data. In short, the PhD project aims at the development of new mathematical tools and algorithms to analyze and search spaces of phylogenetic networks.

Requirements. The successful applicant has a Masters or Honours degree in mathematics or computer science and, preferably, a strong background in graph theory and/or theoretical computer science. An interest in biological questions is desirable, but not a requirement. Candidates must also be eligible for admission to the PhD program at the University of Auckland. For more information on postgraduate studies at the University of Auckland, see the following link: https://www.auckland.ac.nz/en/for/future-postgraduates.html . Scholarship. The PhD scholarship is funded by the New Zealand Marsden Fund and available from March 2016. A later starting date is negotiable. The scholarship is for three years. It covers tuition fees and provides an annual tax free allowance of NZ$27,500. The successful candidate will be based within the Department of Computer Science at the University of Auckland, New Zealand, and supervised by Dr Simone Linz.

Application. To apply, please email your CV and academic transcript, a short statement of research interests, and names and contact details of two referees to Simone Linz (s.linz@auckland.ac.nz). Informal inquiries can be directed to the same address. Applications will be accepted until the position is filled.

Dr Simone Linz Department of Computer Science University of Auckland, New Zealand s.linz@auckland.ac.nz https://simonelinz.wordpress.com "s.linz@auckland.ac.nz" <s.linz@auckland.ac.nz>

UCambridge 2 PlantEvolution

*** PhD Studentships in Ecology and Evolution, Cambridge University *** Two PhD studentships are available in the Ecosystems and Global Change group in the Department of Plant Sciences at the University of

Cambridge.

The studentships are on: * Forecasting shifts in the bioclimatic distributions of canopy trees using genomics * Ecological drivers and consequences of plant evolutionary radiations

Project outlines are available at: * http://essdtp.esc.cam.ac.uk/programme/biology-theme/b214-ecological-drivers-and-consequences-of-plant-evolutionary-radiations * http://essdtp.esc.cam.ac.uk/programme/biology-theme/b215-forecasting-shifts The studentships will be awarded competitively through a Doctoral training partnership (DTP) funded by the Natural Environment Research Council (NERC). UK and EU students who meet residency requirements will be eligible for a full NERC studentship. This will cover a stipend at the standard Research Council rate (Â£14,057 per annum for 2015/16), research costs, and tuition fees at the UK/EU rate. Application and eligibility details are available here: http://essdtp.esc.cam.ac.uk/prospective-students/how-to-apply Interested applicants should contact Dr Andrew Tanentzap (ajt65@cam.ac.uk) in the first instance to discuss an application. The deadline for applications to the NERC DTP is 6th January 2016, with all supporting documentation submitted by 20th Jan.

Andrew J. Tanentzap Head of Ecosystems and Global Change Group Department of Plant Sciences University of Cambridge Downing Street Cambridge, UK CB2 3EA http://www.plantsci.cam.ac.uk/research/andrewtanentzap "A.J. Tanentzap" <ajt65@cam.ac.uk>

UEastAnglia TGAC ConservationGenomics

Would you please help us (TGAC+UEA+NHM) advertise our PhD studentship. We (a collaboration between the Genome Analysis Centre and the University of East Anglia) are currently performing a study into conservation genomics of the Pink Pigeon. We will use the data from this study assist the future management of both the ex situ zoo populations and in situ wild populations, which we believe is pivotal to ensuring the long-term survival of this endangered species. Would you be able to send out to your mailing list the text below (blue) advertising our PhD studentship titled Genome wide analysis of drift and selection using historic and contemporary samples of the endangered Mauritius Pink Pigeon.?

Also if your social media group are happy to tweet/retweet this opportunity then they would find tweets by TGAC (@GenomeAnalysis) EnvEast (@EnvEast) and myself (@LP_Alwyn) about this studentship. Many thanks for your help with this, if you have any questions please don't hesitate to get in touch. NERC funded PhD studentship at the UEA and The Genome Analysis Centre (TGAC)

Genome wide analysis of drift and selection using historic and contemporary samples of the endangered Mauritius Pink Pigeon.

Project Supervisor

Prof Cock van Oosterhout School of Environmental Sciences, University of East Anglia

Email: c.van-oosterhout@uea.ac.uk

Project description

Project background

The Pink Pigeon (Nesoenas mayeri) is an endangered species native to Mauritius. The population has recovered from just 10 to ~400 birds today, but is still threatened by introduced pathogens, predators and habitat loss. This project will study the genetic structure of the Pink Pigeon population, prior to and post, the population bottleneck, to investigate the effect of population decline on genomic diversity and its implications for conservation.

Research methodology

The successful applicant will learn how to perform DNA extractions on historical (1800's) Pink Pigeon skins and NGS library preparation at the ancient DNA laboratory at the Natural History Museum (London). Sequencing will be carried out at TGAC followed by extensive quality control of reads and alignment to the Pink Pigeon reference for variant discovery. Using these resources the candidate will perform temporal population genetic analyses: estimate effective population size prior to the bottleneck; quantify the loss of genetic variation due to the bottleneck; compare the loss of genetic variation against those predicted by population genetic statistics; estimate differentiation between the modern and historic populations; perform statistical tests to determine whether allele loss was random during the population decline or if the population underwent directional selection; infer historical population sizes prior to the 1800's by using Pairwise Sequentially Markovian Coalescent (PSMC analysis).

Training The successful candidate will work at the

Genome Analysis Centre in collaboration with the University of East Anglia and the Natural History Museum. During this multidisciplinary project the student will gain skills and experience in genetics, evolution, molecular biology and bioinformatics including statistical analysis. The student will also receive a broad training in all aspects of science delivery and dissemination, as well as in transferrable skills.

Personal specification

Essential: First or upper second-class degree or Master's in a life or computational science discipline; A self-motivated researcher with an interest in, and understanding of population genetic studies and evolution, willing to develop their technical and analytical skills with strong presentation and written communication skills. Desirable: Experience with bioinformatics tools and/or the ability to write scripts with Python, Perl or similar programming languages.

Shortlisted applicants will be invited to an interview day on the 17th or 18th February 2016.

Funding Successful candidates who meet RCUK's eligibility criteria will be awarded a NERC studentship. In most cases, UK and EU nationals who have been resident in the UK for 3 years are eligible for a full award. In 2015/16, the stipend was ÃÂ£14,057.

Deadline: 6^th January 2016

For more information, please see http://goo.gl/sYoiIo For informal enquiries, please contact Prof Cock van Oosterhout at c.van-oosterhout@uea.ac.uk, or Matt Clark (Matt.Clark@tgac.ac.uk) All the best, Larry

"Lawrence Percival-Alwyn (TGAC)" <Lawrence.Percival-Alwyn@tgac.ac.uk>

UFreibrug 12 ForestBiodiversity

The DFG- funded Research Training Group ConFoBi 'Conservation of Forest Biodiversity in Multiple-use Landscapes of Central Europe' (RTG 2123) invites applications for

12 Ph.D. positions

(salary scale TV-L E13, 65%; including social benefits) for a three-year structured Ph.D. programme. The Research Training Group is based at the University of Freiburg, Germany (www.uni-freiburg.de) and positions will start at the 1.7.2016.

The Research Training Group ConFoBi offers an inter- and transdisciplinary biodiversity research and qualification programme which draws its novelty from the combination of multi-scale ecological studies on forest biodiversity with social and economic studies of biodiversity conservation (for more details see www.confobi.uni-freiburg.de).

Requirements:

We invite applications from highly motivated candidates who have a background in at least one of the scientific disciplines represented in this Research Training Group. These comprise These comprise Wildlife Ecology, Conservation Genetics, Functional Biodiversity Research, Vegetation Ecology , Silviculture, Remote Sensing, Forest Policy, Environmental Governance, Forest Economics, Environmental Systems Analysis. A strong interest in interdisciplinary research and the willingness to engage in scientific exchange with other disciplines is essential. Successful applicants will (1) hold a M.Sc. degree (or equivalent) in a relevant discipline, (2) have experience with methods and/or organisms relevant to the Research Training Group, (3) very good statistical and analytical skills (4) excellent English language skills, and (5) will be motivated to join and actively contribute to an inter- and transdisciplinary research training environment.

Applications:

Detailed information on the application process and the research topics with their specific tasks are available at www.confobi.uni-freiburg.de. Candidates are required to indicate their preferred project and explain their motivation for choosing it. Interviews will take place at Freiburg between late February and mid March 2016.

Please send your application in electronic form by 17.1.2016 to confobi@uni-freiburg.de as a single pdf document. For further information please contact confobi@uni-freiburg.de.

Gernot Segelbacher <gernot.segelbacher@wildlife.uni-freiburg.de>

ULeeds CompEvolBiol

GraduatePositions_CompEvolBiol_ULeeds_UK

Two PhD studentships open to UK and EU citizens available in Dr Mary J. O'Connell's Research Group at Leeds University UK (lab website: www.mol-evol.org)

Closing date for applications on both: 11th January 2016

For a full description of projects and how to apply see:

http://www.findaphd.com/search/ProjectDetails.aspx?PJID=68382&LID=735 http://www.findaphd.com/search/ProjectDetails.aspx?PJID=69420&LID=735 For further information please contact Dr O'Connell:

m.oconnell@leeds.ac.uk

– Dr Mary J. O'Connell, 250 Great Minds University Academic Fellow in Computational & Molecular Evolutionary Biology, Fulbright Scholar, Computational and Molecular Evolutionary Biology Group Leader. www.mol-evol.org Office 9.05 Miall Building, School of Biology, Faculty of Biological Sciences, University of Leeds, Leeds LS2 9JT, UK email: m.oconnell@leeds.ac.uk

"Dr Mary J. O'Connell" <drmary.oconnell@gmail.com>

ULeicester GreatApeGenomics

A fully-funded NERC studentship is available to European/UK Students, as part of the NERC DTP CENTA consortium (www.centa.org.uk), at the University of Leicester, UK

Subject: Genomic approaches to demography, diversity and sex-biased processes in great apes

Supervisors: Prof Mark A Jobling, Dr Jon Wetton, Dr Celia A May (Department of Genetics, University of Leicester, UK)

Informal enquiries to Prof Mark A Jobling, maj4@le.ac.uk, 0116 252 3427

For more details and how to apply, see: www.centa.org.uk/themes/evolution/l35/ Application Deadline: 25 January 2016 Start Date: 26 September 2016

The population genetics and evolution of great apes (chimpanzees, bonobos, gorillas, orangutans) are of particular interest because this group is the most closely related to ourselves, yet critically endangered. Species and subspecies definitions have been labile over the last 20 years, and substantially driven by molecular genetic data. Extant whole-genome data have given insights into gene flow between groups and population structure, with population isolates showing high genetic drift (particularly in mountain gorillas), which has important implications for conservation genetics. Pathogens such as Ebola virus are decimating wild populations and imposing high selective loads that will lead to adaptation. There is a clear need to better understand the structures of wild populations in their existing environments.

The genetic diversity of wild populations is strongly influenced by mating patterns and sex-biased dispersal, including the influence of sperm competition. Analysis of DNA variants in the male-specific region of the Y chromosome (MSY) and mitochondrial DNA (mtDNA) has contributed much to understanding these factors in many mammalian species. Until recently, typing of multiple short-tandem repeats (STRs) has been the only practical way to assess MSY diversity in the great apes. We have sequenced several megabases of MSY DNA in great-ape males via next-generation sequencing (NGS), deriving a detailed MSY phylogeny containing thousands of single-nucleotide polymorphisms (SNPs). In our small zoo-based sample this distinguishes well between (sub)species and reveals dramatic differences that hint at diverse sex-biased processes.

This project aims to expand the MSY tree by NGS analysis of additional great-ape individuals, to properly understand the STR/SNP haplogroup relationships, and to develop methods to type MSY SNPs and STRs, as well as mtDNA, in non-invasive samples such as faeces and hair collected from wild populations. As well as allowing a large-scale approach to gene flow, demography and sex-biased processes in non-invasive samples from natural environments, such methods will be also be adapted for in-field application for analysis of samples connected to the bushmeat trade in order to combat a major threat to wild ape populations, and to aid conservation.

The project will envolve the initial establishment of conventional methods for assessing diversity, including building fluorescent PCR multiplexes, analysis via capillary electrophoresis, set-up of software for automatic allele calling, PCR primer design, SNP typing, and Sanger sequencing.

PCR-based and sequence capture (Agilent) approaches will be established for next-generation (Illumina MiSeq) and third-generation sequencing platforms (MinION; Oxford Nanopore Technologies). Methods will be adapted and validated for non-invasive samples from the wild, and MinION methods established for in-field analysis.

Phylogenetic analysis of DNA sequences and population-genetic statistical analysis will be undertaken to illuminate the population structures and evolution of great ape (sub)species, to understand the roles of sex-biased processes, and to aid in the establishment of conservation strategies.

Prof Mark A. Jobling Professor of Genetics Department of Genetics Room G5, Adrian Building University of Leicester University Road Leicester LE1 7RH UK

tel.: +44 (0)116 252 3427 mob.: +44 (0)7955 882334 fax: +44 (0)116 252 3378 email: maj4@le.ac.uk web: http://www2.le.ac.uk/departments/genetics/people/jobling Mark Jobling <maj4@leicester.ac.uk>

UMuenster 2 Evolution 2

2 PhD stipends within the interdisciplinary "Münster Graduate School of Evolution": PhD projects in Biology and Medicine

Closing date for applications: 10 December 2015

The "Münster Graduate School of Evolution" (MGSE) offers 2 PhD positions funded by DAAD-stipends for international (non-German) students within the stimulating environment of the University of Münster, Germany. As an interdisciplinary graduate school, the MGSE uses the unifying concept of evolution to bridge the faculties of Biology, Medicine, Geosciences, Mathematics, and Philosophy. PhD students work on their diverse disciplinary projects in one of the involved institutes and benefit from interdisciplinary curricular activities as well as a structured supervision and support throughout their PhD. The MGSE is based in the stimulating city of Münster near Münster's City Palace and offers a family friendly and international atmosphere.

Location: Münster, Germany Working language: English Start of the PhD: October 2016 Duration: 3 years (4 years for students from developing and emerging countries)

You can apply for one or several out of nine projects, each of them involving high-quality research and state-of-the-art techniques. The projects are supervised by excellent researchers within the MGSE:

- Prof. Dr. Erich Bornberg-Bauer (Institute for Evolution and Biodiversity, University of Münster) - Prof. Dr. Jürgen Gadau (School of Life Science, Arizona State University) - Prof. Dr. Ulrich Dobrindt (Institute of Hygiene, University Hospital Münster) - Prof. Dr. Joachim Kurtz (Institute for Evolution and Biodiversity, University of Münster) - Dr. Jörn Scharsack (Institute for Evolution and Biodiversity, University of Münster) - Prof. Dr. Norbert Sachser (Institute of Neuro and Behavioural Biology, University of Münster) - Prof. Dr. Stephan Ludwig (Center for Molecular Biology of Inflammation, University of Münster) - Prof. Dr. Wojciech Makalowski (Institute of Bioinformatics, University of Münster) - Prof. Dr. Monika Stoll (Institute of Human Genetics, University Hospital Münster) - Dr. Shirin Glander (Institute of Human Genetics, University Hospital Münster) - Dr. Frank Rühle (Institute of Human Genetics, University Hospital Münster)

Highly qualified and motivated candidates all over the world are invited to submit their application.

For a list of projects and information on requirements and the application procedure, please visit: http://www.uni-muenster.de/Evolution/mgse/jobs/index.html. In case of questions please contact: mgse@uni-muenster.de.

Dr. Vanessa Kloke Coordinator of the Münster Graduate School of Evolution Westfälische Wilhelms-Universität Münster Schlossplatz 6, D-48149 Münster, Germany Â Phone: +49 251 83-21252 E-Mail:Âmgse@uni-muenster.de Website:Âhttp://www.uni-muenster.de/Evolution/mgse/ "Vanessa Kloke, MGSE" <mgse@uni-muenster.de>

UNottingham 2 EvolutionGeneticsConservation

Two BBSRC DTP-funded PhD positions, University of Nottingham.

Closing date for applications is Monday 14th December. All references must be received by Thursday 17th December. Apply here: https://www.nottingham.ac.uk/graduateschool/bbsrc/index.aspx. Successful candidates will be offered four years PhD training. Part of the first year will consist of lab rotations, with the remaining time focused on the main research project. Funding available to UK residents (fees + stipend) and EU citizens (fees only).

Project 1 "Control and conservation of endemic species in the UK and Hawaii"

Dr. Angus Davison and Dr Sara Goodacre, School of Life Sciences, University of Nottingham

Invasive snails and slugs are causing worldwide problems, both in terms of direct damage to crops, and as intermediate vectors for diseases of farm animals. Yet, snails and slugs are difficult to identify and we have little idea of what influences their distributions, hindering appropriate control and conservation efforts. In the UK, modern molecular phylogenetic knowledge of these species - terrestrial and aquatic - and their potential as vectors of disease is relatively limited. In Hawaii, we have recently characterised an aquatic Lymnaeaid snail that has cryptically colonised the archipelago. This snail is endangering the local endemic species, and potentially acts as an intermediate vector for the liver fluke parasite.

The aim of this project, therefore, will be to study the process of invasion, using representative species in the UK and Hawaii (with collaborators in the Bishop Museum, Hawaii and Howard University) to understand the evolution of these snails and their parasites, and including methods that may help refine the identification of the invasive species and species of conservation concern. Although much of the work will be lab-based, with a concomitant bioinformatics element, field collection will be a necessary component. https://www.nottingham.ac.uk/graduateschool/-bbsrc/available-projects/lifesciences/afs-davison.aspx Project 2 “Extreme strength from biomineralisation in molluscs”

Dr. Angus Davison, School of Life Sciences and Dr Nicola Everitt, Faculty of Engineering, University of Nottingham

Nature has inspired some of our greatest inventions, from biomimetic Velcro to sea-water desalinating biological membranes. In this project, we will explore the potential for biomimicry in the design features of molluscs, focussing on their mastery of biomineralisation. For instance, snail teeth are the strongest biological material, and have outstanding mechanical properties, due to their multi-layered structure; also, so-called “love darts” are unique drug-enlaced delivery vehicles that vary markedly between species, yet at present we are quite ignorant of how the function of these organs relates to their microstructure.

In this project, we will use nanoindentation methods to investigate the mechanical behaviour of specimens at a microstructural length scale. Simultaneously, we will investigate the development of the organ(s), through gene expression studies, also combining ecological and phylogenetic information to construct an evolutionary framework which links the microstructure to the mechanical properties. Ultimately, the project will seek to use the information gained to inspire, inform and improve the production of new technologies, perhaps especially with regard to microparticle design, drug delivery and nanocomposite materials, and will of necessity seek out of commercial partners, as discoveries are made. https://www.nottingham.ac.uk/graduateschool/-bbsrc/available-projects/lifesciences/ibb-davison.aspx Dr. Angus Davison Reader in Evolutionary Genetics School of Life Sciences Life Sciences Building University Park University of Nottingham NG7 2RD

0115 8230322 angus.davison@nottingham.ac.uk www.angusdavison.org Angus Davison <Angus.Davison@nottingham.ac.uk>

UPennsylvania MacroEvolutionPaleobiology

GradStudentPositions:UPenn.MacroevolutionPaleobiology

A PhD fellowship in Paleobiology is available in the Department of Earth and Environmental Science at the University of Pennsylvania, starting in Fall 2016. Prof. Lauren Sallan seeks a graduate student to address major questions about the evolution of life. These include: how global change has affected life over time, how life evolves at high levels (macroevolution), the relationships of living and dead animals (phylogeny), and the origins of living biodiversity. While research in the lab has focused on fishes, any suitable group of fossils may be used.

Potential thesis topics include, but are not limited to: the long-term effects of mass extinctions (e.g. the end-Devonian and end-Ordovician), the roles of predation and competition in marine ecosystem evolution, traits of adaptive radiations and living fossils, the effects of long-term climate and environmental changes (e.g. the Late Paleozoic Ice Age) on biodiversity, and major transitions in early vertebrate evolution (e.g. origin of jaws, invasion of land). The student can also develop a novel project that addresses similar questions using quantitative, phylogenetic and/or descriptive methods.

Applicants are encouraged to contact Prof. Sallan (lsallan@sas.upenn.edu) for more details. Additional information on the fellowship is available on the departmental website: www.sas.upenn.edu/earth. Applications for entry in Fall 2015 are due January 15, 2016. Applications to graduate school at Penn must be submitted online at https://www.applyweb.com/upenng/ Lauren Sallan Assistant Professor Earth and Environmental Science & Evolution Cluster University of Pennsylvania Office: Hayden 154B Phone: (215) 898-5650 lsallan@sas.upenn.edu

Lauren Sallan <lsallan@sas.upenn.edu>

UppsalaU DeepSeaSpongeGenomics

Ph.D. position on Metabolomics/Genomics of Deep Sea Sponges,

Dept. of Medicinal Chemistry, Uppsala University, SWEDEN.

I am seeking a highly motivated PhD candidate to work within the frame of the newly EU funded SponGES consortium. This consortium will investigate deep-sea north Atlantic sponge grounds. The candidate will develop a suite of genomic and metabolomic resources to investigate the population diversity of key sponge species and assess connectivity between sponge grounds. These resources will also unlock the potential of sponge grounds for drug discovery, in which the candidate will also play a part.

For more info and to apply, use the link below (in Swedish, for the English version click on "English", upper-right corner). https://mp.uu.se/web/info/vart-uu/lediga-jobb/-/jobb/86997 duration of position: possibly 5 years

application deadline: 18th of January 2016

For specific information about the announced Ph.D. position and details of the project, please contact me (paco.cardenas@fkog.uu.se).

Dr. Paco Cardenas Div. of Pharmacognosy, Dept. of Medicinal Chemistry, Uppsala University BMC Box 574, SE 75123 Uppsala, Sweden paco.cardenas@fkog.uu.se

Paco Cardenas <paco.cardenas@ebc.uu.se>

UPretoria 3 WoodwaspEvolution

ThreePhD positions study the molecular, chemical and behavioral ecology ofSirex woodwasp - University of Pretoria, South Africa

ThreePhD positions are available to study the molecular, chemical and behavioralecology of Sirex woodwasp - Amylostereum fungus - Deladenus nematodesymbioses. These positions have Forestry and Agricultural BiotechnologyInstitute (FABI), University of Pretoria, South Africa as thehome institution, but will involve extensive collaborative work with theCanadian Forest Service (CFS) and the University of the Sunshine Coastin Australia.

Theprojects Invasivepests are one of the most significant threats facing plant ecosystemsand production systems globally; from agriculture to forests andforestry. Sirex noctilio and its fungal mutualist, Amylostereum areolatum,is a growing model system for understanding processes that affectthese invasions, as well as the development and implementation of managementtools for it. One of the primary management tools for this invasivepest is biological control using the nematode Deladenus siricidicola.

1.How and which visual and olfactory stimuli affect the behavior of Sirexnoctilio, and how can these be integrated in management programs? Potentialareas of inquiry may include elucidating kairomone, pheromone, visualand genomic stimuli that influence the behavior of S. noctilio. Theconsequences of these stimuli and their potential to contribute managementtools will be actively explored. 2. What factors influence the reproductive biology of Sirex noctilio, andhow does this influence invasive populations? Potential areas of inquirymay include elucidating physiological and behavioral traits that influencethe complex and fascinating reproductive system of this wasp. Ultimatelythe successful candidate will explore molecular tools to manipulateoutcomes of sexual reproduction. 3. How do invasion processes and micro-evolution affect symbioses, invasivepest adaptation and their biological control agents? The project,termed âPetri-dish Australasia' will use the Sirex noctilio/Amylostereumareolatum/Deladenus siricidicola as a model system tostudy microevolutionary processes in invasion and biological control inAustralia and New Zealand.

Theprojects have the potential to include a combination of field, molecularand chemical ecology and genomics. All three projects will dealwith fundamental questions on the ecology of this intricate, tripartitesymbiosis, but will either include or contribute directly to appliedaspects of the management of this global invasive pest complex. â Requirements Candidatesshould have a Masters or equivalent degree. Candidates are notexpected to possess advanced skills in all the fields linked to the projects,but experience and an interest in at least two of these fields willbe an advantage. Thus a background in molecular genetics and ecology,chemical ecology, behavioral ecology, entomology, microbiology, nematologyor related fields would be considered an asset. Resources andsupport to develop these diverse skills in candidates will be provided.While the projects will explore novel questions at the frontiersof understanding these particular symbioses, as well as symbiosesand invasive pests in general, they are built on strong baselinedatasets, extensive resources and support, and a long history ofexcellence and leading work in the field.

Where Forestryand Agricultural Biotechnology Institute (FABI), University of Pretoria,South Africa. FABI is a global leader in plant biotechnology relatedresearch, with a strong focus on tree health. The successful candidateswill join a vibrant, dynamic, highly international (both in termsof students, postdocs, staff and networks) and interdisciplinary researchteam, which includes strong research groups in tree health research,mycology, entomology, tree and crop genetics, plant-microbe-insectinteractions, genomics, chemistry and more. The laboratoriesinvolved have strong links to industry, government and internationalresearch networks making them a unique and rewarding environmentto work and launch your research career. For more informationplease visit www.fabinet.up.ac.za . Partners ProfBernard Slippers, Dr Brett Hurley, Prof Michael J Wingfield and others DrJeremy Allison, Natural Resources Canada and University of Toronto, Canada DrHelen Nahrung, University of the Sunshine Coast, Australia DrAngus Carnegie, New South Wales Department of Primary Industries, Australia

Remuneration Fullscholarships are offered for all three positions in South Africa thatwill be sufficient to cover accommodation, living costs, registrationfees, and basic medical aid. Additional funds will cover runningcosts associated with the project.

When Weare hoping to fill these positions as soon as possible, but no later thanMarch 2016. The positions will remain open until a suitable candidatehas been identified.

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USheffield SharkEvoDevo

Evolution and development of shark skin teeth inspired surface design for global CO2 reduction

The deadline for submission of applications is Monday 11th January 2016.

A Ph.D studentship is available for an interdisciplinary project focused on evolutionary developmental biology of shark skin teeth and engineering shark-inspired surface geometries for reduced drag leading lower CO2 emissions across several industries. This is an ideal opportunity for an ambitious candidate to work at the interface of evo-devo and engineering. This project aims to explore novel methods to understand the evolution and development of shark tooth patterning and how these data can be modelled in silico for more energy efficient surface design that can be 3D-printed for functional models of drag reduction. This project would suit a candidate interested in skin tooth development in sharks and the diversity of these structures in pattern and morphology across species to understand the most efficient patterns and geometries in nature, and then how nature can help us develop solutions to environmental issues in the engineering industry. This Ph.D studentship will be supervised by Dr. Gareth Fraser, Department of Animal and Plant Sciences, University of Sheffield, and co-supervised by Dr. Mark Johnson at the University of Liverpool, School of Engineering. This research is in collaboration with Dr. Zerina Johanson at the Natural History Museum, London. For further details visit:

https://acce.shef.ac.uk/shark-skin-inspired-surface-design-for-co2-reduction/ All the best, Gareth

Gareth J. Fraser, Ph.D Lecturer in Zoology Department of Animal and Plant Sciences Alfred Denny Building University of Sheffield Western Bank Sheffield S10 2TN UK Phone: +44(0)1142224317 Email: g.fraser@sheffield.ac.uk Website: Fraser Lab Sharks and X-Rays (NERC Shark Team website) Skype: garethjfraser Sheffield Marine Research Forum: http://marine.group.shef.ac.uk/ Gareth Fraser <g.fraser@sheffield.ac.uk>

USouthampton NHM London EcologicalSpeciation

Dear Evoldir,

We are currently looking for applicants for a PhD based partly at the University of Southampton and partly at the NHM, London. Please do contact myself (M.Chapman@soton.ac.uk) or Mark Carine

(M.Carine@nhm.ac.uk) if you have any questions. Application deadline is 4th January.

The genomics of ecological speciation in an endemic plant genus

This SPITFIRE project will analyse the speciation genomics of an endemic genus in the Canary Islands. Several species are endemic to these islands, showing ecological speciation (the origin of species by adaptation to novel environments) within and between islands. The genome of one species is being sequenced at UoS, and the SPITFIRE project will generate sequencing data from multiple individuals of all the endemic species plus mainland congeners. First, phylogenetic analyses will resolve the process of speciation throughout the Islands. Second, the strength of intrinsic reproductive isolation between species pairs will be measured through crossing experiments in situ on Tenerife. Third, through the analysis of linkage disequilibrium, DNA polymorphism and selective sweeps, the genomic regions and candidate genes underlying ecological speciation will be uncovered.

If you are interested in this studentship and would like more information (note the nationality requirements, funding situation and other requirements) please take a look at:

http://noc.ac.uk/gsnocs/project/genomics-ecological-speciation-endemic-plant-genus Dr. Mark A. Chapman M.Chapman@soton.ac.uk +44 (0)2380 594396

Centre for Biological Sciences University of Southampton Life Sciences Building 85 Highfield Campus Southampton SO17 1BJ

Mark Chapman <markchapman4774@gmail.com>

UTromso ModelingDisease

PhD student in Systems Pharmacology (Mathematical Modelling)

A 4-year PhD student position is available immediately in the Systems Pharmacology group of Dr. Pia Abel zur Wiesch. The position is affiliated with the Centre for Molecular Medicine Norway (NCMM), Nordic EMBL Partnership Molecular Medicine and is located at the University of Tromso, Norway. While the primary location is in Tromso, the candidates have the option to visit Yale School of Public Health. The candidate is expected to spend substantial time at ETH Zurich, Switzerland.

About the group

The Systems-Pharmacology group (https://-en.uit.no/om/enhet/ansatte/person?p_document_id=-422372&p_dimension_id=88118) is headed by Dr. Abel zur Wiesch, Tenure Track Associate Professor (seniorforsker) at UiT, NCMM Young Associate Investigator (http://www.ncmm.uio.no/research/-associate-investigators/) and Visiting Assistant Professor at Yale School of Public Health. The aim of our work is to improve therapy in infectious diseases and cancer by using mathematical models to predict how much drug a patient should receive and how long and how often the patient should be treated. Our mathematical models describe both the intracellular reaction kinetics of drug-target binding as well as growth and death of populations of bacterial or cancer cells (Abel zur Wiesch & al., Science Transl. Med. 2015). We collaborate closely with experimentalists and clinicians. Two examples of ongoing projects are:

- link single cell analyses (John McKinney, EPFL Lausanne, http://people.epfl.ch/john.mckinney) to clinical studies (http://www.tballiance.org/ to improve TB therapy, funded by the Bill & Melinda Gates foundation

- develop new extended release technologies together with gastroenterologists at Harvard (Giovanni Traverso, http://www.massgeneral.org/doctors/-doctor.aspx?id=19633) and MIT (Andrew Bellinger http://langer-lab.mit.edu/people/current).

The most important collaborator for the PhD projects is Dr. Roland Regoes (ETH Zurich, http://-www.tb.ethz.ch/research/regoes-group.html). The projects will combine mathematical modeling with the analysis of clinical and experimental data. Both the Systems Pharmacology group and the Regoes group at ETH have documented expertise in all of these areas (Abel zur Wiesch & al., Science Transl. Medicine 2015, Abel zur Wiesch & al., Lancet Infectious Diseases 2011, Abel, Abel zur Wiesch & al., Nature Methods 2015, Diard & al., Nature 2013, Kaiser, Regoes & al., PLOS Biology, Regoes & al. AAC 2004). The project therefore offers a unique opportunity to get experience in a wide range of interesting research topics.

Your profile

We seek candidates that appreciate working in an international and interactive environment, are highly enthusiastic about basic research with medical applicability, motivated and willing to integrate in a young team of researchers. You should have solid programming skills and a strong quantitative background and be passionate about applying your skills to biological and medical questions. A strong interest in Public Health, Pharmacology, Infectious Diseases, Biochemistry and/or Mathematical Biology is desirable. Previous experience with mathematical modeling and/or analysis of large datasets is an advantage. Good command of English and scientific writing skills are required. Applicants must hold a Master's degree (or equivalent).

We offer

The successful candidate will work collaboratively with other faculty, scientists, and students in a dynamic and multi-disciplinary environment. We offer the unique opportunity of being embedded in several scientific environments at the UiT in Tromso, the Centre for Molecular Medicine Norway (NCMM) in Oslo and Yale School of Public Health (YSPH) in Boston. We strongly encourage career development beyond authorship of research manuscripts arising from this work. We will help the successful candidate in developing their own interests and also encourage attending international conferences and visiting collaborators. The salary will be commensurate with experience and in accordance with the Norwegian State salary scale code 1017 (starting approx. at EURO 46'500/ NOK 429'700 per year). UiT is a family friendly work environment and offers very attractive and internationally competitive benefits including pension arrangements, healthcare and other welfare benefits.

How to apply

The application deadline is January 12 2016 and must be submitted in English. The following documents are required:

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UWesternAustralia ClimateAdaptation

We have a fully funded PhD position available to investigate the effects of sociality on physiological responses to high temperatures. Please see following link for full details: http://www.hotbirdsproject.com/blog/phd-babblers Mandy Ridley <amanda.ridley@uwa.edu.au>

UWisconsin Milwaukee PopulationGenomics

Position announcement: PhD position in genomics of captive populations in the lab of Dr. Emily Latch, Department of Biological Sciences, University of Wisconsin-Milwaukee.

The Latch Lab is seeking a highly motivated and enthusiastic graduate student to join the Ecology and Evolutionary Biology program in the Department of Biological Sciences at the University of Wisconsin-Milwaukee. The student would participate in a project focused on integrating molecular data into the genetic management of wildlife breeding programs. Specific aspects of the research will include generating and analyzing genomic (SNP) datasets for captive breeding programs, to be used to develop custom genomic and pedigree-based software tools that can be used by non-experts managing wildlife breeding programs. This project has wide-reaching applications to in situ and ex situ conservation programs. The student will also assist with organizing and participating in training workshops for non-experts, and disseminating research through presentations and publications. This project is a collaboration with the San Diego Zoo, and see also coordinating postdoc position at

http://life.mcmaster.ca/ ˜ brian/evoldir/PostDocs/SanDiegoZooGlobal.CaptivePopulationGenomics Qualified candidates should have completed a B. S. in Biological Sciences or a related discipline, and be broadly interested in the conservation and management of vertebrate populations. Qualified applicants will have a strong background in genetic/genomic analysis, bioinformatics, and/or computer modeling. Proficiency in computer modeling skills and one or more scripting languages is preferred. The applicant should have the ability to collaborate well and communicate scientific materials to non-scientists. Funding in the form of assistantships, research support, and travel grants are available for qualified candidates.

Research in the Latch Lab employs molecular genetic tools and statistical genetic methods to address fundamental questions in vertebrate population genetics and evolutionary ecology. Many projects have an applied focus, helping to inform conservation and management programs. For more information about the Latch Lab, visit: http://www.uwm.edu/ ˜ latch . To learn more about graduate studies in the Department of Biological Sciences at UWM, visit: http://www.uwm.edu/Dept/Biology/Docs/Grad/gradindex.html. The Department has an active research group in Behavioral and Molecular Ecology http://www.preferencefunctions.org/behavioral-molecular-ecology.html If you are interested, please send me an email including a statement of research interests and a CV (including GPA and GRE scores). I will start reviewing applications immediately, and will continue reviewing applications until the position is filled. Qualified candidates will also have to apply to the UWM Graduate School (deadline Jan 1, 2016). Anticipated start date is June or August 2016.

Emily K. Latch Associate Professor Dept. of Biological Sciences University of Wisconsin - Milwaukee 3209 N. Maryland Ave. Milwaukee, WI 53211

Email: latch@uwm.edu Tel: 414-229-4245 Web: http://www.uwm.edu/ ˜ latch "latch@uwm.edu" <latch@uwm.edu>

Vienna PopulationGenetics reminder

reminder: Apply now for PhD positions in Population Genetics in Vienna by January 17, 2016

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

We invite applications from highly motivated and outstanding students with a background in one of the following disciplines: bioinformatics, statistics, evolutionary genetics, functional genetics, theoretical and experimental population genetics. Students from related disciplines, such as physics or mathematics are also welcome to apply.

Topics include:

§Population trees and polymorphism-aware phylogenetic models

§Inferring evolutionary trajectories from time series data

§Wolbachia infection dynamics in evolving Drosophila populations

§Functional characterization of beneficial alleles in Drosophila

§Modified evolve and re-sequence design

§Convergent and adaptive evolution during ecotype formation

§Population history and adaptation in natural Arabidopsis populations

Only complete applications (application form, CV, motivation letter, university certificates, indication of the two preferred topics in a single pdf) received by January 17, 2016 will be considered. Two letters of recommendation need to be sent directly by the referees.

Monthly salary of a successful candidate will be according to the regulations of the Austrian Science Fund FWF. All information about the about available topics, the training program and the application procedure can be found at www.popgen-vienna.at – Dr. Julia Hosp Vienna Graduate School of Population Genetics Coordinator www.popgen-vienna.at *https://twitter.com/PopGenViennaPhD* < http://www.popgen-vienna.at >

c/o Institut für Populationsgenetik Vetmeduni Vienna Veterinärplatz 1 A-1210 Vienna http://www.vetmeduni.ac.at/en/population-genetics/ Tel: +43 1 25077 4338 Fax: +43 1 25077 4390

julia.hosp@gmail.com

Vienna SymbioticSpeciation

PhD Position in Symbiotic Speciation, Genetics & Microbiology at the Medical University of Vienna, Austria

A PhD position funded by the Austrian Science Fund (FWF) is available to study the impact of the endosymbiotic bacteria Wolbachia on physiology, sexual behavior and de novo speciation of the model system Drosophila.

This intracellular bacterium is well known as the prime reproductive parasite of insects by causing cytoplasmic incompatibilities, feminization, parthenogenesis or male killing, but depending on their evolutionary stage, it also can provide adaptive fitness benefits to insect hosts, such as nutritional provisioning or pathogen protection. We recently found that in some Drosophila species Wolbachia specifically colonize defined host brain regions that orchestrate sexual behavior of male and female flies. Furthermore we found that even slight perturbations of this intimate host-symbiont homeostasis can foster de novo speciation of Drosophila in the wild plus under experimental conditions in our laboratory.

In this newly started FWF research project we aim to decipher the temporal and functional dynamics of this Wolbachia-Drosophila symbiosis in two different Drosophila systems, which are currently under speciation in the Neotropics.

The successful candidate will be embedded in the highly multidisciplinary and collaborative environments at the Department of Cell and Developmental Biology of the Medical University of Vienna.

Applicants should hold a master's degree in biology, genetics, microbiology, or a related discipline. We are looking for enthusiastic scientists with proficient communication skills, who are good team players. Previous experiences with DNA & RNA techniques, sequence analyses, fly work, FISH assays, immunocytochemistry and/or microscopy techniques are advantageous.

Please send applications (including CV, a letter of intent and contact information of at least two referees) to the address below.

The call will close on January 31st, 2016 and informal enquiries are welcome. Contact:Wolfgang Miller, Lab Genome dynamics, Center of Anatomy and Cell Biology, University of Vienna, Austria E-Mail: wolfgang.miller@meduniwien.ac.atPhone: 0043 1 40160 37750

Website: Department for Cell and Developmental Biology

| Department for Cell and Developmental Biology | | View on www.meduniwien.ac.at | Preview by Yahoo |

Wolfgang J. Miller, PhD Lab Genome Dynamics, Dept Cell & Developmental BiologyCenter of Anatomy and Cell Biology, Medical University of Vienna, Schwarzspanierstr. 17,HP 36 A-1090 ViennaAUSTRIA.

email: wolfgang.miller@meduniwien.ac.at http://www.meduniwien.ac.at/celldev/miller/ Tel. 0043 1 40160 37750Fax 0043 1 40160 937790

Wolfgang Miller <wolfmanmiller@yahoo.com>

VirginiaCommonwealthU LandscapeGenetics

The Dyer laboratory is in search of a doctoral student in the Integrative Life Sciences (ILS) PhD Program (http://lifesciences.vcu.edu/academic-programs/phd-in-integrative-life-sciences/) at Virginia Commonwealth University to work on theoretical, statistical, and computational problems in modern landscape genetics.

The research in the lab focuses on genetic connectivity predicted by intervening landscape structure. Ongoing projects include studies on pollen-mediated gene flow along urban gradients and spread of the gypsy moth invasion front, both projects have funding and will be incorporating LiDAR & Hyperspectral characterization of intervening landscapes via drones and high-throughput genetic analyses. I'm looking for someone who can aid in the development of conditional genetic and spatial models that can integrate remotely sensed data. Interested students should send a CV to Dr. Rodney Dyer (rjdyer@vcu.edu) before applying.

Rodney J. Dyer, PhD Department of Biology Center for Environmental Studies Virginia Commonwealth University http://dyerlab.bio.vcu.edu rjdyer@vcu.edu

WesternWashingtonU ProteinExpressionQuantGenetics

Graduate Position in Quantitative Genetics of Protein Expression Dynamics

The laboratory of Dan Pollard in the Biology Department at Western Washington University is recruiting a masters-level graduate student to work on an NSF-funded project on the mechanisms by which natural genetic variation in the Saccharomyces cerevisiae population alters protein levels by affecting the rate at which proteins are produced and degraded. The project incorporates yeast genetics, fluorescence microscopy, transcriptomics, proteomics, quantitative genetics, and computational modeling.

Ability to communicate clearly, interact collaboratively, and work independently is essential. Preferred qualifications include a Bachelor's degree in the biological sciences, strong molecular biology training (e.g. PCR, sub-cloning, sequencing), experience with bioinformatics (e.g. Perl/Python, R, Matlab), and excellent organizational skills. Preference will be given to applicants with experience with budding yeast genetics, fluorescence microscopy, and RNA molecular biology.

Western Washington University is a mid-sized public liberal arts university located in Bellingham, WA. Bellingham is a beautiful coastal town in the northeast corner of Puget Sound, 50 miles south of Vancouver, 30 miles west of Mt. Baker, 90 miles north of Seattle, and 20 miles east of the San Juan Islands.

Interested candidates are encouraged contact Dr. Pollard by email (dan.pollard@wwu.edu) with a description of their research interests and a CV including relevant experience, GPA, GRE scores, and the names of three references.

Official application is due February 1st. Application details: http://west.wwu.edu/gradschool/programs/program_details.asp?Program=3D1003 More information: https://cse.wwu.edu/biology-faculty/pollard https://cse.wwu.edu/biology http://www.wwu.edu/http://www.bellingham.org/ “Dan.Pollard@wwu.edu” <Dan.Pollard@wwu.edu>

YorkU SocialInsectGenomics

Multiple PhD positions in honey bee genomics and sociobiology at York University, Toronto.

Are you interested in genomics, population genetics, social insects and a Ph.D.?

The Zayed lab (http://zayedlab.apps01.yorku.ca/wordpress/) in the Department of Biology at York University (Toronto, Canada) is looking for enthusiastic new doctoral candidates in 2016 to work on one of several exciting projects:

1) BeeOMICs ÂV Genome-Wide Association Studies ÂV several positions

Funded by Genome Canada, the BeeOMICs team will apply genome-wide-association mapping and population genomic tools to study the genetics of 12 colony-level traits in honey bees. This will involve sequencing and analysis of 1,000 colony ÂÂgenomesÂÂ. We seek applicants who bring interest and experience in SOME of the following fields: genomics, population genetics, and computing. There will be lots of opportunities to interact with members of the BeeOMICs team. Read more about the BeeOMICs project here: http://www.genomebc.ca/news-events/news-releases/2015/canadian-queens-sustaining-and-securing-canadas-honey-bees-using-omic-tools/ 2) BeeOMICs ÂV Modeling genetic load in social insects ÂV 1 PhD position

We are looking for a PhD student that will work closely with Dr. Amro Zayed and Dr. Jianhong Wu (at York UniversityÂÂs Center for Disease Modeling) http://www.cdm.yorku.ca/wujh/content/about) to develop theory and models for understanding the genetic load in social insects. This will build upon some of our earlier workÂV see Zayed and Packer, 2005, PNAS 102:10742-10746.

3) BeeOMICs - Population genomics of African honey bees ÂV 1 PhD position

We plan to sequence multiple genomes of all honey bee subspecies found in Africa. The dataset will provide a wealth of knowledge about patterns of natural selection in bee genomes and will help us understand the enigmatic biogeographic history of honey bees. It will also allow us to refine a diagnostic tool for detecting Africanized honey bees. Representative pubs include:

Harpur, B.A., Chapman, N.C., Krimus, L., Maciukiewicz, P., Sandhu, V., Sood, K., Lim, J., Rinderer, T.E., Allsopp, M.H., Oldroyd, B.P. and Zayed, A. (2015). Assessing patterns of admixture and ancestry in Canadian honey bees. /Insectes Sociaux/. 62:479-489.

Chapman, N.C., Harpur, B.A., Lim, J., Rinderer, T.E., Allsopp, M.H., Zayed, A., Oldroyd, B.P. (2015) A SNP test to identify Africanized honey bees via proportion of ÂÂAfricanÂÂ ancestry. /Molecular Ecology Resources. DOI: 10.1111/1755-0998./

4) Comparative population genomics of social insects ÂV multiple positions

Funded by an NSERC discovery grant, we plan on carrying comparative population genomic studies across 24 different species that represent different stages of social evolution. Lots of interesting questions to ask, including: What is the relationship between social evolution and genome evolution? Are there common patterns of adaptive evolution associated with the origin of castes and sociality ÂV HamiltonÂÂs proverbial ÂÂ/genes for altruism/ÂÂ ? What kind of mutations underlie adaptive evolution in social insects ? (e.g. coding vs. regulatory, taxonomically-restricted genes vs. conserved genes), and so onÂK

Representative publications include:

Kapheim, K. M./et al. /including Kent, C.F. and Zayed, (2015) A. Genomic signatures of evolutionary transitions from solitary to group living. /Science/, 348:1139-1143.

Kent, C.F. and Zayed, A. (2015). Population Genomic and Phylogenomic Insights into the Evolution of Physiology and Behaviour in Social Insects. /Advances in Insect Physiology/*.* 48:293-342.

Molodtsova, D., Harpur, B.A., Kent, C.F., Seevananthan, K., and Zayed, A. (2014). Pleiotropy constrains the evolution of protein but not regulatory sequences in a transcription regulatory network influencing complex social behaviours. /Frontiers in Genetics/, 5:431.

Harpur, B.A., Kent, C.F., Molodtsova, D., Lebon, J.M.D., Alqarni, A.S., Owayss, A.A., Zayed, A. 2014. Population genomics of the honey bee reveals strong signatures of positive selection on worker traits. /PNAS/. 111:2614-2619

Kent, C.F., Minaei, S., Harpur, B.A., and Zayed, A. 2012. Recombination is associated with the evolution of genome structure and worker behavior in honey bees./ PNAS/. 109:18012-18017.

Successful candidates will receive training in genomics, bioinformatics and sociobiology in a very collaborative environment. Toronto is a great city to live and work in. Funding is available for Canadian students; international students are welcome to apply provided they have access to

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Jobs

CaliforniaStateU MontereyBay AquaticEvolution

Our department at California State University, Monterey Bay is currently looking for a freshwater aquatic biologist. Take a look at the job description and if you are qualified and interested, please apply at https://csumb.peopleadmin.com/postings/961 .Regards, Nate Jue

Position Title: Assistant Professor of Aquatic Ecology and Water Quality Degree/Program BS: Environmental Science & Technology, Environmental Studies, Biology, Marine Science / MS: Applied Marine & Watershed, Marine Science Priority Screening Date: 01/18/2016 Recruitment Status: Open Until Filled Position Description: The Division of Science & Environmental Policy (SEP) at California State University, Monterey Bay (CSUMB) seeks applicants with a demonstrated commitment to teaching and research in freshwater aquatic ecology and water quality within natural, agricultural, and urban landscapes in California's Central Coast region. Projected responsibilities would likely include the following: - Teach upper division course in aquatic ecology (and co-listed graduate course) - Teach upper division course in environmental monitoring - using the study of biological and chemical water quality as a case study in the application of experimental design, contemporary statistics, and quantitative reasoning - Contribute as needed to teaching upper division course in critical thinking and communication in environmental science and/or lower division course in statistics (using R software) - Employ innovative teaching and learning techniques that engage students through the use of technology, hands on experience, and problem solving - Develop and maintain applied research activities with relevance to aquatic ecological and water quality issues within perennial and non-perennial streams, coastal lagoons, vernal pools, lakes, and/or reservoirs in California's Central Coast region - Provide research opportunities for undergraduates, including involving students in field-based sampling of aquatic organisms and monitoring of aquatic biological and chemical variables - Pursue and obtain extramural funding Minimum Qualifications - Ph.D. in a field relevant to the requirements of this position, by date of appointment (August 17, 2016) - Ability to facilitate student learning effectively for diverse learners in a wide range of courses - Demonstrated excellence in instruction and commitment to undergraduate education - Applied expertise in aquatic ecology and water quality - Applied expertise in application of contemporary statistical approaches using R software - Excellent written and oral communication skills Preferred Qualifications - Demonstrated ability and desire to mentor and teach students from diverse cultural, educational, and economic backgrounds, and a commitment to work effectively in a culturally diverse campus community - Research experience and interests that are relevant to freshwater and lagoon environments within 1-hour of the CSUMB campus - Research and teaching interests and expertise that complement and strengthen those of existing faculty in the department - Experience and interest in mentoring undergraduate & graduate student research and/or internships - Successful record in obtaining external funding - Success in obtaining relevant permits e.g. for sampling aquatic organisms - Experience working with Institutional Animal Care and Use Committees (IACUCs)

Nathaniel K. Jue, Ph.D. Assistant Professor Division of Science and Environmental Policy California State University, Monterey Bay Seaside, CA 93955

Nathaniel Jue <njue@csumb.edu>

HarvardU ResAssist MolEvol

Research Assistant in Experimental and Molecular Evolution

Faculty of Arts and Sciences

Organismic and Evolutionary Biology

A laboratory technician (research assistant) position is available with Dr. Betül Kacar, Group Leader within the Edwards Laboratory at the Department of Organismic and Evolutionary Biology, Harvard University.

The researcher will contribute to the development of a new experimental approach that involves reconstructing ancient molecular components and observing their biological function in modern bacterial cells through experimental evolution. This will generate experimental systems consisting of viable modern-ancient hybrid bacterial organisms amenable to biological, biochemical and genetic characterization. The position will be based at the main campus of Harvard University, with access to resources available through the Organismic and Evolutionary Department and the FAS Center for Systems Biology. The position includes competitive salary and full benefits, and is for 1 year in duration with potential extension to 2 or more years.

Requirements:

This opening is for a highly motivated researcher with expertise in any of the following areas: experimental evolution, molecular and cell biology, evolutionary biology, and genetics/genomics. The position includes competitive salary and full benefits, and is for 1 year with potential extension to 2 or more years. The minimal requirement for this position is a bachelors or masters in molecular and cell biology, bacterial genetics, evolutionary biology or a closely related field.

This position is available immediately and will remain open until the position is filled. Interested candidates should contact Betül by email: kacar@fas.harvard.edu with a description of their research interests, skill set and a CV describing relevant experience.

More information:

http://www.oeb.harvard.edu/about/ http://bauercore.fas.harvard.edu/ http://kacarlab.org/join/ Harvard University is an equal opportunity employer and all qualified applicants will receive consideration for employment without regard to race, color, religion, sex, sexual orientation, gender identity, national origin, disability status, protected veteran status, or any other characteristic protected by law.

Betül Kacar <betulkcr@gmail.com>

InBIO Portugal EnvironmentalMetagenomics

ERA Chair in Environmental Metagenomics: InBIO - Research Network in Biodiversity and Evolutionary Biology, Portugal

Applications are open between November 28 to December 31, 2015

Applications are open for a Chair in Environmental Metagenomics to be hosted by CIBIO-InBIO - Research Network in Biodiversity and Evolutionary Biology, University of Porto (Portugal). The Chair position will be contracted in the scope of the project EnvMetaGen - Capacity Building at InBIO for Research and Innovation Using Environmental Metagenomics (Reference NÃÂº 668981), funded by the European Commission under the call H2020-WIDESPREAD-2014-2, and with an overall budget of 2.48M (September 2015 - August 2020). The project aims to expand the research and innovation potential of InBIO, supporting emerging research lines in environmental metagenomics for applications in biodiversity surveys, invasive species control, ecosystem services assessment, and environmental (bio)monitoring. The ERA Chair holder will have a leading role in the development of the project, and he/she will be given responsibilities to select the research and support staff of the ERA Chair team, setting the strategic course and coordinating the scientific, networking and capacity building actions of the project.

CIBIO-InBIO is a young and highly dynamic research centre located near Porto, in Northern Portugal, which conducts world-class research in the fields of biodiversity and evolution. It is an inclusive, equal opportunity employer offering attractive conditions and benefits. The Centre offers great opportunities for multidisciplinary research and hosts 20 research groups, which include over 160 PhD level researchers, and over 100 MSc and PhD students, from across the world. The Centre has state of the art ecology and molecular laboratories and conducts research projects at a global scale. The working language of the institute is English, and it offers a vibrant, multicultural and enthusiastic working atmosphere. In addition, the Northern region of Portugal provides rich cultural and outdoor activities and Porto is a UNESCO world-heritage city and the capital of Port wine.

Requirements

- Internationally Leading or Established Researcher in environmental metagenomics or closely related fields of research - preference will be given to senior researchers (with $>$ 10 years of post-doctoral research experience); less experienced candidates may also be considered in light of their contributions to the research field;

- Proven experience in: managing research teams; supervising graduate students; and in operating with key international funding agencies allowing securing research funding.

- With an established international and cross-disciplinary collaborative network;

- Preference will be given to applicants with experience in the use of metagenomic approaches to address research questions in one or more of the following areas: (i) Biodiversity surveys and assessment; (ii) Environmental biomonitoring; and (iii) Assembling and analysing food webs.

Benefits

- Exceptional research and technical conditions will be offered to the appointed Chair, including:

- Initial appointment for 4.5 years;

- Internationally competitive salary commensurate with qualifications and experience;

- Funding to establish a team of researchers and technical support staff;

- Substantial travel budget for training, conference attendance and networking;

- Access to fully equipped genetics and genomic labs, at the CIBIO-InBIO facilities.

Application

Applicants should submit:

- Detailed Curriculum Vitae;

- The three most important research papers;

- A brief (2-pages) statement of research interests.

Applications should be submitted by mail to cibio.up@cibio.up.pt, in the period between November 28 to December 31, 2015.

The EnvMetaGen project is available upon request to the same mail address.

Evaluation

Candidates will be evaluated by an international selection panel. Short-listed candidates will be invited for an interview.

Employer

ICETA - Instituto de CiÃÂncias, Tecnologias e Agroambiente da Universidade do Porto (ICETA-UP), on behalf of CIBIO-InBIO.

Websites InBIO

CIBIO

Location CIBIO-InBIO, Campus AgrÃÂrio de VairÃÂ£o, Rua Padre Armando Quintas, 4485-661 VairÃÂ£o, Portugal (Coordinates: N41.328940, W8.672635).

CIBIO-InBIO DivulgaçÃ£o

INRA France ComputationalBiol

The INRA laboratory UMR 1290 Bioger (Thiverval-Grignon, France) has a one and a half year open position for a research engineer in genomics and bioinformatics in the EGIP team (Evolution and Genomics of Plant Pathogen Interactions).

Position: We are seeking a motivated applicant interested in providing computational and bioinformatics expertise to different fungal genomics projects developed in the team (Illumina sequencing data handling, de novo genome assembly, polymorphism detection, genome annotation and transcriptomics).

The role of the applicant is to join a multidisciplinary team gathering evolutionary biologists, geneticists, and plant pathologists. Genome annotation will be performed in close collaboration with the JGI-DOE (San Francisco, USA).

Required qualifications: Master in biology or computer science; strong bioinformatics skills ; good practice of scientific English.

Please send a CV and letter(s) of recommendation to : Dr Marc-Henri Lebrun marc-henri.lebrun@versailles.inra.fr and Dr Anne Genissel anne.genissel@versailles.inra.fr. The position is open and review of applications will continue until the position is filled.

BIOGER is located on the ground of the AgroParisTech School for Engineers in Agriculture at Thiverval-Grignon. The Campus is located in the country side South-West of Paris, close to a railway station (Plaisir-Grignon) easily connected to Paris, Gare Montparnasse. (http://www6.versailles-grignon.inra.fr/bioger).

Anne Genissel <anne.genissel@versailles.inra.fr>

InstitutPasteur Bioinformatics

INSTITUT PASTEUR IS HIRING PERMANENT, YOUNG RESEARCHERS

Deadline: Wednesday 6, January 2016 (5:00 pm) http://www.pasteur.fr/en/recruitment-scientists-permanent-contracts Bioinformatics, Biostatistics and Integrative Biology have emerged as strategic priorities for the Institut Pasteur, and a new center (C3BI) to foster research in these domains was set up in 2014. Substantial resources were allocated for the creation and development of the C3BI, with the recruitment of 40 research engineers in bioinformatics and biostatistics between 2014 and 2017. New research groups will start in 2016, and a building will be renovated on the Paris campus to house the C3BI.

In this context, the Institut Pasteur is recruiting permanent, young researchers (typically, PhD+Postdoc, for a position similar to CNRS “Chargé de Recherche”), and a new section of the evaluation committee (COMESP) will be created to examine the candidates in bioinformatics, biostatistics, integrative biology, and modeling.

Applicants must choose a host laboratory among the different entities of the Institut Pasteur and contact the head of this entity before preparing their applications. They should send a copy of their application to the head of the host entity and to the concerned Department Director.

To see the list of labs and departments: https://research.pasteur.fr/en/teams-heads/ All info on the application file, procedure and dates is available from: http://www.pasteur.fr/en/recruitment-scientists-permanent-contracts Deadline: Wednesday 6, January 2016 (5:00 pm)

Contacts: Patrick Trieu-Cuot (Head of COMESP - dcs@pasteur.fr) Olivier Gascuel (Head of C3BI - assistant: johanna.escobar@pasteur.fr)

Olivier Gascuel <olivier.gascuel@pasteur.fr>

OldDominionU PlantEvolutionChair

The Department of Biological Sciences at Old Dominion University invites applications for the J. Robert Stiffler Distinguished Professorship in Botany at the Professor or Associate Professor level.

Minimum requirements include a Ph.D. in Plant Science or a related area, experience in molecular techniques in plant research, substantial research accomplishments with an established record of publications and independent peer-reviewed funding, active competitive grants, and a successful graduate and undergraduate teaching and student mentoring record. We are especially interested in applicants whose research expands the department's expertise in the area of molecular plant systematics and advanced genomics. State salary support and a competitive start-up package are available; additional annual research support funds are provided by the J. Robert Stiffler Professorship endowment.

The department has strong graduate programs, including a Ph.D. in Ecological Sciences, and has four (two endowed) faculty positions in the Plant Sciences (http://ww2.sci.odu.edu/biology/). The incumbent will play a critical role in the future development of botanical sciences in the department. Additional resources available include the Norfolk Botanical Garden, Kaplan Orchid Conservatory, Blackwater Ecological Preserve, and the University's herbarium. Old Dominion University (http://www.odu.edu/) is a state-supported, Carnegie doctoral research extensive institution enrolling approximately 25,000 students.

Applicants should submit a curriculum vitae, a statement of research and teaching interests, and names, telephone numbers, and addresses (postal and email) of four references electronically to https://jobs.odu.edu by clicking on Teaching and Administrative Faculty Opportunities. For full consideration, please apply by January 30, 2016. Questions about the position can be directed to Lytton John Musselman, Mary Payne Hogan Professor of Botany (lmusselm@odu.edu).

Old Dominion University is an equal opportunity, affirmative action institution. Minorities, women, veterans, and individuals with disabilities are encouraged to apply.

https://www.higheredjobs.com/details.cfm?JobCode=176181421&utm_source=12_08_15&utm_medium=email&utm_campaign=JobAgentEmail –

Daniel Barshis, Ph.D. Assistant Professor Department of Biological Sciences Old Dominion University Mills Godwin Building 302J Norfolk, VA 23529 Office: 757-683-3614 Lab: 757-683-5755 Web: www.odu.edu/~dbarshis
Dan Barshis <barshis@gmail.com>

Smithsonian ComputationalGenomics 2

The Center for Conservation and Evolutionary Genetics (CCEG), Smithsonian Conservation Biology Institute (SCBI), National Zoological Park located in Washington, DC, invites applications for a permanent Computational Genomics Scientist position.

The purpose of the position is to conduct independent and collaborative research in bioinformatics as applied to biodiversity genomics and conservation biology, provide bioinformatics and computational expertise and training to scientists, and act as a bioinformatics liaison to the Smithsonian Biodiversity Genomics Institute.

Duties of the position include: * Conducts research projects in the area of bioinformatics as applied to biodiversity and conservation biology, including analyses of genomic, transcriptomic, metagenomic, and next generation DNA sequence datasets. * Develops or implements data analysis pipelines for Next Generation Sequence (NGS) or other genomics datasets. * Publishes scientific papers, chapters and books; prepares independent and collaborative research grant proposals and mentors bioinformatics students and postdocs. * Provides informal and formal bioinformatics and genomics training for other scientists in the Center and institution via workshops, seminars or short courses. * Acts as a liaison for bioinformatics activities of the Smithsonian Biodiversity Genomics Institute. * Keeps abreast of new developments and related research conducted elsewhere in order to improve genomics and related research at SI.

CCEG works to understand and conserve biodiversity through genetic and genomic research. We creatively apply genetic theory and methods to build knowledge about the evolutionary and life histories of animals, to understand the importance of genetic variation to species' survival, and to identify the methods needed to sustain them in captivity and the wild.

To obtain details of the position and to apply, proceed to the USAJOBS website (https://www.usajobs.gov/-GetJob/ViewDetails/421893900). Deadline for applications via USAJOBS website is 18 December 2015. For questions about the position please contact Rob Fleischer (fleischerr@si.edu). Information about CCEG and SCBI can also be found at https://nationalzoo.si.edu/-scbi/cceg/. This position is open to all U.S. Citizens or U.S. Nationals. The Smithsonian Institution is an Equal Opportunity Employer and Provider.

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

StonyBrookU NY Bioinformatician

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The Veeramah Lab in the Department of Ecology and Evolution at Stony Brook (http://life.bio.sunysb.edu/-ee/veeramahlab/index.html) is looking to recruit a bioinformatician on a part time basis for the duration of the 2016 calendar year. The primary focus of the lab is examining genetic diversity in human and non-human primates. The lab currently has ongoing projects examining primate evolution through genomic scale data, as well as a variety of paleogenomic projects involving European human and non-human populations. Details of the position are given below.

This position has been denoted as requisition number 1503578. A link to the online application on the Stony Brook Careers website can be found at: https://stonybrooku.taleo.net/careersection/2/-jobdetail.ftl?job=1503578 Required Qualifications: (Evidenced by an attached resume) Bachelor's Degree in Biology or related disciplines. Bioinformatics or computer programming experience (in python, equivalent or lower level languages). Preferred Qualifications: Master's Degree in Biotechnology/bioinformatics or related field. 2nd generation sequencing experience. Ancient DNA analysis experience. Linux or Unix experience.

Brief Description of Duties: Bioinformatician will assist faculty member with the analysis of 2nd generation sequencing data using model-based qualitative frameworks for two primary projects.

Building and maintaining genomic pipelines (maintain existing human pipelines and creation/adjustment to handle new primate data) Creation and ongoing maintenance of the computer cluster and software installation. Data analysis, preparation of experimental results for publication or for presentations. Coordination of research programs with collaborating labs. assist faculty with grant proposal writing to secure new grant funding. Assisting lab members and grad students with computation scripts. Other duties or projects as assigned as appropriate to rank and departmental mission.

This is a part time, temporary appointment, FLSA Nonexempt position, eligible for the overtime provisions of the FLSA. Stony Brook University will be 100% tobacco-free starting January 1, 2016. See our policy and learn more at stonybrook.edu/tobaccofree.

About Stony Brook: Stony Brook University, home to many highly ranked graduate research programs, is located 60 miles from New York City on Long Island's scenic North Shore. Our 1,100-acre campus is home to 24,000 undergraduate, graduate, and doctoral students and more than 13,500 faculty and staff. SBU is a comprehensive research-intensive university and a member of the prestigious Association of American Universities (AAU), which includes 34 public universities among its 62 members. SBU consists of 12 schools and colleges and a teaching hospital that provides state-of-the-art healthcare in the Long Island region. SBU also manages and performs joint research with Brookhaven National Laboratory, the only Department of Energy Laboratory in the Northeast, and shares doctoral programs with Cold Spring Harbor Laboratory, a world-renowned molecular biology institute. Home to the Emerson String Quartet, the Jackson Pollack House in East Hampton, New York, the Mellon Award winning Humanities Institute, and the Southampton Arts Program, and with endeavors that extend to the Turkana Basin Institute in Kenya and the Ranomafana National Park in Madagascar, SBU sustains an international reputation that cuts across the arts, humanities, social sciences, and natural sciences.

Stony Brook University is an Affirmative Action/Equal Opportunity employer. We encourage protected veterans, individuals with disabilities, women and minorities to apply. If you need a disability related accommodation, please call the University Human Resource Services Department at (631) 632- 6161 or the University Hospital Human Resources Department at (631) 444-4700. In accordance with the Title II Crime Awareness and Security Act, a copy of our crime statistics is available upon request by calling (631) 632- 6350. It can also be viewed on line at the University Police website at http://www.stonybrook.edu/police . Official Job Title: Instructional Support Associate Job Field: Administrative & Professional (non-Clinical) Primary Location: US-NY-Stony Brook Department/Hiring Area: Ecology & Evolution-Stony Brook University Schedule: Part-time Day Shift 1:00pm - 4:00pm Pass Days: Sat, Sun Posting Start Date: Dec 14, 2015 Posting End Date: Jan 13, 2016 Salary: $27,500 - $29,000 at 0.5 FTE Salary Grade: SL2 Appointment Type:Temporary

"krishna.veeramah@stonybrook.edu"
<krishna.veeramah@stonybrook.edu>

UArizona EvolutionaryBiology

EEB at Univ of Arizona is seeking an Evolutionary Biologist at the Asst or Assoc level. This is a broad search - apply if you study evolution!

POSTING: Integrative Evolutionary Biologist Department of Ecology & Evolutionary Biology University of Arizona

We seek applicants with an excellent track record and promising trajectory of research integrating evolutionary biology with other disciplines utilizing transformative, innovative, empirically driven approaches. The ideal candidate will have deep expertise in evolutionary genetics/genomics and related areas and will be expected to continue or build a successful record of extramural funding and to teach at both the undergraduate and graduate levels. We are looking for an early to mid-career scientist, to be appointed as an Assistant or Associate Professor, who is using the power of cutting-edge evolutionary biology and new data streams to break new ground and address real-world biological or biomedical issues. Potential research areas could include, but are not limited to: evolutionary genetics and genomics, population genetics; phylodynamics, epidemiology and disease evolution/ecology; human health/genetics. A focus on any organism or system is welcome.

To apply, please submit and online application for job posting F#20320 at www.uacareers.com. Applications should include: (1) a cover letter describing how the applicants research relates to the focus of this search, (2) a current CV, (3) a Statement of Research Interests, (4) a Statement of Teaching Philosophy, (5) three reprints or preprints of the candidates publications (as publication samples), and (6) 3 letters of recommendation. All the materials except letters of recommendation can be uploaded through this web site; candidates can provide contact details for those providing letters of recommendation through this web site and the UA will contact those individuals directly. Review of applications will begin January 15, 2016 and will continue until the position is filled.

At the University of Arizona, we value our inclusive climate because we know that diversity in experiences and perspectives is vital to advancing innovation, fostering critical thinking, solving complex problems, and creating an inclusive academic community. We translate these values into action by seeking individuals who have experience and expertise working with diverse students, colleagues and constituencies. Because we seek a workforce with diverse perspectives and experiences, we encourage minorities, women, veterans, and individuals with disabilities to apply. As an Employer of National Service, we also welcome alumni of AmeriCorps, Peace Corps, and other national service programs. The University of Arizona is an EEO/AA Employer V M/W/D/V.

The University of Arizona offers outstanding benefits including health, dental, and vision insurance plans; life insurance and disability programs; paid vacation, sick leave, and holidays; UA/ASU/NAU tuition reduction for the employee and qualified family members; state and optional retirement plans; access to UA recreation and cultural activities; and more!

Jeremiah Hackett (hackettj@email.arizona.edu), Chair of the search committee Mike Worobey (worobey@email.arizona.edu), Head of EEB

Katrina Dlugosch <katrina.dlugosch@gmail.com>

UCalifornia LosAngeles PlantEvolution

Assistant Professor in Plant Diversity and Evolution

The University of California, Los Angeles (UCLA) Department of Ecology and Evolutionary Biology (EEB) seeks an organismal biologist with a focus on plant diversity and/or evolution. UCLA has a rich history of work in plant ecology and evolution, and we seek an individual who will help us maintain and grow this critical component of our program. Qualified candidates must have a Ph.D. in a related field of biological sciences, and the search is restricted to the Assistant Professor level. The position is defined broadly within evolution and ecology, but preference will be given to candidates whose research/teaching interests would utilize, at least in part, the UCLA Mildred E. Mathias Botanical Garden and associated UCLA Herbarium. The successful candidate will be expected to establish an internationally recognized and externally funded research program and contribute to EEBÂs teaching needs at the introductory undergraduate level. There are many opportunities for collaboration across a broad group of partners on and off campus, including the UC NRS Stunt Ranch Reserve and White Mountains Research Center, the UCLA La Kretz Center for California Conservation Science, the UCLA Center for Tropical Research, and our Institute of Environment and Sustainability. Information about the Department and the Botanical Garden and may be found at http://www.eeb.ucla.edu and http://www.botgard.ucla.edu/.

Applicants should submit materials online to https://-recruit.apo.ucla.edu/apply/JPF01858 and include 1) a cover letter, 2) curriculum vitae, 3) personal statement that describes current and future research and teaching, a vision of how the candidateÂs research, teaching and/or outreach might include and enhance the Botanical Garden, 4) a summary of ongoing and anticipated activities to promote gender and racial diversity, and 5) names and contact information of three references. Review of candidates will begin on 18 January 2016 and continue until the position is filled. Please use job number JPF01858 in all correspondence.

Individuals with a history of mentoring students under-represented in the sciences are encouraged to apply and to describe their experience in a cover letter.

Inquiries regarding the position should be directed to Grace Angus (gracea@lifesci.ucla.edu) or the Search Chair, Professor Brad Shaffer (brad.shaffer@ucla.edu).

As a campus with a continually growing diverse student body, we encourage applications from women, minorities, and individuals with a commitment to mentoring under-represented demographics in the sciences. 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, sexual orientation, gender identity, national origin, disability, age or protected veteran status. For the complete University of California nondiscrimination and affirmative action policy see: UC Nondiscrimination and Affirmative Action Policy (http://policy.ucop.edu/doc/4000376/-NondiscrimAffirmAct).

Thanks, Mario

Mario Colon I Administrative Assistant I UCLA La Kretz Center for California Conservation Science 818-519-7740 I mario.colon@ucla.edu I http://www.environment.ucla.edu/lakretz/ Mario Colon <mario.colon@ucla.edu>

UCalifornia Merced LabFieldTech PopGenetics

Applications are invited for a lab & field tech position in marine molecular ecology (comparative population genetics / genomics).

The position entails (1) surveys and collection of marine intertidal invertebrates in California, (2) all stages of wetlab analyses for comparative phylogeographic analyses, and (2) preliminary summary analyses of generated data. The technician also is responsible for maintaining a clean, orderly, functioning laboratory.

Full details of the position and application form are available at https://jobs.ucmerced.edu/n/staff/-position.jsf?positionId=3D3D6458 More information about the lab is available @ mnd.ucmerced.edu/

Michael N Dawson Associate Professor University of California, Merced

dawson.mn@gmail.com

UCalifornia Riverside PollinationClusterHire

Tenure-Track Position Announcements: Pollination Cluster Hire ** Bee Health ** Pollinator and Plant Interaction Networks ** Evolutionary Ecology of Pollination Mutualisms from the Plant Perspective **

The University of California, Riverside seeks outstanding candidates for three faculty positions in various aspects of pollinator and pollination biology to be filled at the Assistant, Associate or Full Professor rank. This cluster hire currently seeks collaborative biologists examining issues related to (1) bee health (Open rank), (2) pollinator and plant interaction networks (Assistant rank) and (3) evolutionary ecology of pollination mutualisms from the plant perspective (Assistant rank). The majority of crop systems and over a third of global food production relies on animal pollination, and the value added by managed pollination to US agricultural production exceeds $20B per year. California is home to many of these crops with intensive pollination needs, and accounts for the majority of paid pollination contracts in the US. Research funding for pollinator health is available from a number of national research agencies, and well as a variety of commodity boards. Recognition of the importance of funding research in pollinator health and pollination services has been growing among these agencies in reaction to colony collapse disorder and declining wild bee populations. Maintaining agricultural productivity and natural plant communities will require enhanced knowledge of the pollination interactions in these systems, and solutions to health and management problems facing pollinators. These individuals will build on existing strengths in fundamental and applied research in pollination biology and social insects. Research to maintain agricultural productivity and natural plant communities will require enhanced knowledge of the pollination interactions in these systems, and solutions to health and management problems facing pollinators.

The University of California at Riverside (UCR) is embarking on a major new hiring initiative that will add 300 tenure-track positions in 33 cross-disciplinary areas selected through a peer-reviewed competition (clusterhiring@ucr.edu). Over the next three years, we will hire multiple faculty members in each area and invest in research infrastructure to support their work. This initiative will build critical mass in vital and emerging fields of scholarship, foster truly cross-disciplinary work and further diversify the faculty at one of AmericaÂs most diverse research universities. We encourage applications from scholars committed to excellence and seeking to help redefine the research university for the next generation.

The successful candidates will hold an academic appointment in a department selected during the recruitment, with the option of a secondary cooperating faculty appointment if appropriate. Depending upon the department of appointment, the position may include an appointment in the Agricultural Experiment Station, which includes the responsibility to conduct research and outreach relevant to the mission of the California Agricultural Experiment Station (http://cnas.ucr.edu/about/aes/).

Questions regarding this position should be directed to Dr. Timothy Paine, Chair of the Pollination Cluster Hire Search Committee at timothy.paine@ucr.edu. Review of applications will begin on January 31, 2016 and continue until the position is filled with an anticipated start date of July 1, 2016. Assistant level applicants should apply through https://aprecruit.ucr.edu/apply/JPF00515. The Bee Health Senior applicants should apply through https://aprecruit.ucr.edu/apply/JPF00514. Applications should include a curriculum vitae (6 pages maximum), statements of research interests (3 pages maximum), and teaching interests and philosophy (2 pages maximum). In addition, a statement of contributions to diversity will be required. Candidates applying for the Assistant Professor position will need to provide 3-4 letters of reference. Individuals applying for positions above the Assistant level will be required to provide 3-4 names and contact details for confidential references.

The University of California is an Equal Opportunity / Affirmative Action Employer with a strong institutional commitment to the achievement of excellence and diversity among its faculty and staff. All qualified applicants will receive consideration for employment without regard to race, color, religion, sex, sexual orientation, gender identity, national origin, age, disability, protected veteran status, or any other characteristic protected by law.

UCR is a world-class research university with an exceptionally diverse

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UCambridge Tech EvolutionElephantVocalisations

Research Assistant (Part Time, Fixed Term)

We are looking for a part-time (three days a week) research assistant for up to twelve months to addresses the potential role of vocalisations in individual recognition in African elephants. The candidate will review the literature of the role of vocalisations in individual identity and recognition, participate in recording vocalisations of elephants in zoos, analyse variation in the vocalisations and assist in writing a paper on the topic. The candidate will be involved in coordinating similar data collection by field assistants in South Africa and analysing the data. Short trips to South Africa may be involved, although the post is primarily based in Cambridge.

The project is a collaboration between Dr. Hannah Mumby, a Research Fellow in the Department of Zoology and the South Africa-based non-profit organisation Elephants Alive. The successful candidate will be a graduate with a good understanding of behavioural ecology and bioacoustics.

Skills in recording and analyzing vocalistaions are required as well as the ability to work on aspects of the project from planning fieldwork to synthesising and summarising information for grant applications.

Interviews: the week commencing Monday 18 January 2016

Fixed-term: The funds for this post are available for up to 12 months.

To apply online for this vacancy, please click on the 'Apply' button 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 PF07812 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.

– Dr Hannah S. Mumby Society in Science - Branco Weiss Fellow Drapers' Company Junior Research Fellow, Pembroke College Department of Zoology University of Cambridge Downing Street Cambridge CB2 3EJ

Tel: +44 (0)1223 331698 Twitter: @hannahsmumby hannahsmumby.co.uk

"H.S. Mumby" <hsm29@cam.ac.uk>

UCentralFlorida GenomicsBioinformatics

The University of Central Florida (UCF) is hiring 100 new faculty members to join us in the fall of 2016. As part of this hiring campaign, UCF recently established six interdisciplinary clusters to strengthen its academic and research missions. We are building a new Genomics and Bioinformatics Cluster (http://www.ucf.edu/research/genomics) by the fall of 2017 and we seek to hire a cluster lead to start in the fall of 2016 at the level of either Associate or Full Professor. The cluster lead will immediately participate in the recruitment of four additional cluster members. An ideal cluster lead will have a strong background in genome biology and computational approaches used to analyze large genetic data sets. The cluster lead should have demonstrable leadership experience, preferably with multidisciplinary teams. All cluster members will be expected to function collaboratively in methodology, but research topics are encouraged to be interdisciplinary and cover areas including health and disease, biodiversity, evolution, or computer science.

The Genomics and Bioinformatics cluster members will be expected to have research programs that strengthen their tenure homes as well as the cluster. The new leader can join any host department - Biomedical Sciences (College of Medicine), Biology (College of Sciences), or Computer Science (College of Engineering & Computer Science); or be jointly appointed among them as appropriate to qualifications and interest. Candidates should have a Ph.D. or M.D./Ph.D. and be an established leader in their field. Candidates must apply online at http://www.jobswithucf.com/postings/43545 (Position # 38533) and provide the following materials: a cover letter, curriculum vitae, teaching statement, research statement, and contact information for three professional references. In the cover letter, candidates should address their background in genomics and/or bioinformatics, their leadership experience, and should identify the anticipated department(s) for their potential tenure home.

The search committee will begin reviewing applications in November of 2015 and continue to accept applications until April of 2016.

The University of Central Florida is the nation's second-largest university with more than 60,000 students. UCF has grown substantially in size, quality, diversity, and reputation in its first 50 years. Today, the university offers more than 200 degree programs at its main campus in Orlando and more than a dozen other locations. UCF is an economic engine attracting and supporting industries vital to the region's future while providing students with real-world experiences that help them succeed after graduation. For more information, visit http://www.ucf.edu/faculty/. UCF is an Equal Opportunity and Affirmative Action employer. All applicants are encouraged to apply, including minorities, women, veterans, and individuals with disabilities.

For more information about this positions please contact Sean Moore, the Genomics and Bioinformatics Cluster Search Chair, at genomicscluster@ucf.edu.

"Eric.Hoffman@ucf.edu" <Eric.Hoffman@ucf.edu>

UCentralFlorida SeniorLabTech MolBiol

The Department of Biology at the University of Central Florida is recruiting a permanent Senior Lab Technician to maintain and operate a core molecular lab facility. The position will involve basic DNA skills (DNA/RNA extraction, PCR and standard DNA sequencing, fragment purification, gel electrophoresis, restriction enzyme digestion), as well as next-generation sequencing (Illumina) methods, included but not limited to: whole genome library preparation, microbial metagenomics, reduced representation libraries using probe hybridization, and RNAseq/whole transcriptome library preparation. The technician will maintain, troubleshoot and perform day-to-day lab upkeep and coordinate sample shipment for sequencing at off-site core Illumina facilities. S/he will also help design and execute next-generation sequencing data generation workflows; oversee sequencing projects conducted in the lab as part of undergraduate courses and faculty research; analyze current process procedures and provide feedback for their optimization and improvement; document processes and improvements to methods; perform Quality Control on samples and raw sequence data; consult on research projects with other laboratories; develop, assess and adapt new technologies, protocols and software; supervise and train graduate and undergraduate students; and conduct other laboratory work as needed.

Complete details on salary, benefits, eligibility and how to apply can be found at:

http://www.jobswithucf.com:80/postings/44207 Applications will be reviewed starting in January 2016 and accepted through February 2016.

For additional information, please contact Anna Savage at Anna.Savage@ucf.edu

"Anna.Savage@ucf.edu" <Anna.Savage@ucf.edu>

UCollegeLondon ResAssist TetrapodEvolution

University College London: Research Assistant in Tetrapod Modularity and Morphological Evolution

We are now accepting applications for a one-year research assistant post to work on a European Research Council-funded project reconstruct morphological evolution and modularity across tetrapods. The successful applicant will be employed to work as part of a team conducting a large-scale quantitative analysis of evolutionary rates, morphological disparity, and phenotypic integration across tetrapods through deep time. The research assistant will focus on synapsids (including their living representatives, mammals), assisting primarily with the collection and processing of 3-D surface scans from international museum collections. They will be responsible for working closely with Dr. Goswami towards the goal of building a comprehensive dataset of 3-D images spanning the living and extinct diversity of synapsids and extracting surface morphometric data from images. There may be scope for involvement in conducting analyses to reconstruct the patterns and processes underlying ecomorphological evolution and identify the major intrinsic and extrinsic factors shaping clade diversity. Further duties may involve logistical assistance and uploading new data to online resources for free dissemination.

The successful candidate must be capable of independent, international travel to collections in the US and Europe with fragile scanning equipment and responsible, careful handling of irreplaceable fossil specimens. Previous experience with image analysis and museum specimens will benefit this position. This post is now open for applications, with a deadline of January 17,

2016. Further details and a link to the online application form can be found at goswamilab.com. Informal enquiries can be directed to Dr. Anjali Goswami (a.goswami@ucl.ac.uk), or speak to Dr. Goswami in person at SICB in Portland.

Dr. Anjali Goswami Reader in Palaeobiology Department of Genetics, Evolution, and Environment and Department of Earth Sciences University College London Darwin Building 218A Gower Street London WC1E 6BT +44 (0)20 7679 2190 www.goswamilab.com "Goswami, Anjali" <a.goswami@ucl.ac.uk>

UFlorida LandscapeGenetics

Title: Assistant Professor of Landscape Ecology Location: Fort Lauderdale Research and Education Center University of Florida Institute of Food and Agricultural Sciences (IFAS) Davie, Florida Salary: Commensurate with Qualifications and Experience

Review Date: For full consideration, candidates should apply and submit additional materials by February 15, 2016. Position will remain open until a viable applicant pool is determined.

Duties and Responsibilities:

This is a 12-month tenure-accruing position that will be 60% research (Florida Agricultural Experiment Station) and 40% extension (Florida Cooperative Extension Service), available at the Fort Lauderdale Research and Education Center, Institute of Food and Agricultural Sciences, at the University of Florida. This faculty member is expected to develop a productive, interdisciplinary, extramurally funded research program with emphasis on landscape structure and function over a range of spatial and temporal scales in South Florida. This may include application of climate change, including sea-level rise, to ecological landscape analysis; biogeochemical processes and modeling including carbon sequestration and greenhouse gas emissions; evaluation of species and community responses to changes in landscape structure and function or invasive species; and integration of multidisciplinary science into restoration of damaged landscapes or response to sea-level rise. Extension responsibilities will include developing education programs on the interaction of Everglades restoration with natural and man-made ecosystems and on impacts of sea-level rise. The incumbent will provide leadership, training, and assistance to county faculty. The position will be located at the Fort Lauderdale Research and Education Center, Institute of Food and Agriculture Sciences (IFAS), University of Florida (Davie, Florida). Tenure will accrue in the most suitable department (Soil & Water Science or School of Forestry & Resource Conservation), based on the successful applicant's credentials.

Please refer to Requisition # 495173 Dr. Henry Hochmair Chair, Landscape Ecologist Search and Screen Committee University of Florida Fort Lauderdale Research and Education Center 3205 College Avenue Davie, FL 33314

Telephone: 954.577.6317 Facsimile: 954.475.4125 E-Mail: hhhochmair@ufl.edu

Application Information:

Individuals wishing to apply should go online to http://explore.jobs.ufl.edu/cw/en-us/job/495173 and submit: * Application * Cover letter that states applicant's interest in the position and qualifications relative to the credentials listed above * Curriculum vitae * Names and contact information (email address and phone number) of three individuals who may be contacted to provide letters of recommendation

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Mathieu Basille basille@ufl.edu | http://ase-research.org/basille +1 954-577-6314 | University of Florida FLREC

≪ Le tout est de tout dire, et je manque de mots Et je manque de temps, et je manque d'audace. ≫ Paul Ãluard

This message is signed to guarantee its authenticity. For a true private correspondence, use my public key to encrypt your messages: http://mathieu.basille.net/pub.asc Learn more: http://mzl.la/1BsOGiZ Mathieu Basille <basille@ufl.edu>

UFlorida SharkResearchDirector

The Florida Museum of Natural History, University of Florida, invites applications for the position of Director of the Florida Program for Shark Research. The position is tenure-track and open rank (Assistant/Associate /Full Curator) with the potential for tenure-upon-hire based on qualifications. The Florida Program for Shark Research is engaged in a broad spectrum of elasmobranch research addressing issues in fishery management and conservation including life history, ecology, behavior, genetics, systematics, and population dynamics. Education/outreach activities have included graduate, undergraduate and intern mentoring, classroom teaching, capacity-building workshops for international biologists, hosting of workshops for environmental educators, web-based outreach through a highly visited web page, and frequent interaction with journalists.

The Director will oversee the activities of this program. Qualified candidates must have a Ph.D. in Biology or related field, a proven record in elasmobranch biological or conservation research, fundraising, grantsmanship, outreach (including media interviews and effective use of social media), as well as teaching and mentoring.

The appointee will be expected to grow the successful program in elasmobranch conservation, which includes maintaining and acting as the spokesperson for the existing International Shark Attack File and the International Sawfish Encounter Database, both housed at the Florida Museum of Natural History. The Director will be expected to conduct dynamic, externally funded research, oversee education/mentoring/outreach activities, and supervise staff. The Dorian-Springer endowment is dedicated to the support of the appointee's research program and the two databases mentioned above. Expected start date is July 01, 2016. Salary is competitive and commensurate with experience.

The search committee will begin reviewing applications on December 14, 2015 and will continue to receive applications until this position (Job No. 495354) is filled. Applicants must apply on-line by December 31, 2015 at http://explore.jobs.ufl.edu/cw/en-us/job/495354/. Applications received after this date may be considered at the discretion of the Committee and/or hiring authority. The application should include: (1) cover letter; (2) curriculum vitae; (3) statement of research, teaching, and outreach experience; (4) digital copies of no more than three publications; (5) the names of three colleagues who might be contacted for letters of recommendation.

The University of Florida is one of the most comprehensive high-quality public universities in the country. UF is a land grant, sea grant, and space grant university and on-campus home to the most comprehensive academic health center in the southeast. The Director will oversee a program located in one of the nation's largest natural history museums, and will benefit from close collaborations with the Whitney Lab, Seahorse Key Marine Laboratory, and a strong collaborative culture across all disciplines at UF. UF counts among its greatest strengths – and a major component of its excellence - that it values broad diversity in its faculty, students, and staff and creates a robust, inclusive and welcoming climate for learning, research and other work. UF is committed to equal educational and employment opportunity and access and seeks individuals of all races, ethnicities, genders and other attributes who, among their many exceptional qualifications, have a record of including a broad diversity of individuals in work and learning activities. The University of Florida is an Equal Opportunity Employer.

For additional information, please contact David L. Reed

David L. Reed, Ph.D. Curator of Mammals and Chair, Department of Natural History Florida Museum of Natural History 1659 Museum Road (Dickinson Hall) University of Florida Gainesville, FL 32611 (352) 273-1971 (voice) (352) 846-0287 (fax) e-mail: dlreed@ufl.edu<mailto:dlreed@ufl.edu> http://www.flmnh.ufl.edu/mammals/

UFribourg Switzerland EvolutionaryBiol

The Faculty of Science of the University of Fribourg/Switzerland and the Department of Biology invite applications for a tenured position of an

Associate Professor in Evolutionary Biology studying adaptive processes using empirical or experimental approaches

Qualified applicants must have an outstanding track record of successful independent research. We are looking for a population biologist with interest in evolutionary genetics/genomics. Possible research topics include experimental evolution, local adaptation, species interactions, speciation and invasion. The successful candidate is expected to develop an internationally recognized competitive research programme sustained by external funding. More information about the application procedure (deadline February 15, 2016) is available at : http://www.unifr.ch/science/fr/faculte/postes/49_EvolBiology Prof Louis-Felix Bersier University of Fribourg Department of Biology - Ecology and Evolution Ch. du Musee 10 CH-1700 Fribourg, Switzerland

louis-felix.bersier@unifr.ch

UGottingen ForestGenetics

Please note an exceptional career opportunity at the University of Göttingen, Germany, for a full Professor of Forest Genetics and Forest Tree Breeding.

The core activities of the professorship are:

- Research into the genetic diversity of tree species in terms of genetics and genomics relating to population ecology and molecular ecology

- Research into the genetic basis of the stability of forest ecosystems, in particular with regard to climate change

- Research into the conservation of forest genetic resources.

Please see the full position announcement at https://www.uni-goettingen.de/de/w3—professor-of-forest-genetics-and-forest-tree-breeding-/528379.html The application deadline is March 1st, 2016.

In case of any questions, please contact Dr. Hiltscher at whiltsc@gwdg.de

Niko Balkenhol, Ph.D. Professor of Wildlife Management Dept. of Wildlife Sciences Georg-August-University Göttingen Büsgenweg 3 37077 Göttingen GERMANY Tel. +0049-551-39-33622 nbalken@gwdg.de

niko.balkenhol@forst.uni-goettingen.de

UMassachusetts Lowell FishEvolution

Title: Post-doctoral Research Associate Institution: University of Massachusetts Lowell Description:

One postdoctoral fellow position is immediately available in the Fish lab (http://faculty.uml.edu/-jennifer_fish) in the Department of Biological Sciences at the University of Massachusetts Lowell (MA, USA). We seek a talented and motivated scientist to join our team focused on understanding molecular mechanisms underlying variation in craniofacial morphogenesis and osteogenesis. The potential candidate should have an M.D. and/or Ph.D. degree and a strong background in molecular and developmental biology. Preference will be given to those with significant experience in molecular cloning, gene expression analyses, cell culture, and/or microscopy and image analysis. Experience working with mice or other animal models is desirable. Applicants should have demonstrated scientific productivity, good inter-personal and communication skills, and be able to conduct independent research.

Contact person: Jennifer Fish (jennifer_fish@uml.edu)

Link to job posting:

https://jobs.uml.edu/applicants/jsp/shared/frameset/-Frameset.jsp?time=3D1 448920004013

Please let me know if you need any other information.

Thanks,

Jennifer

Jennifer L. Fish, Ph.D Assistant Professor Department of Biological Sciences University of Massachusetts Lowell

"Fish, Jennifer L" <Jennifer_Fish@uml.edu>

UNorthCarolina Wilmington EvoDevo

The Department of Biology and Marine Biology at the University of North Carolina Wilmington invites applications for the position of tenure-track Assistant Professor in Evolutionary Developmental Biology starting August, 2016. The successful candidate will contribute to undergraduate and graduate courses in developmental biology and other topics depending on area of expertise, as well as maintain a vigorous, extramurally funded research program involving both undergraduate and graduate students. Candidates with a research program that targets the interface of evolution and development, including those that study evolutionary developmental biology from an environmental perspective, are especially encouraged to apply. The department has an excellent record of faculty development and mentorship, and is committed to assisting new faculty to succeed. The department is especially interested in qualified candidates who can contribute, through their research, teaching, and/or service, to the diversity and excellence of the academic community. Graduate curricula in the department include M.S. programs in Biology and Marine Biology, as well as a Ph.D. program in Marine Biology. Preference will be given to candidates able to complement existing disciplinary strengths and leverage departmental facilities (http://www.uncw.edu/bio/) and who can interact with and contribute to our Ph.D. program in Marine Biology. Excellent support for research is provided in Departmental facilities on campus and at the CREST Research Park (http://uncw.edu/CREST/-), including the Center for Marine Science, Shellfish Research Hatchery, and Biotechnology Center.

To apply, complete the online application available at https://jobs.uncw.edu/ by electronically submitting separately:

(1) a letter of application that includes:

a) A brief statement of teaching philosophy,

b) A brief statement of research interests with particular attention to the applicant's fit to this department,

c) A separate statement that addresses how the candidate's cultural, experiential, or academic background contributes to building an equitable and diverse scholarly environment; see www.uncw.edu/bio/-diversitystatement.html for further details,

(2) a curriculum vitae,

(3) contact information for three references.

For questions about the position, contact the Search Chair, Dr. Heather Koopman (koopmanh@uncw.edu). For questions about the online application process, contact Ms. Tracie Chadwick (chadwickt@uncw.edu). Priority consideration will be given to applications submitted before January 4, 2016, however applications will be accepted until the position is filled.

Stephanie Kamel, Assistant Professor Department of Biology & Marine Biology Center for Marine Science University of North Carolina Wilmington 601 South College Rd., Wilmington, NC 28403 Tel (910) 962-2841 kamels@uncw.edu

"Kamel, Stephanie" <kamels@uncw.edu>

UOklahoma 2 Microbiome

Title of Position: Tenure/Tenure-track Professor

The University of Oklahoma (OU), Norman is excited to announce the first phase of a planned six-faculty cluster hire in the areas of Microbiome and Anthropological Sciences. In this first phase, we seek to fill two newly-created, full-time academic, tenured or tenure-track open rank professorships, beginning Fall 2016. The primary appointment would be within the Department of Anthropology, with potential joint appointments in other departments and/or centers. Successful applicants will have a PhD, strong research program, and demonstrated commitment to teaching excellence. The review of applications will begin December 15th and continue until the positions are filled.

The goal of the cluster hire initiative is to build a collaborative team of scientists that lead in their respective fields, but who also create synergies through large, team science approaches that are typical of current microbiome research. OU already has a strong presence in microbiome research. For example, OU's Institute for Environmental Genomics (IEG: http://ieg.ou.edu) is an award winning research group focusing on the soil microbiome with over 30 publications annually. OU's Laboratories of Molecular Anthropology and Microbiome Research (LMAMR) are home to leaders in the study of the ancestral state of the human microbiome. This research has included partnerships with extant traditional peoples and investigating archaeological remains. LMAMR also houses the largest ancient DNA facility in the U.S. (http://lmamr.org). Moreover, IEG and LMAMR have aligned to build a joint core for genomics, bioinformatics and computational research, providing exceptional infrastructure for multi-omic studies of the microbiome. Two new informatics staff positions are now being filled and a new consolidates sequencing lab is being developed, for which a lab manager position also is being advertised. This broad, multidisciplinary research and education consortium is well situated on OU's award winning Research Campus (http://urc.ou.edu/video/).

OU is a Carnegie Very High Research institution that comprises three campuses. The University was established in 1890 and enrolls over 30,000 students and more than 2600 full time faculty. It ranks first among all universities in the number of National Merit Scholars enrolled and has developed an award-winning Research Campus, contiguous to the Main Campus, that houses more than a dozen private companies, several Federal agencies, and numerous research programs in a unique synergistic ecosystem. More than a million square feet of new, fully-occupied space now exists on the Research Campus, with the latest additions including a Radar Innovations Laboratory, Life Sciences Complex, and an Innovation Hub that will open in about a year. Norman, with a population of 110,000 has a vibrant arts community with outstanding public schools and a variety of recreational resources. It was ranked #6 among the best places to live by CNN/Money Magazine on America's best small cities.

Interested individual should email a 1) cover letter describing research and teaching interests, 2) complete CV, and 3) names and email addresses of three references to:

Dr. Cecil M. Lewis, Jr. Search Committee Chair Email: cmlewis@ou.edu Subject line: ATTN - Faculty Search.

The University of Oklahoma is an Affirmative Action/Equal Opportunity employer and encourages diversity in the workplace. Protected veterans and individuals with disabilities are encouraged to apply. See http://www.ou.edu/eoo for more information.

"cmlewis@ou.edu" <cmlewis@ou.edu>

USouthFlorida DeanScienceMath

The Position:

The Founding Dean of the College of Science and Mathematics will lead a dynamic and growing program. The Founding Dean will be expected to lead the new College, participate in leadership efforts for the USFSM campus, manage external partnerships, engage with the relevant external communities, and actively participate in university events. The Dean will be expected to foster a culture of academic excellence among the faculty and students within the College by working with faculty to encourage high level scholarly activity, attract and maintain grants and nurture undergraduate research programs. The College will be non-departmentalized, so the Dean can fully engage with all of the faculty, curricula, and students.

The College:

The College of Science and Mathematics (CSM) at USFSM will provide an intellectual, collaborative, ethical, inclusive and challenging learning environment for students pursuing bachelor's degrees in Biology, Communication Sciences & Disorders, and Psychology. The College will also offer courses in Chemistry, Physics, Mathematics, and Statistics. The new College of Science and Mathematics will permit USFSM to actively respond to the state and national demands on improving STEM programs in the sciences, anticipate future growth of our Biology,Communication Sciences & Disorders, Psychology, and possible new programs, and build research synergies among colleagues in the disciplines of the college.

Qualifications

Minimum Qualifications:

* Earned doctorate in a field related to Natural Sciences, Health Sciences, Psychology, or Mathematics.

* Documented leadership responsibility in an academic or a professional setting.

* Evidence of strong teaching and nationally recognized scholarship that earned tenure (or equivalent) previously.

Preferred Qualifications:

* Documented experience as an academic administrator with budget line authority.

* Evidence of success attracting and maintaining grants.

* Evidence of success developing undergraduate research programs.

* Experience with new program development.

* Evidence of success in public-private collaborations.

* Evidence of success engaging external communities.

Any interested people can go to http://www.usf.edu/-about-usf/work-at-usf.aspx look under USF Sarasota-Manatee and find position number 9155.

Carlos A. Santamaria / Assistant Professor, Biology csantamaria@sar.usf.edu

University of South Florida Sarasota-Manatee Fax: 941-359-4489 8350 N Tamiami Trail C263Sarasota, FL 34243 http://usfsm.edu "Santamaria, Carlos" <csantamaria@sar.usf.edu>

UToronto GenomicsDataAnalyst

Institution/Company: University of Toronto

Location: Toronto, ON

Job Description:

Purpose

In support of research by PIs in the Department of Ecology and Evolutionary Biology (EEB) the Genomics Data Analyst is expected to conduct genome and transcriptome assembly and analysis of NGS (next-generation sequencing) data, by using off-the-shelf software and by writing and implementing scripts, to help solve important questions about the evolution of plant and animal genomes.

Qualifications Required

Education: Bachelor's degree in biological sciences, bioinformatics or computer sciences, engineering, or statistics, or acceptable equivalent combination of education and experience.

Experience: Minimum 3 years experience working with genomic and/or transcriptomic datasets; demonstrated experience working in a Linux/Unix shell environment; competency with at least one scripting language (e.g. Perl, Python, R). Demonstrated experience in analysis of NGS (next-generation sequencing) with plant and polyploid genomes, particularly whole genome assembly of large plant genomes, genome annotation, and DNA and RNA structural modeling, is required.

Skills: High proficiency with programming languages is required (e.g. C/C++, Python, Java). Unix server administration and hardware specification. A broad range of bioinformatics competencies demonstrated at a high level. Basic understanding of statistics, probability, genetics, and molecular biology. Good written and verbal communications skills, organization skills, initiative, tact and analytical skills. Reliability and good time management skills.

Other: Ability to interface with diverse personnel and to work productively both in collaborations with other team members and individually; ability to balance workloads from multiple competing tasks; able to effectively mentor and assist graduate students and postdoctoral fellows in bioinformatics analyses.

If you are interested in applying for this position, please apply online:

https://utoronto.taleo.net/careersection/10000/jobdetail.ftl?job=3D1501336 Stephen Wright <stephen.wright@utoronto.ca>

UTromsa Norway Biosystematics

Researcher in Biosystematics at TromsÃ University Museum

Application deadline: 03.01.2016

Ref.2015/4603

University of TromsÃ - The Arctic University of Norway (UiT), TromsÃ University Museum, has vacant a researcher position in Biosystematics. The period of appointment is up to a period of four years.

The position is attached to TromsÃ University Museum, Department of Natural Sciences.

For further information, please contact Prof. Inger Greve Alsos, e-mail inger.g.alsos@uit.no, tel +47 77 62 07 96, head of Department of Natural Sciences, Karl Frafjord, e-mail karl.frafjord@uit.no, tel + 47 77 64 57 25, or or Museum Director Marit Anne Hauan, e-mail marit.hauan@uit.no, tel. + 47 77 64 50 30

The position's affiliation

This position is attached to the Department of Natural Sciences, which is responsible for developing and maintaining scientific collections of objects (animals, plants, fossils and minerals) as well as public outreach including TromsÃ Arctic Alpine Botanical Garden. The department has a permanent staff of 16, of which 9 are in academic positions. The department includes a research group in taxonomy and biodiversity, which focuses on diversity, phylogeography and taxonomy of northern organism using molecular as well as traditional methods. The department has laboratories for modern and ancient DNA analyses, and is currently involved in two large project: Ancient DNA of Norwest Europe and Norwegian Barcode of Life. The latter includes full genome sequencing of the entire Norwegian flora. For more information about the Department of Natural Sciences, visit this site.

The position's field of research and other duties

The position is associated with the Norwegian-Swedish Research School in Biosystematics, ForBio (http://www.forbio.uio.no/). ForBio is a teaching and research initiative coordinated by the Natural History Museum (University of Oslo), with Bergen Museum (University of Bergen), TromsÃ University Museum (UiT The Arctic University of Norway) and the Museum of Natural History and Archaeology (Norwegian University of Science and Technology) as collaborators. ForBio is funded by the Norwegian Taxonomy Initiative/Norwegian Biodiversity Information Centre and the Research Council of Norway. Most students at our courses are postgraduate students (PhD or post doc students), but some are graduate and some courses are also aimed at e.g. management employees etc.

The position involves 50 % research and 50 % teaching and administration at the ResearchSchool. The successful candidate will work strategically and practically with the development of ForBio, and teach on theoretical and/or field courses offered through this research school. The development of the Research School will take place in cooperation with representatives of the other Norwegian university museums.

http://www.jobbnorge.no/ledige-stillinger/stilling/119862/researcher-in-biosystematics-at-tromsoe-university-museum Alsos Inger Greve <inger.g.alsos@uit.no>

UTromso Biosystematics

The TromsÃ University Museum, University of TromsÃ - The Arctic University of Norway (UiT), is recruiting a ForBio coordinator/researcher in Biosystematics.

This is a four year research position that includes 50% research and 50% coordination of ForBio.

We are looking for an enthusiastic and active researcher willing to organize ForBio courses and meetings and participate in teaching activities. The role of ForBio coordinators is to continue, expand and improve the work that ForBio has done during the last five years, by training the next generation of biosystematist in Scandinavia, strengthen their networks and improve the quality of the scientific outcomes. The full announcement with requirements and specifications is here: http://www.jobbnorge.no/nn-no/ledige-stillingar/-stilling/119862/researcher-in-biosystematics-at-tromsoe-university-museum Application deadline is January 3rd 2016.

The position's affiliation This position is attached to the Department of Natural Sciences, which is responsible for developing and maintaining scientific collections of objects (animals, plants, fossils and minerals) as well as public outreach including TromsÃ Arctic Alpine Botanical Garden. The department has a permanent staff of 16, of which 9 are in academic positions. The department includes a research group in taxonomy and biodiversity, which focuses on diversity, phylogeography and taxonomy of northern organism using molecular as well as traditional methods. The department has laboratories for modern and ancient DNA analyses, and is currently involved in two large project: "Ancient DNA of Norwest Europe" and "Norwegian Barcode of Life". The latter includes full genome sequencing of the entire Norwegian flora. For more information about the Department of Natural Sciences, visit: https://en.uit.no/-om/enhet/tmu The position's field of research and other duties The position is funded the Nordic Research School in Biosystematics, ForBio (http://www.forbio.uio.no/). ForBio is a teaching and research initiative coordinated by the Natural History Museum (University of Oslo), with Bergen Museum (University of Bergen), TromsÃ University Museum (UiT The Arctic University of Norway) and the Museum of Natural History and Archaeology (Norwegian University of Science and Technology) as collaborators. ForBio is funded by the Research Council of Norway and the Norwegian Taxonomy Initiative/Norwegian Biodiversity Information Centre. Most students at our courses are postgraduate students (PhD or post doc students), but some are graduate students and professionals.

For further information, please contact Prof. Inger Greve Alsos, e-mail inger.g.alsos@uit.no, tel +47 77 62 07 96, head of Department of Natural Sciences, Karl Frafjord, e-mail karl.frafjord@uit.no, tel + 47 77 64 57 25, or Museum Director Marit Anne Hauan, e-mail marit.hauan@uit.no, tel. + 47 77 64 50 30. For further information about the work for ForBio, contact ForBio leader Hugo de Boer, hugo.deboer@nhm.uio.no, tel +47 98 12 60 30.

Please forward to relevant candidates!

Best, Hugo

Hugo de Boer

Natural History Museum University of Oslo P.O. Box 1172 Blindern 0318 Oslo, Norway Phone: +47 22851875

Leader of ForBio - the Scandinavian Research School in Biosystematics www.nhm.uio.no/english/-about/organization/research-collections/people/-hugode/ www.forbio.uio.no/ "h.d.boer@nhm.uio.no" <h.d.boer@nhm.uio.no>

UVienna GroupLeader EcolEvolGenomics

UVienna.GroupLeaderEcolEvolGenomics

An academic Group Leader position is available in the context of several new hirings in the Department of Botany & Biodiversity Research of the Faculty of Life Sciences at University of Vienna, Austria. Building on its broad and long-standing expertise, the Department is currently aiming to strengthen its research focus on the ecological & evolutionary genomics of plant adaptation, speciation, and species diversification / radiation, including the formation of plant species ranges and evolution of biotic interactions in rapidly changing environments. We are hence looking for a person with experience in the use of current DNA / RNA sequencing technologies to address fundamental questions in evolutionary biology and / or biogeography. This includes a keen interest in integrative approaches towards understanding the origin, maintenance, and functioning of biological diversity.

University of Vienna offers an attractive and dynamic research location in a city with exceptional quality of life and in a country with excellent research infrastructure and funding provision.

Extent of Employment: 40 hours/week. Salary grading in accordance with relevant work experience.

Job Description: Participation in research, teaching and administration - Participation in research projects - International publication and presentation activities - Preparation of high-quality external (third-party) research grant applications - Preparation / Finalization of a (publishable) habilitation thesis - Giving classes in accordance with country-wide university regulations - Examination activities - Supervision / mentoring of students.

Profile: Doctoral degree in biology or equivalent field / Focus on molecular evolutionary biology or biogeography of plants - Experience in population genetics, evolutionary genomics, and/or systems biology, especially the use of current DNA / RNA sequencing technology - Excellent written and oral communication skills in English - Computer literacy, including experience with Unix / Linux based analysis software and R - Ability to work in teams - Experience in teaching / experience in e-learning - Experience in external (third-party) fundraising. Duration of the contract: 6 years.

To apply: Your application must include the following documents: motivation letter (<1 page)- Scientific CV - List of publications - Draft of research interests / habilitation project - Contact details of three references. Please see full job description and submit your application via the website of the Job Center at the University of Vienna (http://jobcenter.univie.ac.at; email: jobcenter@univie.ac.at) no later than 01.02.2016, mentioning job reference no. 6252. For more information please contact: Christian Lexer, christian.lexer@univie.ac.at and christian.lexer@unifr.ch.

LEXER Christian <christian.lexer@unifr.ch>

UVienna SeniorScientistBioinformaticsCompBiol

Job: UVienna.SeniorScientistBioinformaticsCompBiol

A permanent, full-time Senior Scientist position is available in the Department of Botany and Biodiversity Research, Faculty of Life Sciences, University of Vienna, Austria. The position is initially for 6 years with the possibility of subsequent unlimited employment. You will take the lead role in the implementation of research activities and approaches in bioinformatics and computational biology in our group. Our research focus is on the ecological & evolutionary genomics of adaptation to changing environments, speciation, and species diversification / radiation in plants and associated organisms. We address these topics using the latest DNA / RNA sequencing technologies in combination with spatial, ecological, and phenome data at different hierarchical levels of biological diversity.

University of Vienna offers an attractive and dynamic research location in a city with exceptional quality of life and in a country with excellent research infrastructure and funding provision.

Extent of Employment: 40 hours/week. Salary grading in accordance with relevant work experience.

Job Description: Participation in cutting-edge research projects involving bioinformatics and computational biology, including the development / validation of new bioinformatic pipelines - Responsibility for the operation and maintenance of high performance computing resources - Liaison point for collaboration with external high performance computing centres - Participation in international publication and presentation activities - Supervision / mentoring of students engaged in bioinformatics and computational biology projects - Assistance with teaching in the department.

Profile: MSc or doctoral (or equivalent) degree in the natural or computer sciences - Experience with the analysis of so-called 'Next Generation Sequencing' (NGS) data, i.e. second or third generation DNA / RNA sequence datasets - Extensive experience with computational work within a Unix / Linux based environment - Programming skills (bash scripting; R; basic skills in either Python or Perl) - Excellent written and oral communication skills in English - A keen interest to keep abreast with ongoing developments in bioinformatics and computational biology - Ability to work in teams - If from an educational path other than biology: basic understanding of biology including evolution.

To apply: Your application must include the following documents: 1-page motivation letter - Educational and scientific CV - List of publications - Contact details of three references. Please see full job description and submit your application via the website of the Job Center at the University of Vienna (http://jobcenter.univie.ac.at; email: jobcenter@univie.ac.at) no later than 01.02.2016, mentioning job reference no. 6254. For more information please contact: Christian Lexer, christian.lexer@univie.ac.at and christian.lexer@unifr.ch.

"christian.lexer@unifr.ch" <christian.lexer@unifr.ch>

WadsworthCenter NGS Bioinformatics

Research Scientist for Next Generation Sequencing, Bioinformatics and Statistics

A permanent Staff Scientist position in Next Generation Sequencing, Bioinformatics and Statistics is available at the Wadsworth Center, NY State Department of Health, Albany, NY. We seek applications at the Research Scientist 2 level from highly motivated individuals with practical experience in bioinformatics analysis of NGS data with an emphasis on microbial genomes, including pathogen identification and outbreak tracking, mapping drug-resistance determinants, development of novel genetic tests, variant analysis, genome annotation and phylogenetics, In addition, he/she is expected to serve as the statistics resource for the Center's research and regulatory programs. Alternatively, we are looking for an Assistant Research Scientist or Research Scientist 1 with strong molecular biology skills and with practical experience in NGS and an interest in the development of new methods and applications for NGS in microbial diagnostics.

The Wadsworth Center (www.wadsworth.org) is the country's most comprehensive state public health laboratory with a staff of about 750. The Center provides a dynamic research environment focused on infectious, genetic and environmental diseases and their impact on human health. Through its initiative for Public Health Genomics the Center will bring NGS and other advanced molecular technologies to public health testing, diagnosis, and research, further develop these technologies to address new and emerging challenges, and become a regional center of excellence for NGS in the area of public health genomics.

For the Research Scientist 2 position, a Ph.D. or M.S. degree in the biological or physical sciences or equivalent and research experience in NGS data analysis and statistics is preferred. Knowledge of Unix, Python, PERL and similar is highly desirable. For the Assistant Research Scientist or Research Scientist 1 position, a B.S. or M.S. in biological sciences or equivalent and experience with NGS and strong molecular biology skills is required. Applicants should submit their curriculum vitae, and contact information for at least three references to wcphgc@health.ny.gov, referencing "Item 12294" in the subject line and indicate which position they are applying for. Applications will be accepted until the position is filled and reviewed as they are received. AA/EOE.

"Lapierre, Pascal (HEALTH)" <pascal.lapierre@health.ny.gov>

Other

AmericanGeneticAssoc Awards

Application Deadline 31 January 2016

Awards announced 31 March 2016

The American Genetic Association grants awards each year for support of special events that advance the mission of AGA, particularly to support students to attend the event.

Eligible events include specialized workshops and short courses in topical areas of organismal genetics and genomics, but any event relevant to AGAs purpose will be considered. Events that could lead to Journal of Heredity articles will receive special consideration. Awards are usually between ,000-5,000, with a total of 0,000 available for 2016.

Funding is competitive, and applications must follow the guidelines. Details and instructions for preparing applications can be found at http://www.theaga.org/

The American Genetic Association grants Evolutionary, Ecological, or Conservation Genomics (EECG) Research Awards to graduate and post-doctoral researchers who are at a critical point in their research, where additional funds would allow them to conclude their research project and prepare it for publication.

These awards are open to any graduate student or postdoctoral fellow who is a member of the American Genetic Association at the time of application V visit http://www.theaga.org/ for membership details.

The program is not intended to fund an entire research project, to initiate new research projects, or to provide salary support. Proposals addressing genome-scale questions, or ecological, evolutionary and conservation genetics questions best addressed with genome-scale data, will be given priority for funding. Awards will generally range from ,000 to 0,000, awarded to the PI or institution (no overhead is provided).

Application deadline is 1 Feb 2016; award outcomes will be announced 15 Apr 2016.

Details and instructions for preparing applications can be found at http://www.theaga.org/ AGA-JOH@oregonstate.edu

AmericanGeneticAssoc Awards 2

Application Deadline 31 January 2016

Awards announced 31 March 2016

The American Genetic Association grants awards each year for support of special events that advance the mission of AGA, particularly to support students to attend the event.

Eligible events include specialized workshops and short courses in topical areas of organismal genetics and genomics, but any event relevant to AGAÂÅs purpose will be considered. Events that could lead to Journal of Heredity articles will receive special consideration. Awards are usually between $5,000-$15,000, with a total of $60,000 available for 2016.

Funding is competitive, and applications must follow the guidelines. Details and instructions for preparing applications can be found at http://www.theaga.org/

The American Genetic Association grants Evolutionary, Ecological, or Conservation Genomics (EECG) Research Awards to graduate and post-doctoral researchers who are at a critical point in their research, where additional funds would allow them to conclude their research project and prepare it for publication.

These awards are open to any graduate student or postdoctoral fellow who is a member of the American Genetic Association at the time of application. Visit http://www.theaga.org/ for membership details.

The program is not intended to fund an entire research project, to initiate new research projects, or to provide salary support. Proposals addressing genome-scale questions, or ecological, evolutionary and conservation genetics questions best addressed with genome-scale data, will be given priority for funding. Awards will generally range from $5,000 to $10,000, awarded to the

PI or institution (no overhead is provided).

Application deadline is 1 Feb 2016; award outcomes will be announced 15 Apr 2016.

Details and instructions for preparing applications can be found at http://www.theaga.org/ AGAJOH@oregonstate.edu

AGAJOH <AGAJOH@oregonstate.edu>

Bootstrapping Trees

Hi,

I'm creating a tree from a distance matrix using phylip neighbor and phylib drawgram. I would like to have bootstrap values for the branches but all I have is this one distance matrix. Is this possible?

The distance matrix is calculated from a Genotyping by Sequencing (GBS) dataset with a few thousand SNPs. For each individual pair, the distance is basically the proportion of genotypes that differ for loci where both individuals are genotyped.

I could easily create different distance matrices by randomly sampling only some of the SNPs to calculate the distances, but that would not make much sense. For example, if I use a low proportion of the SNPs (ie: 5%), the bootstrap values will end up being lower because the matrices will be more different from one another than if I use a high proportion of the SNPs (ie: 50+%). It feels like I can control the bootstrap values artificially, so that is not a good avenue.

Is there a way, given a single distance matrix, to create a tree with bootstrap values?

I'll be happy to summarize the answers and post them back on EvolDir.

Eric

–

Eric Normandeau - Bioinformaticien Laboratoire de Louis Bernatchez Ressources Aquatiques Québec (RAQ)

Institut de Biologie Intégrative et des Systèmes (IBIS) Pavillon Charles-Eugène-Marchand 1030, Avenue de la Médecine Local 1143 Université Laval Québec (Québec) G1V 0A6 Canada

Tél: 418 656-2131 poste 8455 Courriel: eric.normandeau@bio.ulaval.ca

"eric.normandeau@bio.ulaval.ca"

DryadLab TeachingEvolution

"DryadLab - Using real data to engage students in scientific inquiry": a QUBES Faculty Mentoring Network

Spring 2016

Apply by January 1, 2016

DryadLab and Quantitative Undergraduate Biology Education Synthesis (QUBES) are pleased to offer a unique networking and professional development opportunity from January V April 2016 for faculty interested in bringing authentic research data into undergraduate classrooms. DryadLab is an educational extension of the Dryad Digital Repository, which contains freely available research data from thousands of published scientific papers. DryadLab provides open, high-quality, hands-on, data-driven educational modules suitable for use in undergraduate classrooms, developed by the authors of the original publications in collaboration with experienced educators. Over the course of this network, faculty will implement selected DryadLab < http://datadryad.org/-pages/dryadlab > modules in their courses with a focus on providing students with quantitative skills.

QUBES (https://qubeshub.org) is an NSF-funded virtual center that supports collaboration to promote quantitative biology education at the undergraduate level.

Benefits of Participation

-

Access to ready-to-use teaching modules. Participants will incorporate at least 1 of the selected DryadLab modules in Spring 2016 classes -

Access to peer mentors for effective teaching tips and strategies in small group virtual meetings every two weeks -

Letter sent from QUBES to your department chair recognizing your contribution to teaching scholarship

Please visit qubeshub.org/groups/dryadlab/dryadlabfmn for more details and to apply.

Questions? Contact Sam Swauger (samswauger@datadryad.org) or Alison Hale (anm116@pitt.edu).

– Kristin P. Jenkins, PhD Director

BioQUEST Curriculum Consortium bioquest.org (608)

622.9394 POBox 45032 Madison, WI 53744

Kristin Jenkins <kristin.jenkins@bioquest.org>

ESEB funding

** ESEB EQUAL OPPORTUNITIES FUND ***

*The European Society for Evolutionary Biology is pleased to announce the first open call for proposals**for activities that increase awareness of the problem and possible solutions. Such proposals can include, but are not limited to, short workshops (for instance, on unconscious bias) and/or seminars (with invited speakers) at your home organization, data collection, publication activities and similar events. It must be clear from the proposal how the activity will improve our knowledge and awareness of unequal opportunities, or how the activity will improve equal opportunities directly, in the ESEB specifically, or Evolutionary Biology as a field in general. There are two calls per year, with the next upcoming deadline being the 31^st of March 2016. More information about the Equal Opportunities Initiative is available at http://eseb.org/prizes-funding/equal-opportunities-initiative/ *ELIGIBILITY* - Applicants must be ESEB members (for becoming a member of ESEB, please visit http://eseb.org/society/membership/) - Applications can be submitted by scientists at any stage of their professional career (e.g., Masters and PhD students, postdocs, and lecturers). - Applicants must provide proof of support of the host institution where the activity should take place (letter from head of department) - Applicants must explain explicitly how their activity will improve our knowledge, awareness of unequal opportunities, or how the activity will improve equal opportunities directly, in ESEB specifically, or Evolutionary Biology as a field in general. - Applicants must detail which group of people, and how many, will benefit from this activity (for instance, 50 undergraduates, 10 graduate students, 15 faculty members) - Budgets should be reasonable (usually not exceeding 1000,- EUR), and detail costs per person (that benefit from this event).

HOW TO APPLY

The application should be no more than 3 pages long (excluding CV and support letter) and include:

- Name of the applicant(s) - A proposal of the activity - A short summary to be published on the website (100-150 words) - An justification of how the activity will improve our knowledge, awareness of unequal opportunities, or how the activity will improve equal opportunities directly, in ESEB specifically, or Evolutionary Biology as a field in general. - Which group of people will benefit (students, staff, general public), and how many - A detailed, justified budget (including cost per beneficiary) - A time schedule - CVs of the applicants - A letter of support of the host institutionÂs head of the department

Please submit the application as a single PDF-file by email to Ute Friedrich <office@eseb.org; Subject: EO Fund> at the ESEB Office and take care to limit the size of attachments (total < 10 MB) in any one email.

Successful applications must hand in a report about the activity and including details how funds were spent within 3 months after the event.

Kind regards, Ute Friedrich

– ESEB Office Manager European Society for Evolutionary Biology Email: office@eseb.org Website: eseb.org

office@eseb.org office@eseb.org

FrenchGuiana Biodiversity CallProposals

Annual call for proposals CEBA 2016, French Guiana

The CEntre for the study of Biodiversity in Amazonia (CEBA) is a Laboratory of Excellence based in French Guiana aimed at fostering knowledge on terrestrial biodiversity. The Labex CEBA aims to coordinate research capacity in France on the topic of Amazonian terrestrial biodiversity, and to reinforce collaborations with South American and other international partners. Details are available at http://www.labex-ceba.fr The Labex CEBA opens an annual competitive call for proposals to encourage innovative research on biodiversity in French Guiana. Projects will be evaluated by the Scientific Board and by external referees. The submission deadline is February 12^th, 2016. To access the call for proposals form: http://www.labex-ceba.fr/en/appel-a-projets-annuel-ceba/ – Amaia IRIBAR-PELOZUELO

Chargée de coordination scientifique CEBA

Laboratoire Evolution et Diversité Biologique UMR 5174 Université Paul Sabatier, bât 4R1, bureau 124 118 route de Narbonne, 31062 Toulouse Cedex 9 - France

tél : + 33 (0)5 61 55 64 95 fax : + 33 (0)5 61 55 73 27

link: www.labex-ceba.fr Amaia Iribar-Pelozuelo

<amaya.pelozuelo@univ-tlse3.fr>

Hokkaido Japan VolResAssist SeabirdEvolution

Behavioural Ecology of seabirds by using bio-logging techniques.

Location: Teuri and Rishiri Islands, Hokkaido, Japan. Duration: 3 months. Job Type: Volunteer.

We use bio-logging devices (e.g. geolocators, GPS recorders) on two species (Rhinoceros Auklets and Black-backed Gulls) to study behavioural ecology of colonial seabirds. Most work will involve assisting a long-term monitoring project and behavioural studies of post-doc fellows and graduate students from Hokkaido University coordinated by Yutaka Watanuki, with the daily monitoring breeding birds and their chicks, and the deployment and retrieval of tracking devices. It will also involve entering data collected in the field into databases.

We are looking for an enthusiastic, hardworking young biologist to work as a voluntary Research Assistant to help with our seabird research on Teuri/Rishiri Island, Hokkaido, Japan, between May and July 2015. Previous experience in the field or in harsh conditions is desirable, but not essential. Work on Teuri/Rishiri requires long hours (with some work at night and at dawn) spent in a cold and wet environment and considerable manual work. A successful candidate should be able to work independently and have a reasonable level of fitness. Planning to embark on further research degrees in the future would be preferable. It is also important that the assistant feels comfortable sharing sometimes crowded accommodation with a number of colleagues over long periods of time, and can cope with the occasional untidiness inevitably associated with fieldwork.

Unfortunately we cannot provide a stipend but accommodation (shared and basic) on Teuri/Rishiri will be covered. However, the project is a great opportunity to gain valuable experience in modern field ornithology, with bio-logging techniques. There will also be opportunities for the assistant to learn some analytical techniques applied to animal movement data. Teuri/Rishiri has mobile coverage and some access to Internet, however movements to and from the mainland are limited because of unpredictable wind conditions. Teuri/Rishiri is an inhabited island and there are small restaurants and grocery stores. There is a small community of other researchers, ringers and volunteers at our shared accommodation.

If you are interested, please email a CV and a statement of interest and arrange for two letters of reference to be emailed to akikosho@gmail.com (with ywata@fish.hokudai.ac.jp in cc). The deadline for submitting applications (including reference letters) is the 31st January 2016. We will interview the shortlisted candidates (on Skype) shortly after and we expect to make a decision by late February.

akikosho@gmail.com

IUCN subspeciesListing

Hello Everyone!!

I am Dr. Mukesh Thakur from Amity Institute of Wildlife Sciences, Amity University, India. I am an early career scientist, working in conservation genetics for approximately one decade.

I request you kindly share your views regarding red list (IUCN) assessment at subspecies level and what the IUCN should do regarding subspecies assessment. I will be highly interested to read if any one of you has faced the same problem with their species or subspecies form or know a similar case where a widely distributed species has several subspecies form and has not assessed accordingly under IUCN.

I look forward to hear you. Thanking you.

Cordially yours, Mukesh Thakur

Mukesh Thakur, Ph.D.

Assistant Professor

Amity Institute of Wildlife Sciences,

Amity University, Sector 125, Noida 201 313, Uttar Pradesh E. mail: mthakur2@amity.edu; thamukesh@gmail.com Mob.:+91-9639026807; Skype ID: mukeshthakur Mukesh's website: https://sites.google.com/site/thakurmukeshprofile/home Institute's website: http://amity.edu/aiws/ mukesh thakur <thamukesh@gmail.com>

IUCN subspeciesListing answers

Subspecies diversification and its importance in conservation

Dear all,

This is in reference to the issue I raised last week whether the subspecies should be considered as a conservation unit for the assessment under IUCN Vred list. I emphasise this particularly for those species whose mulitple forms (subspecies) exists and they have not accorded separately instead lumped to a species complex under IUCN.

The responses I received are overwhelming and some of you were also experiencing the same problem that I am facing here in India. I have seriously considered each of your response/reply to compile my view point for the species of my concern.

thanking you so much for writing, sharing your experiences, views and suggesting me the possible way to look forward and convince the authorities. I greatly acknowledge those who shared articles in support of their views and had discussion with me. I am herewith sharing you the compilation report of responses.

Thanking you so much.

Regards

Mukesh Thakur

1 # Ron Okimoto replied:

Get some population geneticists involved. We are just starting to get a glimpse of what a genetic load is for a population. My take is that all endangered species should be classified and managed by sub species. The evolutionary facts of life are that nearly all the sub species are going to go extinct for one reason or another. We are just getting data on what the genetic load is for a population in terms mutations in the genome. It may be that some populations will survive their genetic load upon population reduction and most will not. The more populations the better the chance that one will survive. If you start mixing the populations artificially to increase current reproductive success you may be dooming the species to extinction by just making all the populations the same in terms of their chance at ultimate survival.

Trying to maintain the largest effective population may be the simplest to manage, but it may not be the best solution in terms of ultimate survival of that lineage. We only see the survivors in the current biosphere and the survivors have been few and the failures have been many.

Ron Okimoto

2 # Dr. Acacia Alcivar-Warren replied:

Dear Mukesh,

Thank you very much for raising this very important IUCN issue.

On a separate but related concern related to marine shrimp populations in their natural range in the Pacific coast of Latin America, I have not succeeded in encouraging IUCN leaders to take action to review the penaeus taxon.

The natural populations of the Pacific whiteleg shrimp, *Litopenaeus (Penaeus) vannamei,* from northern Peru to northern Mexico, may be at risk. The unregulated international trade threatens food safety, food security and national security. There are no international authorities, or concerned veterinarians, in charge of addressing the lack of supervision for the massive translocation of a subspecies from one continent to another -without quarantine!. Nobody seems to take responsibility for this.

The severe *Vibrio* spp-causing disease (AHPND/EMS) of fast growing SPF *L. vannamei *from US, which first appeared in China in 2009 and quickly spread to other countries in Asia and then to Mexico in April 2013, is of concern to conserve healthy biodiversity in light of climate change.

My requests to international agencies and governments to protect the natural populations of *L. vannamei* have received no replies, not from IUCN, FAO, World Bank, US authorities, or the authorities of the leading shrimp producing-countries (Ecuador, India and Indonesia), that claim to be EMS-free (unconfirmed - we are checking into these claims).

My requests to AVMA leaders and US government's health officials in charge of protecting our food supply have gone nowhere. Nobody seems to care, in spite of my repeated calls for action at meetings of the World Aquaculture Society (https://www.was.org/meetingabstracts/ShowAbstract.aspx?Id=32080). A group in France, supported by IUCN, is actually working on an industry-sponsored project to 'address the safety and nutrition of current feeds used in shrimp aquaculture'.

Can I do something to help you *bring together the basic researchers on population genetics and the leaders of IUCN?*, to address the issues of concern to both of us?

Would you be interested in *organizing a Biodiversity Conservation meeting, *to invite the IUCN leaders to address our issues of concern?. Friends of the FUCOBI Foundation of Ecuador, of which I was the Founder and first President, would be very happy to support an international meeting like this, *if *you include collaborators from our 'ONE HEALTH Epigenomics Educational Initiative (OHEEI)' in India and Nigeria. Indeed, we just sent a message out to a 'ONE HEALTH' list, offering travel awards to pay for expenses of speakers and students to attend conservation meetings

— / —

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

KluaneYukon RedSquirrelVolunteers SpringSummer2016

Field Assistants Required-North American red squirrels

Kluane, Yukon, Canada

We are looking for volunteers to assist with fieldwork for a number of different time periods: (a) 1 March-30 April/15-May (b) 1 May-15 July, and (c) 1 September-15 October. We will also have two positions that extend from 1 March to 15-Aug.

The positions are part of a long-term study of red squirrel ecology, evolutionary biology and physiology. As a member of the study, assistants will be involved with monitoring the reproduction and survival of individuals. Fieldwork will involve live-trapping and handling of animals, radio-telemetry, behavioural observation, and climbing trees to find young in nests. Some positions will also require handling for physiological assays (e.g., blood sampling) This is an excellent opportunity to gain experience working with a collaborative research team on a long-term study of a wild mammal.

All fieldwork is carried against the beautiful backdrop of southwestern Yukon, Canada. We will be staying at a rustic field station two hours from Whitehorse, and ~30 min to the nearest town (Haines Junction). Food and accommodation are provided. Volunteers are required to provide for their own travel to Edmonton, Alberta; however, travel from Edmonton to the field station (and back again!) is provided.

Training will be provided and no experience is necessary. An on-site head technician will coordinate the project, in coordination with the PIs. Candidates should have an interest in a number of the following (the more the better!): ecology, evolutionary biology, wildlife, field biology, and animal behaviour. The field camp is remote and low tech (no showers, cell phone service, or internet), so successful applicants must enjoy the outdoors and be able to remain a positive and responsible team member under relatively isolated and demanding conditions. Candidates must be in good physical condition, be willing to climb trees, and have an enthusiasm for learning. We work on 'squirrel time', which often involves long work days; as such, applicants must have a strong work ethic. That said, the atmosphere at squirrel camp is friendly and inclusive, and this area is one of the most beautiful in Canada. All nationalities are welcome.

If you wish to apply for one of these posts then please send a CV with a cover letter and contact details for three references (with e-mail addresses), by email to Ainsley Sykes (contact info below), by January 30, 2016. Please also indicate the time period(s) you are interested in.

Contact:

Ainsley Sykes via email: asykes@ualberta.ca

Department of Biological Sciences, University of Alberta

"jeffrey.lane@usask.ca" <jeffrey.lane@usask.ca>

MaxPlanckInst Seewiesen Volunteers AvianFieldwork

The Department of Behavioural Ecology and Evolutionary Genetics at the Max Planck Institute for Ornithology in Seewiesen, Bayern, Germany (see http://www.orn.mpg.de/2622/Department_Kempenaers), is seeking two volunteers to work from 15 February 2016 to 30 August 2016.

The volunteers will assist in the collection of courtship displays and egg laying data. This work would be part of a project that aims to understand the evolution of sexual selection in parrots of the world. The work will be done at the facilities of the Loro Parque Foundation, located in Tenerife, Spain.

Work will include: * recording courtship displays * following up reproduction (egg laying, hatching, and fledging) * maintenance of electronic equipment * setting up experimental equipment * data collection, entry, and management

Successful candidates should have experience with video-recording equipment. Experience with monitoring animals, especially birds, is desirable. Applicants should also be highly motivated and well organised, with capabilities of working both in a group and independently. Work will be 5-6 days per week starting early in the morning and potentially continuing into the evening. The working language at the Institute is English, so good knowledge of the language is required. A basic working knowledge of the Spanish language would be advantageous. Eligibility is sadly restricted to UK and EU students. The Max Planck Institute for Ornithology employs a dynamic, dedicated, and international group of researchers who are focused on exploring the fields of evolution, ecology, genetics, and neurobiology.

Benefits will include accommodation and travel-related expenses in Tenerife.

If you are interested in applying for one of the volunteer positions as described above, please apply (including your CV) by 15 January 2016 at the latest, via email to lcarballo@orn.mpg.de

Luisana Carballo Department of Behavioural Ecology and Evolutionary Genetics Max-Planck-Institute for Ornithology Eberhard-Gwinner-Straße, House 8 82319 Seewiesen Germany

"Dobus, Carmen" <cdobus@orn.mpg.de>

Namibia VolFieldAssist Baboons

Tsaobis Baboon Project 2016 - Volunteer Field Assistants

The Tsaobis Baboon Project is a long-term study of desert baboons in Namibia. Based at the Institute of Zoology (the research arm of the Zoological Society of London), and affiliated with the Gobabeb Research and Training Centre (Namibia), our aim is to carry out fundamental research in behavioural ecology and population ecology, and to inform conservation policy and practice for social species.

We are seeking to appoint four volunteer field assistants for periods ranging from 3-5 months between 1 May and 30 September 2016. The fieldwork will primarily involve daily follows of baboon troops on foot, collecting data on the behaviour and ecology of individually recognisable animals. Our research focus this year is on both baboon cognition and collective behaviour.

Further information about the Tsaobis Baboon Project, the volunteer field assistant positions, and the application procedure can be found on the Project's webpages:

www.zsl.org/science/research/baboon The deadline for applications is 6pm Sunday 10 January 2016

Claudia Martina <claudia.martinala@gmail.com>

Panama Intern ButterflySpeciation

Internship on butterfly speciation project in the tropics (re-posting)

We are seeking a research intern to work at the Smithsonian Tropical Research Institute (STRI) in Panama from ˜mid March 2016 for a period of at least one year. The internship will focus on speciation in Heliconius butterflies (for more information please see http://heliconius.zoo.cam.ac.uk/).

The intern will join a vibrant community of scientists studying the origins and maintenance of tropical diversity (see http://www.stri.si.edu). The project is based in Gamboa and the intern will be assisting a project investigating the genetic basis of reproductive and ecological isolation between two sympatric Heliconius species. The project involves breeding butterflies, managing crossing experiments and conducting behavioural assays. Applicants must be able to work independently and be committed to spending considerable time in Panama. A knowledge of Spanish and the ability to drive would be useful but are not essential.

A stipend of US$800/month will be provided to cover accommodation and living costs in Panama .

Please send applications (with a CV and the names and contact details of two referees), or questions, to Richard Merrill (r.merrill@zoo.cam.ac.uk). Please use the subject header: "PANAMA RESEARCH ASSISTANT" before 15th December 2015

Dr. Richard Merrill Department of Zoology | University of Cambridge

Panama: (+507) 64267029 UK Office: (+44)(0)1223 336644 UK Mob: (+44)(0)7590 984754 Email: r.merrill@zoo.cam.ac.uk Web: http://-

www.zoo.cam.ac.uk/directory/richard-merrill @dickmerrill

"rmm60@hermes.cam.ac.uk"
<rmm60@hermes.cam.ac.uk>

RequestComments EvoinEvoDevo

.. might be of interest, particularly because aim of this paper is to stimulate discussions on evo-devo and its possible future directions, and we are thinking about expanding the subject in a book, so any comments/thoughts are welcome (send them directly to me, to avoid multiple messages circulating).. here's the paper and pdf: https://www.researchgate.net/publication/285579741_Where_is_the_Evo_in_Evo-Devo_%28Evolutionary_Developmental_Biology%29 Thanks, Rui Diogo

Rui Diogo <rui_diogo@hotmail.com>

Software DAMBE update

Dear All,

I just noticed that I have packed an outdated NucSubMat.BIN file (dated 2003) with DAMBE. This file contains a collection of nucleotide score matrices for sequence alignment in binary format. The new function for phylogenetics with pairwise alignment uses a matrix that is not in that file, resulting in wrong output for nucleotide sequences (amino acid and codon sequence alignment will be fine). I have uploaded a new version with the correction.

Merry Christmas!

Best Xuhua http://dambe.bio.uottawa.ca http://science.uottawa.ca/biology/people/xia-xuhua "Xuhua.Xia@uottawa.ca" <Xuhua.Xia@uottawa.ca>

Teaching HumanGenetics

If you teach Human Genetics for non-majors or know someone who does, I'd appreciate hearing from you. I would especially like to know which textbook do you use, the reasons that you selected this textbook, and whether or not are you happy with this book.

Thank you

Dan Graur Department of Biology & Biochemistry University of Houston dgraur@uh.edu Twitter: @DanGraur Tumblr: http://judgestarling.tumblr.com/ Dan Graur <dgraur@gmail.com>

UPittsburgh FieldExperience

PLE Early Career Fellowship

Pymatuning Laboratory of Ecology

The University of Pittsburgh's Pymatuning Laboratory of Ecology (PLE) is pleased to offer a summer research fellowship of $10,000 plus up to three months of station fees and residency costs for the primary investigator (PI). PLE is a vibrant research and education facility located on Lake Pymatuning in Northwest Pennsylvania. PLE's research facilities are spread across 350 acres and include access to a variety of aquatic and terrestrial ecosystems. Its 10,000+ square feet of laboratory facilities include a field laboratory adjacent to an open field that can be used for large-scale replicated experiments, a modern molecular laboratory, and facilities for animal, plant and aquatic studies.

This opportunity is open to researchers holding PhD degrees in any science discipline that can benefit from PLE's resources (http://www.biology.pitt.edu/facilities/pymatuning). The purpose of the fellowship is to permit researchers to explore new projects or collect preliminary data. Fellowship funds can be used at the PI's discretion to facilitate the research but not for compensation. Preference will be given to individuals and projects with the potential to develop into long-term research activities at PLE. We especially encourage applications from individuals in the postdoctoral or early faculty phases of their careers but researchers holding PhD degrees at all stages of their careers are encouraged to apply.

For more information about the fellowship program or research opportunities at PLE, please contact the Director, Dr. Cori Richards-Zawacki (cori.zawacki@pitt.edu).

Applicants should submit a single .pdf file including their CV, a 2-3 page proposal outlining the proposed research, a budget detailing how the fellowship funds will be spent, and planned dates of residence to cori.zawacki@pitt.edu, placing the words "PLE Early Career Fellowship" in the subject line of the email. Review of proposals will begin *February 1, 2015*.

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Corinne L. Richards Zawacki, Ph.D. email:cori.zawacki@pitt.edu <email%3Acori@tulane.edu>

Associate Professor, Department of Biological Sciences and Director, Pymatuning Laboratory of Ecology University of Pittsburgh

"At night I went out into the dark and saw a glimmering star and heard a frog and nature seemed to say, well do not these suffice?" - Ralph Waldo Emerson

"cori.zawacki@pitt.edu" <cori.zawacki@pitt.edu>

UTelAviv Israel VolResAssist RoyalIrisEvolution

Opportunity available to participate in an ongoing project on Floral Evolution and Ecology of the Royal Irises in Dr. Yuval SapirÂs lab (http://labsapir.wix.com/labsapir) at Tel Aviv University, Israel. We are seeking one or two motivated volunteer research assistants to help with field data collection, to perform experimental work at the botanical garden and to assist in data analyses.

The positions are most suitable for graduates in Biology seeking to gain further research experience. Candidates who are still undergraduates will be also considered. Candidates should have good organizational skills, high interest to work in the field and fluent English. International driving license is essential. Positions start early February and will continue until early April, but a partial term is also possible.

About Tel Aviv University: Tel Aviv University (https://english.tau.ac.il/) is considered the best university in Israel for life sciences. It is located in the city of Tel Aviv, an international and vibrant coastal city. The University has a wide representation of International students.

Israel is culturally and ecologically diverse. The country has approximately 3000 plant species growing along a climate gradient, from sub-alpine mountain through Mediterranean maquis to extreme desert. Alongside the natural settings, Israel is rich in history, with archaeological sites dated thousands years old and sites that are sacred to three religions.

The volunteer will have an opportunity to travel throughout the country during the project work and experience the diversity in vegetation, especially the coastal and desert vegetation, as well as the culture.

If you are interested please e-mail your cv to Dr Yuval Sapir (sapiryuval[at]gmail.com) or to Dr. Mahua Ghara (mahuaghara[at]gmail.com). You could also write to us for further information and queries regarding the opportunity.

mahuaghara@gmail.com

PostDocs

AarhusU QuantGenomics

Dear All,

I would like to draw you attention to the post doc position in QGG, Aarhus University, described below.

Best regards, Louise

Postdoctoral Fellow on robust and efficient dairy cows

Center for Quantitative Genetics and Genomics (QGG < http://mbg.au.dk/forskning/forskningscentre/center-for-quantitative-genetics-and-genomics/ >), at the Department of Molecular Biology and Genetics, Aarhus University, is seeking a creative, motivated and productive Postdoctoral Fellow to conduct research on dairy cattle phenomics and genetics.

Project In dairy cattle breeding, definition and measurement of new phenotypes like rumen microbial composition, feed intake, and methane emission, is important in order to continuously improve the genetic potential and management of the dairy cattle population and to accommodate for new breeding goals. However, an important issue regarding many of these new phenotypes is how to measure them in large scale in commercial dairy cattle herds as they are difficult and expensive to measure. Therefore, measurement techniques need to be further developed and validated. In this post doc project, the successful candidate will work on data collection, analysis and validation of phenotypes related to robustness and efficiency on a large scale in commercial farms and in our research farm. The project will be very industry oriented, but have a high scientific focus on novel phenotypes. The genetic evaluation of the new phenotypes will give us insight in the underlying biology of complex traits like feed efficiency and methane emission.

The position is open for 2 years with a possibility to extend for another year and the expected starting date is the 1st of March 2016.

Qualifications and competences * PhD or equivalent in quantitative genetics, statistical genetics, or related fields * Documented experience in multivariate statistics. * Preferably experience working with unix/linux systems for high performance computing. * Preferable experience in scripting and/or programming in e.g. SAS, R/Matlab or C * Strong skills in oral and written communication in English * Ability to work independently in a large and diverse group of researchers, and collaborate with national and international research partners. * Being able to see opportunities rather than limitations.

Place of work The place of work will be the Center for Quantitative Genetics and Genomics (QGG), which is a major center for research and education in quantitative genetics, quantitative genomics, and breeding. QGG has large experience in development and implementation of methods for genetic studies and software that is routinely used by several Danish and international research groups and commercial breeding companies. It comprises 20 senior staff and a large group of PhDs and postdocs. The center is part of the Department for Molecular Biology and Genetics and is located at the AU Foulum campus (for the locations of the department see http://mbg.au.dk/en/contact/how-to-find-the-department/). QGG provides a very dynamic and internationally orientated environment with strong collaborations with relevant industrial partners and with several other leading international research groups in the area.

Further information For further information, please contact Project Senior Scientist Jan Lassen (jan.lassen@mbg.au.dk)

Formalities and salary range Science and Technology refers to the Ministerial Order on the Appointment of Academic Staff at Danish Universities under the Danish Ministry of Science, Technology and Innovation. The application must be in English and include a curriculum vitae, degree certificate, a complete list of publications, a statement of future research plans and information about research activities, teaching portfolio and verified information on previous teaching experience (if any). Guidelines for applicants can be found here. Appointment shall be in accordance with the collective labour agreement between the Danish Ministry of Finance and the Danish Confederation of Professional Associations. Further information on qualification requirements and job content may be found in the Memorandum on Job Structure for Academic Staff at Danish Universities. (in Danish). Salary depends on seniority as agreed between the Danish Ministry of Finance and the Confederation of Professional Associations. All interested candidates are encouraged to apply, regardless of their personal background.

Deadline

All applications must be made online and received by: 11.01.2016

The formal announcement of the position and information on how to apply can be found here

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ArizonaStateU EvolutionMedicine

Postdoctoral Fellow in Evolution & Medicine: Education Resources Development and Online Learning

Salary: $40,000 “ 48,000, Salary is negotiable based on the candidate’s experience and ASU salary scales.

Reference # 11450

Full-time

The Center for Evolution & Medicine (CEM) at Arizona State University (ASU), and Founding Director Dr. Randolph Nesse, invites applications for a Postdoctoral Fellow in Education Resources Development and Online Learning. Anticipated start date is August 1, 2016. This is a full-time (1.0) benefits -eligible, fiscal year (July 1 - June 30) appointment. The successful candidate will be co-mentored by Dr. Nesse, an expert in evolutionary medicine and Dr. Sara Brownell, an expert in undergraduate biology education research. As a physician, Dr. Nesse’s research on the neuro-endocrinology of anxiety led to a series of publications that established the field of evolutionary medicine. Dr. Brownell is a neuroscientist whose research is focused on biology education.

Renewal is possible on an annual basis contingent on satisfactory performance, availability of resources, and the needs of the program. For additional information and policies regarding postdoctoral scholars at ASU, please see http://provost.asu.edu/postdoc.

The successful candidate will help curate existing online resources in evolutionary medicine, participate in the development and delivery of new innovative evolutionary medicine courses, both in-person and online, and will evaluate and study the impact and effectiveness of these resources and courses. The Fellow will help develop a project plan to build courses that will initially be offered to ASU and ASU online students and later to medical personnel all over the world. This is an exciting opportunity to work with an interdisciplinary faculty in a growing field of study to develop, implement, and research innovative curriculum and other resources related to evolution and medicine.

While specific technology expertise is not required, an ideal candidate would demonstrate a strong interest in the applications of technology in higher education, and would have an aptitude for developing and assessing new approaches to learning and how they are best supported by new technologies. This, together with experience in curriculum development and teaching, will allow the Education Resources Fellow to provide disciplinary and pedagogical expertise in creating innovative and rigorously assessed learning experiences. The Fellow may have supervisory responsibilities that include the training and mentoring of staff and/or student interns.

This Postdoctoral Fellows Program is a service and training program designed for early career scientist-teachers who are interested in an academic pathway involving curriculum development, teaching, and educational programming in the interdisciplinary field of Evolutionary Medicine. Fellows will receive mentorship to support their development as educators throughout the duration of the fellowship and have an opportunity to participate in the ASU Science Education Group, the Evidenced-based Teaching Seminar series, as well as the Biology Education Research Lab.

The Center for Evolution & Medicine is a university-wide Presidential Initiative whose mission is to establish evolutionary biology as an essential basic science for medicine, worldwide. As an interdisciplinary unit, and a member of ASU's BioDesign Institute, the postdoctoral fellow will have multiple opportunities to work in collaboration with faculty from a wide-range of disciplines. The Center brings leading scientists to ASU to join existing faculty in research that demonstrates the power of evolutionary biology to address problems in medicine and public health.

The School of Life Sciences (SOLS) is a creative hub for research and teaching excellence at Arizona State University. Fast becoming a global leader in life science education and discovery faculty, graduate students, postdoctoral fellows and staff, work together to support an environment of interdisciplinary research to inspire and transform life science students by providing an innovative learning experience that prepares them to thrive in a dynamic and demanding world. SOLS aims to improve life by stimulating scientific discovery and solving critical problems at the intersection of the life sciences and society.

By the start date, candidates must have completed a Ph.D. in anthropology, biology or other natural science or science education field that provides an extensive background in evolutionary biology. Cross-training and experience in education is desirable. Candidates with experience in the following are preferred: developing and assessing education resources; conducting educational research; and using developing digital resources for online and classroom use. The successful candidates will have a commitment to science

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

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Auckland EvolutionMetabolicSystems

Post Doctoral Research Fellow

Institute of Natural and Mathematical Sciences, College of Sciences Albany

The Institute of Natural & Mathematical Sciences and The NZ Institute of Advanced Study seek to appoint a Postdoctoral Research Fellow for the research group of Prof. Thomas Pfeiffer.

In this appointment you will be expected to contribute to the group's research activities in the modelling of metabolic systems and their evolution. You will have a strong background in mathematical modelling, theoretical biology or computational biology is of advantage, as is a track record in metabolic modelling and the analysis of genomic data.

This position is for three years, requires a PhD qualification, and is based at the Auckland campus. Please contact Prof. Thomas Pfeiffer for further information (email: T.Pfeiffer@massey.ac.nz).

Closing date: 17 January 2016 Reference number: A403-15SF

For further information and to apply online, visit: http://www.massey.ac.nz/joinus/ Dani Smith | Account Executive DDI ÂÂ 04 914 4652 Â

AUCKLAND | WELLINGTON | CHRISTCHURCH 0800 170 019 Â

Dani Smith <dani.smith@hainesattract.co.nz>

BangorU LinkageMapping

Applications are invited for a 3 year fixed-term, full-time post working in the School of Biological Sciences at Bangor University. Closing date 1st Feb.

We are looking for a dynamic researcher to fulfil a leading role in a new Leverhulme Trust-funded project aimed at developing a linkage map of the gerbil genome. Desert-dwelling rodents have great potential to provide insight into the genetic basis of physiological adaptation to restricted diets and lack of water, and can inform understanding of human diseases such as diabetes. The primary objective of this project is to develop a single nucleotide polymorphism (SNP)-based linkage map of the gerbil genome to reveal gene order and provide a scaffold for data from whole genome sequencing efforts.

Duties will include maintenance and breeding of Mongolian gerbils (Meriones unguiculatus); RNA-Seq analysis of multiple tissues and developmental stages; generation and development of SNP markers via genotyping by sequencing (GBS); and the creation of high-density genetic linkage maps.

Candidates should be educated to PhD standard (or equivalent) and have previous experience in relevant techniques, including the development of genetic markers and linkage analysis in plant or animal systems. Familiarity with bioinformatic tools for analysis of RNA-Seq experiments is desirable, but not essential.

The successful candidate will be expected to commence 1st April 2016 or as soon as possible thereafter.

Informal enquiries should be directed to Dr John Mulley (email: j.mulley@bangor.ac.uk), www.johnmulley.com, @JohnMulley.

Further information: https://jobs.bangor.ac.uk/ Dr John Mulley School of Biological Sciences Bangor University Deiniol Road Bangor Gwynedd LL57 2UW United Kingdom

Tel: +44 (0)1248 383492 Email: j.mulley@bangor.ac.uk Web: www.johnmulley.com Twitter: @johnmulley < https://twitter.com/JohnMulley >

John Mulley <j.mulley@bangor.ac.uk>

BangorU MolEvolPollen

Using molecular genetics to understand aerial dispersal of grass pollen and linkages to human health

We are looking for a dynamic postdoctoral researcher to fulfil a leading role in a multidisciplinary team working at the interface between the molecular genetic analysis of aerial pollen composition and human health (http://mefgl.bangor.ac.uk/news/3–25077). Approximately 20% of the UK population suffer from summer allergies and the primary outdoor allergens are grass pollens. Nevertheless, there is currently no easy way of discriminating different species of grass pollen using traditional morphological approaches. Molecular biodiversity identification is emerging as a high throughput and cost effective alternative to existing approaches to assess grass pollen mixtures both quantitatively and qualitatively. The primary objectives of the broader project will be to (a.) develop a species level, spatio-temporal grass pollen molecular genetic assessment framework throughout the UK and (b.) develop novel pollen bio aerosol models in order ultimately to (c.) identify linkages between species-specific grass pollen loadings and human health (i.e. asthma exacerbations).

The Â£1.2M project is funded by the NERC Standard Grant blue sky funding stream and involves collaboration with Aberystwyth University (Natasha DeVere; Gareth Griffith; Matt Hegarty), The National Pollen and Aerobiological Research Unit (NPARU), University of Worcester (Carsten SkjÃ̃th), Exeter University (Nick Osborne) and the UK Met Office. The leading Bangor component of the project will utilise molecular ecology, including high throughput qPCR and genomic approaches to assess biodiversity, bioinformatics and ecological modelling, with the PDRO working closely with a diverse team of collaborators both in the UK and overseas. The project will also benefit from close links with a range of charities providing support in the broad field of allergenic and respiratory health.

Candidates should possess a doctoral degree in related areas such as natural sciences, ecology, botany, molecular taxonomy, evolution/genomics and should ideally have previous experience of fieldwork, molecular ecology, bioinformatics and ecological data handling. The successful candidate will be expected to commence 1st March 2016, or as soon after this as possible.

Applications will only be accepted via our on-line recruitment website, jobs.bangor.ac.uk (REF: BU01042). However, in cases of access issues due to disability, paper application forms are available by telephoning 01248 383865.

Post details: 3 year, full time postdoctoral researcher (Â£31,656 - Â£37,768 (Grade 7) p.a.). Closing date for applications: 21st December 2015, with interviews predicted to take place in the 2nd half of January 2016.

In the meantime, informal enquiries should be sent to Dr S. Creer, email s.creer@bangor.ac.uk; http://-mefgl.bangor.ac.uk/staff/si.php; @spideycreer or members of the broader team where appropriate.

Many thanks and best wishes

Si Creer

Simon Creer Senior Lecturer Molecular Ecology and Fisheries Genetics Lab Environment Centre Wales Building School of Biological Sciences Bangor University Bangor Gwynedd LL57 2UW UK

e-mail: s.creer@bangor.ac.uk

Tel: +1248 382302 Fax: +1248 382569

Home Page: http://mefgl.bangor.ac.uk/staff/si.php Skype: spideycreer Twitter: @spideycreer

Simon Creer <s.creer@bangor.ac.uk>

Basel Switzerland HostParasiteCoevolution

University of Basel, Switzerland Zoological Institute

Postdoc position in host-parasite population genetics and genomics

A postdoc is available in the research group of Dieter Ebert, at the Zoological Institute at Basel University in Switzerland. I am looking for a highly motivated post-doc with interest in the (co-)evolutionary genetics of host-parasite interactions. This position is funded to work on the coevolutionary genetics/genomics of Daphnia and its microparasites. A background in evolutionary genetics and bioinformatics skills are welcome. Excellent written, verbal, and interpersonal skills, a superb work ethic, and the ability to think creatively and critically are desired. The starting date is flexible. The position is initially for 2 years, but can be extended to 3 years.

The post-doc will be part of Dieter Ebert's research group, working on the co-evolution of host-microbe interactions. Our experimental work uses Daphnia as the host system. Details about the group can be found under: http://evolution.unibas.ch/ebert/ Please send application by E-mail to Dieter Ebert (dieter.ebert@unibas.ch). Applications (all in one single pdf file with your name as file-name, please) should include a CV, a list of publications and a 1-page description of your research interests and motivation. Please give names and email addresses of two persons who are willing to write a letter of recommendation. Deadline for applications is 31. January 2016.

Contact information: Prof. Dr. Dieter Ebert, University of Basel, Zoological Institute, Vesalgasse 1, 4051 Basel, Switzerland, Email: dieter.ebert@unibas.ch Tel. +41-(0)61-267 03 60 http://www.evolution.unibas.ch/ebert/ "dieter.ebert@unibas.ch" <dieter.ebert@unibas.ch>

CityUNewYork ButterflyPhylogenomics

POSTDOCTORAL POSITION IN BUTTERFLY PHYLOGENOMICS

The Lohman Laboratory at the City College of New York (CCNY), the flagship campus of the City University of New York (CUNY), is seeking a motivated and productive postdoctoral researcher in phylogenomics and comparative life history evolution.

MAJOR RESPONSIBILITIES The postdoc will join a team of researchers from the University of Florida, Harvard, Yale, and Georgetown University to reconstruct a phylogenetic tree of all butterfly species using anchored hybrid enrichment of marker genes followed by next-gen sequencing. A parallel effort will mine existing databases and literature to synthesize data on species ranges and traits and deliver these data through an online portal. Subsequent analyses will use these tools to examine biogeography, macroecology, and life history evolution of these charismatic insects. The project, ButterflyNet, is funded by a Genealogy of Life grant from the National Science Foundation.

The successful candidate will have three primary responsibilities: 1) coordinating a large, global network of collaborators and contributors to obtain specimens and tissues; 2) traveling to several countries including China, India, and Sri Lanka to perform next-gen library preparation in host laboratories; 3) undertaking large-scale phylogenetic/ phylogenomic analyses and evolutionary comparative studies. The position requires prolonged travel to Asia, and the postdoctoral fellow must be willing and able to travel outside the United States for several months at a time. The postdoctoral researcher will have the option to spend time visiting the laboratories of other participants of ButterflyNet to work on comparative analyses, particularly in later phases of the project: Akito Kawahara and Rob Guralnick at the University of Florida, Leslie Ries at Georgetown, Walter Jetz at Yale and/or Naomi Pierce at Harvard University.

The Biology Department of CCNY has a large and thriving community of faculty, students, and post-docs studying ecology, evolution, and behavior (EEB). The CCNY EEB group interacts with the larger community of biologists in New York at other CUNY campuses and at the American Museum of Natural History, the New York Botanical Garden, and other universities, including Columbia, Rockefeller, and NYU.

QUALIFICATIONS > Ph.D. in systematics, evolutionary biology, behavioral ecology, > genomics and/or related fields > Fluency in written and spoken English > Computational proficiency with bioinformatics, phylogenetic inference > software, and other analytical programs, including command-line > computing > Laboratory experience with PCR, DNA sequencing, and sequence editing > Ability to meet deadlines, work in a team, and gather data in > challenging conditions > US citizenship or permanent residency is not a requirement.

ADDITIONAL RESPONSIBILITIES > The postdoctoral scientist will be expected to teach an undergraduate > elective course on a topic of his or her choice to gain teaching > experience. > Participation in multidisciplinary ButterflyNet workshops will help > broaden the postdoctoral scientist's skill set. > Assist with purchasing and other laboratory management activities > Assist with grant applications and publication writing > Participate in mentoring graduate and undergraduate students

OTHER DESIRABLE SKILLS > Prior experience studying insects, especially butterflies or other Lepidoptera > Laboratory experience with next-gen library preparation and/or phylogenomics > Proficiency in spoken Mandarin Chinese would be useful but is not required

APPLICATION INFORMATION To apply, please submit your CV, a cover letter, and the names, phone numbers, and email addresses of three referees using this link at rfcuny.org>About RF>Careers>Research

https://www.rfcuny.org/careers/postings?pvnID=CC-1508-000694 Click on "Apply" under the "Actions" header. In addition, please ask two of your referees to email letters of support to butterflyphylogenomics@gmail.com.

The cover letter should discuss your previous research and training, your qualifications for the position as detailed in this advertisement, and how this postdoctoral position will further your long-term research/career aspirations.

The salary will be commensurate with experience; generous benefits are included. The appointment is initially for one year, with up to two additional years possible given satisfactory progress.

Review of applications will begin 15 October 2015 and will continue until the position has been filled. The successful applicant may begin as early as 1 November 2015, and should ideally begin within the first quarter of 2016.

Any questions about this position should be addressed to David Lohman at butterflyphylogenomics@gmail.com.

For more information about the Lohman Laboratory, please visit:

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ClarkU FungalEvolutionaryGenomics

Postdoc:fungal evolutionary genomics

TheHibbett lab at Clark University seeks a highly motivated, independent postdoctoralfellow to conduct research in evolutionary genomics in mushroom-formingfungi. The postdoctoral fellow will be involved in oneor more of the following projects: (1) Evolutionary developmental biologyof Agaricomycetes; (2) Evolution of substrate-specificity inwood-decay fungi; or (3) Phylogenomics of Lentinula (shiitake mushroomsand relatives). All three projects require expertise in evolutionarygenomics and molecular phylogenetics. Experience in fungalgenetics is also desirable. Research could include Ãâ¬*Åwetbench Ãâ*¬ï?‘1$_{\overline{2}}$techniques, including culturing and production of fruitingbodies for transcriptomics, or could be entirely analytical, dependingon the candidate's skills and interests. Applicants should havea PhD in genomics, evolutionary genetics, fungal biology, or a relevantdiscipline, a strong publication record (appropriate for careerstage), and excellent communication skills. Willingness to involvestudents in research is also important. Preferred starting dateis June 1, 2016, but this is (somewhat) flexible. Up to threeyears of support is available, contingent on progress. For moreinformation, including application instructions, please see: https://hibbettlablog.wordpress.com/2015/12/28/-post-doc-available-june-2016/ Applicationsfrom women and members of underrepresented groups in scienceare encouraged. Clark University is an EEO/AA Employer.

DavidHibbett <DHibbett@clarku.edu>

CornellU CassavaStatisticalGenetics

Post Doctoral Position in Statistical Genetics in Cassava - Cornell University

This position is within the Section of Plant Breeding and Genetics at Cornell, within the NEXTGEN cassava research program (www.nextgencassava.org). Cassava is a critical food security crop in sub-Saharan Africa for which genomic resources are only now being rapidly developed.

NEXTGEN Cassava researchers at Cornell work with primary collaborators in Nigeria and Uganda and a wider network of collaborators at other research programs. The hired person will join this team to aid genomic analyses and interaction with new collaborators. Analyses will include genomic prediction training population design, experimental design for trait evaluation, and understanding breeding goals to implement selection decision support.

In addition to direct work with collaborators, the postdoc will pursue research to improve the team's analysis capacity overall by developing new methods or data, extending analyses of existing data, or improving implementations of existing methods. Possibilities include:

§Identifying and implementing models to jointly analyze populations from multiple collaborators where the data exhibits sub-population structure;

§Developing algorithms for automated training population design, requiring exploration of a large repository of cassava data (www.cassavabase.org);

§Low-depth sequencing of parents used in African cassava breeding programs to obtain ultra-high density marker profiles of their progeny for prediction and association studies;

§Implementing algorithm-based experimental design methods to lower error variance of collaborator phenotyping efforts;

§Method development for selection by identifying and selecting for greater recombination in genomic regions where such recombination is low;

§Maintaining diversity during genomic selection;

§Selecting on traits to improve stability in the presence of genotype by environment interaction.

There is tremendous scope within the lab for research that will have high impact on this important crop and on plant breeding in the genomics era generally. Travel and teaching in sub-Saharan Africa will also be possible within this position.

The position term is one year, renewable to two years contingent on performance. Extending beyond two years contingent on funding.

Anticipated Division of Time

Applied research providing genomic predictions and selection decision support with collaborators 40%

Basic research to improve NEXTGEN Cassava team analysis capabilities 40%

Participation in preparation of annual reports and publications 10%

Formal and informal training of lab members and collaborators in statistical genetics and genomics 10%

Position Requirements

Ph.D. in statistics or applied mathematics with experience in predictive modeling or Ph.D. in plant or animal breeding with emphasis on statistics; or in statistical or computational areas of genetics. Specific technical/administrative skills required:

§High-dimensional data analysis

§One or more programming languages

§Proven scientific writing ability and communication skills

Preferred Qualifications:

§Experience in plant breeding practice, analysis of plant breeding data, statistical genetics, and crop physiology

§Knowledge of databases / database programming

How to Apply

Please send the following in a single PDF to daniel.torrington@cornell.edu with the subject "Statistical Genomics Post Doctoral Position Application":

1. A letter of interest

2. A current CV

3. Contact information (email and phone number) for three references

Review of applications will begin in mid to late January and will continue until the position is filled.

Dan Torrington <daniel.torrington@cornell.edu>

CUNY NewYork EvolutionAdaptation 2

Brooklyn College - CUNY Research Associate (Post-Doctoral Fellow) - Biology CUNY Job ID: 13931

The Brooklyn College Department of Biology seeks applications for a research Associate (Post-Doctoral Fellow) who will assist the Principal Investigator with research activities in evolutionary biology, and work with student researchers. The Principal Investigator's research uses computation and theory to explore how complex adaptations evolve.

Under the mentorship and guidance of the Principal Investigator, the Research Associate (Post-Doctoral Fellow) will perform the following duties:

- Develop plans, and collect and analyze data based on projects prepared by the Principal Investigator. - Prepare reports of completed projects for publication in scientific journals, academic presentations or for further applied or theoretical research activities. - Develop, plan and conduct new research projects. - Provide administrative support to the Principal Investigator including, but not limited to: managing laboratory budgets and ordering supplies. - Maintain laboratory computers and research equipment for accurate operation. - Train and supervise undergraduate and graduate researchers.

Potential projects include: - Extending a model of stochastic gene networks to answer evolutionary questions about plasticity and evolvability - Applying math and computation to understand adaptation on fitness landscapes, with applications to evolution experiments. - Modeling virus life-histories to make predictions about host shifts.

For more information, please contact the Principal Investigator, Dr. Jeremy Draghi, at Jeremy.Draghi21@brooklyn.cuny.edu or visit www.jeremydraghi.com . *This appointment is for one year and, any reappointment is contingent upon satisfactory performance and financial availability.

MINIMUM QUALIFICATIONS Doctoral Degree in a related field and demonstrated research ability.

OTHER QUALIFICATIONS - Published research in evolutionary biology. - Experience with one or more programming environments, especially C, R, and Mathematica. - Experience with the mathematical analysis of models. - Outstanding communication and writing skills. - A history of successful collaborative work and mentoring.

COMPENSATION $44,849; All appointments are subject to financial availability.

BENEFITS CUNY offers a comprehensive benefits package to employees and eligible dependents based on job title and classification. Employees are also offered pension and Tax-Deferred Savings Plans. Part-time employees must meet a weekly or semester work hour criteria to be eligible for health benefits. Health benefits are also extended to retirees who meet the eligibility criteria.

HOW TO APPLY Applicants must upload their cover letter (referenced Job ID # 13931), resume, and contact information (name, phone number and email address) for three references in rtf, doc or pdf format.

To apply, please visit www.brooklyn.cuny.edu/-adminjobs.

For more information, please visit www.jeremydraghi.com. To apply, please visit www.brooklyn.cuny.edu/adminjobs . CLOSING DATE

Revised

Review of applications will begin December 14, 2015 and continue until position is filled.

EQUAL EMPLOYMENT OPPORTUNITY We are committed to enhancing our diverse academic community by actively encouraging people with disabilities, minorities, veterans, and women to apply. We take pride in our pluralistic community and continue to seek excellence through diversity and inclusion. EO/AA Employer.

Jennifer Tsui <JTsui@brooklyn.cuny.edu>

DukeU RecombinationMolecularEvolution

A postdoctoral position opening is anticipated in the Noor laboratory at Duke University to study temperature effects on crossover rate variation in Drosophila pseudoobscura and consequences of that variation on molecular evolution. Specific duties will include performing Drosophila crosses, purification of DNA from individual flies for genotyping-by-sequencing (GBS), analysis of GBS data to assess recombination rate, and various computational molecular evolutionary assays. Details of the project are available upon request. The supported postdoc will work closely with the PI and other trainees in the laboratory, and participate in weekly group lab meetings, weekly one-on-one meetings, and departmental journal clubs and other activities. The Duke Office of Postdoctoral Services also offers diverse professional development programs in which the supported postdoc will be encouraged to participate.

Minimum qualifications:

* PhD degree anticipated by June, 2016, in field related to proposed research (e.g., genetics, genomics, evolution) * Basic computer coding skills and familiarity with command line tools * Basic molecular laboratory skills * Evidence of writing skills and completion of research projects through research publications * Evidence of ability to work both independently and as constructive member of a team

Desirable traits:

* Experience with genotyping-by-sequencing, experimental portions and especially data analysis * Advanced skills listed in minimum qualifications above * Love of Star Trek (though this one will not factor in hiring decision)

If interested, please send brief statement of relevant experiences & why you're interested, your publication list (with links to papers), and names/ contact info for 2 references, to Mohamed Noor at noor@duke.edu<mailto:noor@duke.edu> Please DO NOT send attachments– just send requested items in text of e-mail, and please send the e-mail with subject line saying only "postdoctoral position". Anticipated start date is late spring/ summer of 2016, but this is potentially negotiable. Duke University is an Equal Opportunity/ Affirmative Action Employer.

https://sites.google.com/site/noorlabduke/home
"noor@duke.edu" <noor@duke.edu>

IAST Toulouse EvolutionaryBiology

The Institute for Advanced Study in Toulouse (IAST), France, invites applications for Research Fellowships from 1st September 2016.

We welcome applications from researchers within a large range of disciplines in the social and behavioral sciences: anthropology, biology, history, law, philosophy, political science, psychology and sociology, though motivated applications from outside these disciplines will be given full consideration. We seek candidates with a strong research background in their own discipline, but willing and able to develop research projects drawing on IASTs substantial interdisciplinary resources, including particularly the proximity of strong groups in economics (Toulouse School of Economics, TSE).

Eligible applicants: Active researchers who have or will have completed their PhD after January 2014 and before September 2016. The IAST offers candidates an opportunity to devote themselves full time to their research at the start of their careers. Motivated applications will be considered from candidates whose PhDs were completed in 2013 or earlier; please explain your reasons in your cover letter.

Conditions: Fellows are provided with office space, computer facilities and a contract for two years, renewable for a third year.

Deadline to apply: 31st December 2015

For information on how to apply, visit: http://www.iast.fr/applications/research-fellowship Ingela Alger <ingela.alger@gmail.com>

Kiel Germany EvolutionaryGenomics

Postdoc Position on Evolutionary Genomics in Kiel, Germany

Basic Information

Postdoctoral Scientist position for 2x 3 years, starting date 1 July 2016, salary at level TV-L E14

Area of Work

Up-to-date research work on genome evolution - with a focus on either antibiotic resistance evolution or the evolution of C. elegans-microbe-interactions. Within the 3+3 years-time frame, an innovative research program in one of these fields shall be developed. In addition, contributions to the teaching activities of the Schulenburg group within the fields of evolutionary ecology, biostatistics, and/or genomics at both Bachelor- and Master-level (four hours per week).

Expectations and Requirements

University degree and PhD in the general area of evolutionary genomics with one of the above listed foci. Experience in the independent performance of research in these areas (e.g., based on a first postdoc project). Excellent knowledge of genome analysis, including population genetics. High competence in English. Ideally, experience in teaching students, supervision of BSc and MSc projects, experience in procurement of third-party funding, and international experience(s) (e.g., postdoc outside of Germany). Kiel University aims at a higher proportion of women in research and education, and, therefore, specifically encourages qualified female scientists to apply. Female scientists will be preferentially considered in case of equivalent qualification, competence and achievements. Kiel University specifically supports employment of severely handicapped people. Therefore, severely handicapped applicants will be preferentially considered in case of suitable qualification. Kiel University specifically welcomes application from people with migration background.

Location

The position will be based in the Schulenburg group at the University of Kiel, Northern Germany. The department provides an international and interactive atmosphere, while Kiel University and connected institutes (e.g., Max Planck Institute in Ploen) offer a stimulating research environment with a particular focus on evolutionary biology and also C. elegans genetics. The city of Kiel is a medium-sized town located at the coast of the Baltic Sea. It is the capital of the most Northern state of Germany, Schleswig-Holstein. It offers many opportunities for leisure activities, including theatres, an opera, the Schleswig-Holstein classical music festival, the heavy metal festival in Wacken, sailing, surfing, cycling, and the famous festivities of the “Kieler Woche” - one of the largest sailing events in Europe.

Applications

Applications should include a motivation letter (max. 2 pages long), CV, publication list, names and contact details of two referees (who are familiar with the applicant’s work), and copies of certificates. Deadline for applications is 20.01.2016. Applications should be sent as a single pdf-document by Email to Hinrich Schulenburg (hschulenburg@zoologie.uni-kiel.de).

Deadline for applications

20 January 2016.

Further questions

Send an Email to Hinrich Schulenburg (hschulenburg@zoologie.uni-kiel.de).

Hinrich Schulenburg

Zoological Institute Christian-Albrechts-Universitaet zu Kiel Am Botanischen Garten 1-9 24118 Kiel Germany Tel: +49-431-880-4143/4141 Fax: +49-431-880-2403 Email: hschulenburg@zoologie.uni-kiel.de Web: www.uni-kiel.de/zoologie/evoecogen/ Hinrich Schulenburg <hschulenburg@zoologie.uni-kiel.de>

LakeBaikal MolluscanRadiation

Short term post-doctoral position - Lake Baikal, Russia

9-12 month position from February 2016 working on molecular biology of an endemic molluscan radiation from Lake Baikal, Siberia. This project is a collaboration between molluscan taxonomist Tatiana Sitnikova and the molecular biology lab of Dmitri Sherbakov at the Limnological Institute, Russian Academy of Sciences, Irkutsk, Siberia, studying the endemic gastropods of the worlds most ancient and diverse freshwater lake. More specifically, the project aims at the elucidation of the discrepancies between the diversity patterns obtained from mitochondrial DNA and nuclear DNA data in order to obtain a better evolutionary history of the group and to fit it to the well-studied history of the Baikalian eco-system transformations.

The project is funded for Sanger sequencing and some NGS (obtaining depleted libraries or 2-3 transcriptoms). It also includes participation in 10-15 days expedition around Lake Baikal.

The successful applicant should have skills in molecular laboratory and analytical work (general lab routines, PCR, purification of amplicons, dealing with DNA sequences and phylogenetic analysis of various kinds). The applicant will also be involved into analysis and publication of the data already obtained.

The project will deliver publications with the successful applicant as co-author or lead author as appropriate.

The position includes salary at local level. Knowledge of Russian is not required, though willingness to learn is an advantage.

This is a great opportunity for a young researcher with a sense of adventure and good academic research skills. Siberia is a region of can-do optimism and Lake Baikal is one of the most interesting systems for an evolutionary biologist to study.

For further information on outputs from our lab see the Limnological institutes webpage http://lin.irk.ru and https://www.researchgate.net/profile/Dmitry_Sherbakov . Contact Professor Dmitry Sherbakov dysh007@gmail.com for specifics on the application process.

Ellinor Michel <e.michel@nhm.ac.uk>

MaxPlanck FishBehaviour

Collective Cognition in Animal Groups

We seek a postdoctoral scientist to explore experimentally how perception, learning and strategic decision-making enhance the capabilities of group-living animals. Due to their diversity of cognitive capabilities and social organisation, and their suitability for both laboratory and field studies, this study will focus on fish, which offer a powerful opportunity to explore the relationship between individual-level cognition and effective collective response in a wide range of ecologically-meaningful contexts. The successful candidate will have access to brand new state-of-the-art experimental facilities, including our sophisticated computational tracking, body posture and visual field reconstruction system. Embedded in a multidisciplinary research team, the candidate will have the opportunity to work closely with experts in computer vision and machine learning, as well as in biology, to explore sensory integration and decision-making in animal groups. The successful candidate will work both at Princeton University (where experiments will be conducted) and at the Department of Collective Behaviour at the Max Planck Institute for Ornithology, Konstanz, Germany.

Information Processing and Computation in Fish Schools

We seek an outstanding scientist for a postdoctoral position that brings together dynamical self-organisation and information-theoretic analyses to probe how collective intelligence emerges within animal groups, using fish schools as a model system. Rather than assume an ad-hoc model and tune it to âreproduce' group behaviours, in this project we will employ data-driven dimensionality-reduction and probabilistic models from neuroscience, combined with state-of-the art automated tracking and visual field reconstruction to investigate the computations performed by group members when making decisions under conditions of uncertainty and risk.

Investigating the Social Behavior of Fish Using Immersive Closed-Loop Virtual Reality

We seek an outstanding scientist for a postdoctoral position to develop, and employ, immersive 3D closed-loop virtual reality (VR) environments to investigate visually-mediated social behaviours in fish. Like other group-living vertebrates fish must respond rapidly to changing visual cues in order to effectively employ social information when making movement decisions. Consequently they are an excellent system for investigating the process by which complex, high-dimensional visual information is translated into low-level movement decisions. Candidates must hold a Ph.D. in computer science, robotics, biophysics, neuroscience, physics, or a related field. Expertise in developing closed-loop VR environments is not essential, but applicants must be skilled in C++ and/or Python and have experience with computer vision / 3D computer graphics.

Open Postdoctoral Fellowships

We seek outstanding postdoctoral candidates from any background to conduct research in experimental and/or theoretical studies of collective animal behaviour. We are particularly interested in quantitative studies of field and laboratory systems, although purely theoretically focused applicants are also encouraged to apply. Our department is a vibrant and highly international and interdisciplinary environment and we welcome informal inquiries. Multiple positions are available to be filled immediately. See also below for further funded projects.

Alex Jordan Principal Investigator Department of Collective Behaviour Max Planck Institute for Ornithology www.alexjordan.org collectivebehaviour.com

"Jordan, Alex" <ajordan@orn.mpg.de>

McGillU Montreal ComputationalGenomics

Postdoctoral position in computational genomics

A postdoctoral position is available immediately in the Computational Genomics Laboratory (http://functionalgenomics.ca), Lady Davis Institute of Medical Research and the Ludmer Centre for Neuroinformatics and Mental Health. The center focuses on understanding the genetic, epigenetic and environmental influences that shape brain development, including structure and function, and the risk for mental disorders. This Centre spans the Lady Davis Research Institute, the Douglas Mental Health University Institute and the Montreal Neurological Institute, all affiliated with McGill University, Montreal, Quebec, Canada.

Our lab uses genome-wide approaches to understand mechanisms regulating gene expression and RNA processing in the developing brain, their interplay with genetic and epigenetic factors, and how they cause disease. We work in an interdisciplinary environment, interacting with statisticians, physicists and molecular biologists. Successful candidates will conceive and develop algorithms and analytical approaches to integrate large genetic/epigenetic/expression datasets, generated both in-house and from public sources, primarily from next-generation sequencing technologies.

Qualifications and Experience We are looking for a very motivated individual capable of carrying out independent research, and to interact in a collaborative setting

-> Doctoral degree in computer science, bioinformatics, statistics, molecular biology, genetics or a related field

-> Strong programming skills are essential

-> Experience within one of the following areas is an asset, but not required: genomics, neuroscience, statistical interpretation and analysis of next-generation sequencing datasets.

For applying, please send a CV, a brief statement of scientific interest and contact information for at least two references to claudia.kleinman@mcgill.ca

cl.kleinman1@gmail.com

Minnesota EvolutionaryBiol

The College of Biological Sciences at the University of Minnesota is accepting applications for an independent postdoc – Grand Challenges in Biology post-doc program [link https://goo.gl/ca6CSY]. The award provides two years of funding to pursue an interdisciplinary project mentored by two or more faculty advisors (faculty advisors must be from more than one department). If you are interested, contact potential faculty mentors (https://cbs.umn.edu/research/faculty-research) – who can talk about ideas and potential collaborators.

This position has much to offer for an evolutionary biologist - Two years of independent funding, Minneapolis-St. Paul is a great place to live, and there is an active community of evolutionary biologists working on campus.

The application requires a short description of the proposed research, a 1 page statement on previous research, a CV, and letters of support from the proposed faculty advisors. The application deadline is soon – February 1st.

ybrandvain@gmail.com

MissouriBotanicalGardens ModelingGlobalChange

The Center for Conservation and Sustainable Development (CCSD) at the Missouri Botanical Garden seeks to hire a full-time postdoctoral scholar. The postdoc will work closely with Dr. Adam Smith in the CCSD's Global Change Program to develop methods for applying next-generation species distribution models to data that traditionally has been difficult to model. In collaboration with Dr. Smith the postdoc will 1) develop novel modeling algorithms; 2) test these algorithms with simulations and high-quality specimen data obtained in collaboration with taxonomists at the Missouri Botanical Garden; 3) prepare and submit manuscripts for publication; 4) develop R packages that encapsulate these novel methods; 5) craft project specifications for a programmer who will create stand-alone software using these methods; 6) actively consult with collaborators at

UC Berkeley. The successful candidate will:

* Have a solid background in applied mathematics and statistics (including Bayesian methods).

* Have expertise in R or related programming languages.

* Excellent communication skills, with experience presenting results and publishing in peer-reviewed journals.

* Understand and appreciate the difficulties of working with occurrence data that may have been collected in an opportunistic fashion, e.g., data from natural history museum specimens.

* Be enthusiastic about developing tools that enable conservation practitioners to avert loss of biodiversity and be able to translate complex ideas into straightforward procedures.

Candidates with a completed Ph.D. or that will soon graduate with a Ph.D. in ecology, wildlife biology, environmental science, statistics, or applied mathematics are encouraged to apply. Ideal start time is early 2016, but this is negotiable for applicants who may be graduating in the spring. The term for this grant-funded position will be 1 year, with renewal for an additional two years or more contingent on satisfactory performance. Salary will be commensurate with experience, and this position includes a comprehensive benefits package.

The position will be based in St. Louis, where a vibrant community of ecologists, conservation practitioners, and evolutionary biologists that interact through partnerships among MBG, Washington University, the University of Missouri-St. Louis, Saint Louis University, plus other area institutions. The position will be seated in the CCSD, which explores and implements new, science-based approaches to the conservation and sustainable use of plant diversity. CCSD's strategies for conservation are based on a sound, scientific understanding of the occurrence and distribution of plants. CCSD applies the knowledge of plant diversity accumulated by Missouri Botanical Garden researchers over many years, making that knowledge usable for conservation planning and decision-making. Operating under the auspices of the Garden and as part of its division of Science and Conservation, CCSD builds upon the Garden's institutional expertise, scientific programs, influence and resources.

To be considered, applicants should apply on-line by February 5, 2015 at: https://missouribotanicalgarden.applicantpro.com/jobs/310082-18077.html Please direct questions to Dr. Adam Smith (adam.smith@mobot.org).

Adam B. Smith, Ph.D. Assistant Scientist in Global Change Center for Conservation & Sustainable Development Missouri Botanical Garden PO Box 299 Saint Louis, MO 63166

314-577-9473 ext. 6314

http://www.earthskysea.org Adam Smith <Adam.Smith@mobot.org>

NewYorkU PlantSystemsBiol

Post-doctoral Position in Plant Systems Biology & Evolutionary Genomics

New York University Center for Genomics and Systems Biology

A post-doctoral position at NYU's Center for Genomics and Systems Biology - in the laboratory of Dr. Gloria Coruzzi - is available as part of our newly awarded 5 year DOE Grant entitled: EvoNet: A phylogenomic and systems biology approach to identify genes underlying plant survival in marginal, low-N soils.

The successful applicant will have skills and experience in Genomics, Bioinformatics and Phylogenetics. The position will include experimental/informatic analysis on NextGen datasets (e.g. overseeing laboratory work, planning, leading and conducting analyses on RNASeq data). Skills in R, Perl, Python or other programming language are strongly preferred. This position also includes Project Management duties, which involve coordinating scientific activities at six participating institutions, organizing group meetings, writing grant reports, paper writing and communicating our work in conferences and meetings.

This project involves the collaboration of plant systematists, molecular biologists, genome scientists and bioinformaticians. PI: Gloria Coruzzi (NYU Center for Genomics and Systems Biology); Co-PI(s): Rodrigo Gutierrez (Chile); Robert DeSalle (AMNH); Dennis W Stevenson (NYBG); W. Richard McCombie (CSHL); and Jean-Michel Ane & Heidi Kaeppler (UW-Madison).

Project description: This collaborative project exploits the genomes of extreme survivor plants adapted to thrive in marginal, extremely nitrogen (N) poor soils in the arid Chilean Andes. It uses a previously validated phylogenomic pipeline we previously developed (Lee et al 2011) and a paired species sampling strategy, to identify the genes that distinguish these extreme survivors in Chile from their related species adapted to similarly dry regions in California (CA) that are not constrained by N. These Ãâ¬$\mathring{A}extremesurvivor\tilde{A}\hat{a}$¬ï?‘$1_{\overline{2}}$ species cover the main branches in flowering plants. To maximize our ability to separate the trait-relevant signature from overall speciation events, the paired species sampling will cover multiple independent origins of the low-N adaptive trait. Our project aims are:

Aim 1. Paired-species collection and sequencing: Use a paired-species sampling strategy to capture genes involved in adaptations of extreme survivors which grow on dry, N-poor soils (Chile) compared to their paired species from California adapted only to drought.

Aim 2. Phylogenomic and Network Analysis: (A) Perform phylogenomic analysis of the extreme survivors in a paired-sampling strategy to identify genes supporting evolution of adaptations to marginal, low-N soils. (B) Perform gene network analysis based on gene expression and interactions.

Aim 3. Integrate Phylogenomic and Network signatures: Combine phylogenomic signals and gene networks to prioritize candidate genes associated with adaptations to marginal, low-N soils.

Aim 4. Functional validation of candidate genes: Functionally validate top-ranked candidate genes for low-N adaptations in the model plants Arabidopsis and Brachypodium.

This project presents an excellent opportunity to work with scientists from a broad range of expertise. It also includes opportunities to develop new methods and algortihms for integrating phylogenetics with systems biology approaches. Therefore, the ideal candidate would have excellent communication skills and would be motivated in developing novel analyses methods.

The Coruzzi lab

Coruzzi lab web page: http://coruzzilab.bio.nyu.edu/ Coruzzi Biology Faculty web page: http://biology.as.nyu.edu/object/GloriaCoruzzi.html is located in the historic and vibrant Greenwich village in downtown Manhattan in New York City. NYU is one of the world's leading research universities and its Center for Genomics and Systems Biology is housed in a new, state-of-the-art facility with 14 faculty members who study Genomics and Systems Biology across all kingdoms of life. For more information on the Center, please go to http://cgsb.as.nyu.edu Please send cover letter, resume and 3 letters of reference by email to: coruzzi.lab.nyu@gmail.com. Please mark the subject line of your email: DOE Post-doc

Applications received by December 31, 2015 will receive full consideration for the position.

Coruzzi Lab

New York University Center for Genomics and Systems Biology

12 Waverly Place, New York, NY 10003

Amanda Heim Lab Manager New York University Center for Genomics & Systems Biology 12 Waverly Place New York, NY 10003 212.998.3960

Amanda Heim <amanda.heim@nyu.edu>

NewZealand FishPhylogenetics

SUBJECT: Postdoc.NewZealand.Fish phylogenetics and community ecology

Postdoctoral Research Fellow Institute of Natural & Mathematical Sciences, College of Sciences, Massey University, Auckland, New Zealand

Apply here: http://massey-careers.massey.ac.nz/9100/-post-doctoral-research-fellow We are seeking a Postdoctoral Research Fellow to contribute to the project “Synergising ecology and evolution: discovering patterns of functional and phylogenetic diversity of New Zealand's marine fishes versus depth”, funded by the Marsden Fund, Royal Society of New Zealand. Applications close: 19 January (11:45pm, New Zealand Standard time).

Project Overview Biologists know least about the largest habitat on earth - the deep sea. Fundamental patterns of functional and phylogenetic biodiversity, from coastal waters to the abyss, have never been quantified. Do biodiversity trends in the ocean follow the patterns in alpha and beta diversity seen in the terrestrial environment? New ZealandÂs latitudinal range and nearshore continental shelf offers a unique opportunity to address trends in biodiversity and community structure and to disentangle the evolutionary and ecological drivers of these patterns. This project will complement an existing stratified and replicated depth by latitude dataset describing fish community composition. Specifically, this project aims to combine phylogenetic and functional information with knowledge of community composition for the fishes of New Zealand and to understand the ecological and evolutionary drivers of community composition from the sub-tropics to the sub-antarctic, and from the shallows to the abyss. The results of these analyses will have a major impact on the interpretation of the ecology and evolutionary history of New ZealandÂs fish communities and biodiversity patterns in the ocean, and will contribute novel methods of analyses for biodiversity research.

Position Overview We are seeking a motivated and innovative researcher, keen to make their mark in the field of quantitative biodiversity research. The ideal candidate will have a PhD in biology and will have experience in phylogenetics, diversification analyses, biogeographic analysis, comparative methods, trait-based analyses, ecological modeling, multivariate statistics, macroecology, and community ecology. Applicants with only a subset of these skills are encouraged to apply. A track record of publication in international journals and relevant statistical, computational and programming skills are expected. The appointed Fellow will conduct phylogenetic analyses of new and data-mined sequence data, and will combine these data with existing community data, and functional trait data to describe biodiversity patterns. The Fellow will contribute to the development of statistical methods to help test explicit hypotheses that will disentangle evolutionary and ecological drivers of diversity and turnover. The Fellow is not expected to have any prior experience in marine fieldwork, molecular genetic benchwork, or ichthyology. The appointee will be encouraged to supplement the primary research goals of the project with their own research objectives, in consultation with the wider research team that includes Prof. Marti J. Anderson (co-Primary Investigator, Chair in Statistics, Massey University), Dr. Clive Roberts (co-Primary Investigator, Head Curator of Fishes, Museum of New Zealand Te Papa Tongarewa), Dr. Libby Liggins (mentor/supervisory role, Lecturer in Marine Ecology, Massey University) and a recruited PhD candidate (responsible for functional trait analysis, Massey University). The Fellow will be expected and supported to publish and present their findings to international peers. Proficiency in written and spoken English is required.

Position specifics The position is three years, starting March 2016 (a later start date may be negotiated for an exceptional candidate). The Fellow will be based in the Institute of Natural and Mathematical Sciences (INMS) at Massey UniversityÂs campus in Auckland, New Zealand. INMS is a recently formed multi-disciplinary research and teaching Institute incorporating Biology, Chemistry, Computer Science, Mathematics, Physics and Statistics. In conjunction with world-class researchers in the closely-linked Institute for Advanced Study (IAS), INMS has special strengths in quantitative biology and ecology, evolution, genetics, mathematical biology, computational science and modelling of complex systems. Massey University is in the north of Auckland, with easy access to the city of Auckland (New ZealandÂs largest and most culturally diverse city) and recreational areas such as the harbour, islands, beaches, and forest parks. The Fellow will be joining a dynamic team of researchers working on the frontier of statistics, ecology, and evolution. The Fellow will also work closely with

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NHM London AncientDNA

Post-Doctoral Research Assistant in Ancient DNA of Pleistocene faunal remains.

Salary: Â£28,470 per annum plus benefits Contract: 36 months fixed term contract Location: Natural History Museum, London, UK. Closing date: 9am on Monday 7 December 2015

We are currently seeking applications for a PDRA to contribute to the Palaeolithic colonisation and cultural diversification in unfamiliar landscapes (UP-NORTH) project. The post-holder will be responsible to Professor Ian Barnes, and will work closely with Dr Rhiannon Stevens at UCL Institute of Archaeology. The candidate will have demonstrable knowledge and experience of generating and analyzing ancient DNA using next generation sequencing technologies.

For further information go to PDRA-UpNorth here: https://nhm.irecruittotal.com/CONFIG/NHM/StaticPages/CAC/SearchVacancy.aspx?EmploymentTypeID=0&Intranet=0 or contact i.barnes@nhm.ac.uk

“I.Barnes@nhm.ac.uk” <I.Barnes@nhm.ac.uk>

NIST RockvilleMD Bioinformatics

The US National Research Council offers a limited number of fellowships for work at NIST (my employer), based on a competitive review of proposals (http://sites.nationalacademies.org/pga/rap/). The award is extremely generous ($67K plus $3K travel allowance), the location is Rockville (MD), the time-period is 1 or 2 years, and the scope is flexible– so long as it is consistent with my interests and my ability to provide effective mentorship. These interests are in two main areas: computational studies (simulations, data analysis) of evolution, such as the role of mutation in evolution (e.g., [1-3]), Constructive Neutral Evolution [4], and diverse other aspects of molecular evolution from tree calibration to population genetics theory (e.g., [5-8]); and developing cyberinfrastructure to facilitate interoperability of data and software (e.g., [9, 10]). For instance, anything related to the works listed below, the Phylotastic project [10], structural variant-calling, or deep mutational scanning data, would be welcome.

I encourage you to consider applying if you are a US citizen or permanent resident with a Ph.D. and a compelling idea for a project. The upcoming deadline for NIST proposals is February 1, 2016, and there is another deadline August 1. If you are interested, contact me with a brief introduction and a pitch for your idea, and we'll go from there.

Arlin Stoltzfus (arlin@umd.edu)

Research Biologist, NIST (Genome-scale measurements group) Fellow, IBBR; Adj. Assoc. Prof., UMCP; IBBR, 9600 Gudelsky Drive, Rockville, MD, 20850 tel: 240 314 6208; web: www.molevol.org 1. Stoltzfus, A. and R.W. Norris. 2015. On the causes of evolutionary transition:transversion bias. MBE, in press (see http://bit.ly/1NU0fGC)

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10. Stoltzfus, A., H. Lapp, N. Matasci, et al. 2013. Phylotastic! Making tree-of-life knowledge accessible, reusable and convenient. BMC Bioinformatics 14:158. http://www.biomedcentral.com/1471- 2105/14/158

Arlin Stoltzfus (arlin@umd.edu) Research Biologist, NIST; Fellow, IBBR; Adj. Assoc. Prof., UMCP IBBR, 9600 Gudelsky Drive, Rockville, MD, 20850 tel: 240 314 6208; web: www.molevol.org arlin@umd.edu

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NorthCarolinaStateU AppliedEvolBiology

Postdoc: Applied Evolutionary Biology

PROJECT DESCRIPTION:

Selfish genetic elements have been studied for over a century, and as far back as the 1960's researchers became interested in using the power of selfish genetic elements to drive genes into pest species to suppress their impacts (Gould et al. 2006). Until recently, the focus of applied work was on naturally occurring elements. In the past decade some progress was made on developing synthetic elements that mimicked natural meiotic drive and selective embryo-killing, but de-novo creation of a gene-drive system in a pest species was elusive. With the harnessing of the bacterial CRISPR-Cas9 system in the past few years there has been a revolution brewing in this field (Esvelt et al. 2014, Oye et al. 2014). In March 2015 a pivotal article by Gantz and Bier (2015) came out in Science demonstrating a CRISPR-Cas9 construct in Drosophila with strong gene drive.

In the past month, two empirical papers came out that demonstrate CRISPR-Cas9 gene drive in the mosquito that transmits malaria and the mosquiot that transmits dengue (Gantz et al. 2015, Hammond et al. 2015). Not everyone is comfortable with these developments and there has even been a call for a moratorium on certain experiments. There are also concerns about nefarious use of the technology.

The bottom-line is that progress in molecular biology is ahead of the population genetic work needed to build systems that are less risky but accomplish changes in the public interest.

We have been funded by the NIH and the W. M. Keck Foundation to conduct this kind of population genetic research. Our focus has been on mosquitoes that transmit dengue and malaria, but we are also interested in other biological systems (There is hope that these selfish genetic elements can save endangered species like Hawaiian honeycreepers and specific seabirds (Gould 2008, Esvelt et al. 2014).

The postdoc in this position will build a set of simple to complex models to examine the expected dynamics of gene drive systems in mosquitoes and other taxa.

The most detailed model that we have developed simulates the population dynamics and population genetics of Aedes aegypti, the vector of dengue, in a city on the Amazon river, Iquitos, for which there are rich data sets on both mosquito dynamics and dengue epidemiology (e.g. Magori et al. 2009, Okamoto et al 2014). An accompanying epidemiological model is currently under development. The goals of two other postdocs in our group are to expand the mosquito model and the human epidemiology model to encompass the entire city of about 400,000 people. The postdoc in this new position will collaborate with the other postdocs to use these detailed models to test gene drive systems, but will also develop more generic models (e.g. Huang et al. 2010).

In addition to working on model development and analysis, the person in this position will have the opportunity to collaborate in an interdisciplinary research group composed of mosquito ecologists, disease epidemiologists, molecular biologists, biomathematicians, ethicists, and scientists from disease-endemic countries. We are dedicated to taking seriously the ethical and political issues surrounding this technology.

DESIREABLE SKILLS: A background in population genetics and the ability to program in C++ (or knowledge of a related programming language), and training in evaluation of mechanistic models.

TO APPLY: email a cover letter and CV to Fred_Gould@ncsu.edu

References:

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Huang, Y., Lloyd, A.L., Legros, M., Gould, F. 2010. Gene-drive into insect populations with age and spatial structure: a theoretical assessment. Evol. Appl. ISSN 1752-4571.

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OpenUIsrael EvolutionaryGenomics

Our group at the Open University, Raanana, Israel, invites applications for a postdoc position in Evolutionary Genomics.

Our group research interests are focused on Endosimbiotic Gene Transfer. In our research we use computational approach the study the abundance and significant of naturally occurring organelle-to-nucleus gene transfers.

Candidate qualifications: (1) Highly motivated person with a PhD degree in Molecular Evolution, Bioinformatics or related fields (2) Proficiency in computer programming (preferable - PERL/Python). (3) Any of following expertise is an advantage: phylogenomics, genomics, biostatistics. (3) Good oral and written communication skills (English is required). (4) Skills and motivation to communicate and interact with other scientists.

This position is funded by the German-Israeli grant (awarded to Dr. Hazkani-Covo and Prof. Dr. William Martin, Heinrich Heine University Duesseldorf, Germany). Applicant will have the opportunity to travel to the German partner lab. Initial appointment will be for 1 year with a possible extension to a total of 3 years.

Applicants should send curriculum vitae with a list of publications, a motivation statement and contact addresses of at least two referees to Dr. Einat Hazkani-Covo (einatco@openu.ac.il). For enquiries regarding the position please contact Dr. Einat Hazkani-Covo (einatco@openu.ac.il).

Dr. Einat Hazkani-Covo, Department of Natural and Life Sciences The Open University of Israel 1 University Road P.O Box 808 Ra'anana 43537 ISRAEL

Tel: 972-9-7780981 http://www.openu.ac.il/Personal_sites/einat-hazkani-covo/

PompeuFabraU Barcelona InsectEvoDevo

Postdoc position: "Origin of insect metamorphosis: dissection and evolution of themetamorphic gene toolkit"

OUR RESEARCH OBJECTIVE: Insects have undergone radical evolution in their development since theirorigination from arthropod ancestors, such that three types of metamorphosis haveemerged: ametaboly, hemimetaboly and holometaboly. These three forms ofmetamorphosis represent an evolving sequence from the primitive ametabolous(direct-developing) to hemimetabolous (incomplete metamorphosis) to the mostderived holometabolous type of metamorphosis (complete metamorphosis).Unfortunately, the nature of the changes underlying the appearance ofHolometaboly remains a puzzling problem in evolutionary and developmentalbiology. To this aim, the main goal of the EvolMeT project is to characterize themolecular mechanisms underlying the origin of complete holometabolanmetamorphosis.

ELIGIBILITY The successful applicant will hold a PhD in the biological sciences with a strongbackground in Drosophila genetics, and/or developmental biology. A provenexperience in molecular biology, and genetics is essential. Microscopy techniquesare desirable although not essential. We are looking for highly motivatedapplicants that feel comfortable undertaking the challenges of learning newexperimental techniques. You must have excellent scientific communication,presentation and writing skills, as well as very good critical and analytical problemsolving skills.

CONDITIONS We offer a two-year position, starting ideally by 01/01/2016. This position may be further extended, subject to satisfactory progress. We offer an exclusive working environment in a modern research institute with anexcellently equipped laboratory. The Institute of Evolutionary Biology (SpanishResearch Council-Pompeu Fabra University) (see http://www.ibe.upf-csic.es/) islocated in BarcelonaÂÂs seafront, adjacent to the Biomedical Parc of Barcelona(PRBB) and Hospital del Mar. The candidates will join the Evo-Devo Lab (PIs:Xavier Franch-Marro, David Martin and Elena Casacuberta).

If interested, please apply by sending a cover letter that describes the motivation to workon the project, a CV with detailed technical experiences, and contact information for atleast two academic references as PDF files to elena.casacuberta@ibe.upf-csic.es,xavier.franch@ibe.upf-csic.es, david.martin@ibe.upf-csic.es. Application can be inCatalan, Spanish or English.

ComunicaciÂÂ IBE <comunicacio@ibe.upf-csic.es>

RBG Kew OrchidEvolution

Early Career Research Fellowships (Sainsbury Orchid Fellowships) at RBG Kew

The Royal Botanic Gardens, Kew seeks outstanding postdoctoral candidates to take up two Early Career Research Fellowships focusing on orchid diversity, taxonomy, systematics and evolution. The successful candidates will establish their own independent research programmes closely aligned with Kew's Science Strategy, developing funding streams, producing excellent publications, and engaging fully with science life across the institution. They will be future leaders in the science disciplines pursued at Kew.

We seek applicants who are outstanding early career scientists with a PhD in a relevant subject area (awarded within the past eight years) and, ideally, some postdoctoral experience. Applicants will have a proven aptitude for delivering excellent science publications and demonstrated potential to raise science income. Applicants should also be outstanding and enthusiastic communicators who are ready to engage with students, peers and the general public.

Closing date for applications: 10 January 2016

For further details, follow this link: https://careers.kew.org/vacancy/early-career-research-fellow-sainsbury-orchid-fellow-241235.html W.Baker@kew.org

RiceU EvolutionHumanHealth

INDEPENDENT POSTDOCTORAL FELLOWSHIPS AT RICE UNIVERSITY

Rice University is pleased to announce the establishment of the Rice University Academy of Fellows (RUAF). This new program fosters intellectual exchange and advancement of research through the creation of an interdisciplinary community of Rice Academy Faculty Fellows and Rice Academy Postdoctoral Fellows (http://www.riceacademy.rice.edu). With the 2016-2017 cohort, the Rice Academy will focus on scholarship and creative activities broadly related to health. Academy Postdoctoral Fellows can be housed in any department at Rice University. Postdoctoral Fellows are appointed to a two-year term, and they take a concurrent complementary non-tenure track faculty appointment in an appropriate department at Rice. Applications are due January 11, 2016. The following faculty in the EEB program in the Department of BioSciences are interested in hosting and working with a Fellow:

Amy Dunham (aed4@rice.edu): impacts of conservation and development projects in Madagascar on human health and well being; to be co-hosted by a faculty member in anthropology (tbd); other interests - tropical ecology, conservation biology, evolutionary ecology applied to conservation issues in tropical rainforests. http://www.owlnet.rice.edu/~aed4/amydunham/ Scott Egan (scott.p.egan@rice.edu): eco-evolutionary dynamics, plant-insect interactions, evolution, speciation, population genetics and genomics, conservation and invasions. https://sites.google.com/site/scottpegan/ Volker Rudolf (volker.rudolf@rice.edu): Infectious disease; Community, population, & evolutionary ecology, climate change, biodiversity, host-pathogen dynamics. http://www.owlnet.rice.edu/~volker.rudolf/ Julia Saltz (julia.b.saltz@rice.edu): Development and evolution of individual differences in behavior, behavioral genetics, evolutionary feedbacks, phenotypic plasticity, learning. https://saltzlab.wordpress.com Rice Academy Postdoctoral and Faculty Fellows hold regular gatherings that support social interactions, as well as intellectual and academic pursuits. Fellows should attend regularly and present their work at least once a year. Professional development is a central focus, and Academy Postdoctoral Fellows will receive close mentorship in pursuit of the NIH K99 or other career development awards. The path to tenure-track professorships will be guided through Rice$B!G(Bs very successful $B!H(BNegotiating the Ideal Faculty Position$B!I(B workshops.

The standard stipend is $60,000. National standard stipends in a few research areas are above that level, and those departments may augment the stipend. Academy Fellows will be provided with an office, a computer, $5,000/year in a research fund, and access to university resources. Fellows who need substantial research infrastructure or supplies will generally work closely with a faculty mentor, who would supply research funding for appropriate projects of mutual interest. Academy Postdoctoral Fellows are encouraged to pursue outside funding when appropriate.

Prospective Academy Postdoctoral Fellows should have an exceptional record of scholarship, unusual promise for future intellectual achievement, and a commitment to build a community with the Rice Academy. Applicants should have completed all requirements for the doctorate between September 1, 2012, and August 31, 2016. All applications should be submitted electronically at https://jobs.rice.edu/postings/6090 by January 11, 2016. Rice Postdoctoral Fellows are expected to begin September 1, 2016.

Scott Egan <scott.p.egan@rice.edu>

SanDiegoZooGlobal CaptivePopulationGenomics

Post-doctoral Associate for San Diego Zoo Global

San Diego Zoo Global invites applications for a 3-year post-doctoral research associate to participate in a project focused on integrating molecular data into the genetic management of wildlife breeding programs. Specific aspects of the research will include analyzing genomic (SNP) datasets for captive breeding programs, modeling alternate approaches for integrating genomic data into pedigree-based breeding pair selection strategies, and developing custom genomic and pedigree-based software tools that can be used by non-experts managing wildlife breeding programs. This project has wide-reaching applications to in situ and ex situ conservation programs. The research associate will also be responsible for organizing and participating in training workshops for non-experts, administering and analyzing evaluation surveys at the beginning and end of the project period, and disseminating research through presentations and publications. This project is a collaboration with the

Latch Lab at the University of Wisconsin Milwaukee (http://www.uwm.edu/~latch).

Qualified applicants should have completed a Ph.D. in Bioinformatics, Computer Science, Statistics, Biology, Genetics, or a related field and have a strong background in genomic (SNP) analysis and/or computer modeling. Proficiency in computer modeling skills and one or more scripting languages will be necessary for testing alternate approaches for integrating genomic data into pedigree-based breeding pair selection strategies and for developing custom software tools. Experience with a C-based programming language and/or python are preferred. The applicant should have the ability to collaborate well and communicate scientific materials to non-scientists.

Opportunities exist for the position to be based at either the San Diego Zoo (San Diego, CA) or San Diego Zoo Safari Park (Escondido, CA). The application deadline is December 23rd. For more information or to apply go to: http://www.sandiegozoo.org/jobs/

Jamie A. Ivy, Ph.D. Population Biologist San Diego Zoo Global p. 619-557-3905 (Zoo) p. 760-738-5056 (Safari Park) p. 760-747-8702 x5709 (Institute) P.O. Box 120551 San Diego, CA 92112-0551

JIvy@sandiegozoo.org

SunYatsenU PlantMacroevolution

Macroevolution of Land Plants at SYSU V Exploring the link between genome evolution and plant diversity

Postdoctoral research positions (2 years) are open at the new research team “Macroevolution of Land Plants” led by Harald Schneider located at the School of Life Sciences, Sun Yatsen University, Guanzgou, Guangfdong, China. The position holder is expected to carry out a research program exploring the evolutionary consequences of polyploidy in selected groups of seed-free land plants, e.g. derived ferns. The research involves the integration of genomic evidence (e.g. transcriptome sequences), genome size (DNA C-values), chromosome numbers, and morphological evidence in a dated phylogenetic framework. The main issues addressed are (1) the consequences of polyploidy on the assembly of morphological disparity, (2) ecological and phylogenetic constraints in the assembly of polyploidy; and (3) intrinsic and extrinsic constraints on the accumulation of large genomes via polyploidy.

Key roles: carrying out research on the topic outlined at the postdoctoral level / First author of at least two publications in scientific journals with a SCI > 2.0 based on the research carried out / contribute to other publications of the research team / contribute to or lead the writing of grant proposals of the research team / presenting of the research results at international scientific meetings (e.g., IBC 2017) / contribute to the training of bachelor and master students / contribute to the success of the research team

Qualifications of the post-doctoral applicants Required: Phd in Biology (e.g., Evolutionary Sciences) or Bioinformatics/ General understanding of plant genomes and plant evolution/ Proven publication record (in English) / Good communication skills/ Ability to work in teams / Self motivated work habit

Preferred: Experience with the handling of transcriptome data or other next generation sequence data using bioinformatic pipelines / Experience in statistical analyses using R or similar platform/ Experience in phylogenetic analyses and/ or divergence time estimates/ Experience in plant cytogenetics including cytofluometry or chromosome painting

The call for positions will be open until the positions are filled. Interviews will be held based on availability.

For informal enquiries please contact Prof Harald Schneider (haralds@mail.sysu.edu.cn)

Prof Harald Schneider School of Life Sciences Sun Yat-Sen University Guangzou, Guangdong, China.

Prof Harald Schneider, PhD FLS School of Life Scienes, Centre of Ecology and Evolution Sun Yatsen University, Guangzhou, Guangdong, China & Department of Life Sciences Natural History Museum, London SW7 %BD, UK

Harald Schneider <h.schneider@nhm.ac.uk>

Texas BiomedicalResInst MalariaEvolution

Searching for an enthusiastic postdoctoral researcher to work on the biology of the malaria parasite, Plasmodium falciparum. Plasmodium parasites are of huge medical importance, causing ~700,000 deaths per year and millions of infections. P. falciparum parasites are a highly tractable organism which can be reared in the laboratory and placed under strong selection. This project will use a combination of flow cytometry, genome/transcriptome sequencing and experimental evolution to identify the genetic underpinnings of disease related traits of the parasite, including drug resistance, host-cell invasion and growth rate. A large component of this project will be based at new flow sorting facilities at Texas Biomed. The postdoctoral scientist will report to Dr. Ian Cheeseman. The successful applicant will join a new lab in a vigorous infectious disease program at Texas Biomed (including work on malaria, schistosomiasis, ebola, HIV, and hepatitis C). The Genetics department at Texas Biomed provides a stimulating environment with work on statistical and quantitative genetics, metabolomics, and proteomics and has outstanding computational, sequencing and wet lab facilities. San Antonio is a vibrant, rapidly growing city with an interactive research community.

RELEVANT PUBLICATIONS

Nair S, Nkhoma SC, Serre D, Zimmerman PA, Gorena K, Daniel BJ, Nosten F, Anderson TJ, Cheeseman IH. Single-cell genomics for dissection of complex malaria infections. Genome Res 2014; Jun; 24(6):1028-38. PMCID: PMC4032849

Nkhoma SC, Nair S, Cheeseman IH, Rohr-Allegrini C, Singlam S, Nosten F, Anderson TJ: Close kinship within multiple-genotype malaria parasite infections. Proc Biol Sci 2012; 279(1738):2589-2598. PMCID: PMC3350702.

Cheeseman IH, Miller BA, Nair S, Nkhoma S, Tan A, Tan JC, Al Saai S, Phyo AP, Moo CL, Lwin KM, McGready R, Ashley E, Imwong M, Stepniewska K, Yi P, Dondorp AM, Mayxay M, Newton PN, White NJ, Nosten F, Ferdig MT, Anderson TJ. A major genome region underlying artemisinin resistance in malaria. Science 2012; Apr 6; 336 (6077):79-82. PMCID: 22491853

Education REQUIRED: Ph.D. in genetics, parasitology, molecular biology or a related discipline.

Experience/Skills Required: Substantial experience in flow cytometry and cell culture work, need not be limited to work on malaria parasites.

Potential Hazards This position may involve exposure to cryogenics and infectious materials (BSL-2). Participation in a medical monitoring and surveillance program is required. Safety training and protective clothing, equipment and supplies will be provided.

Other This is a full-time salaried (exempt) position. Texas Biomedical Research Institute business hours are Monday through Friday - 8:00 a.m. to 5:00 p.m. Application packets are accepted electronically or in hard copy. A completed application packet is a requirement for all positions. Incomplete applications will not be accepted. EOE

Please apply online at http://www.txbiomed.org/-about/employment/job-detail?id=3D550 job ID: 15-079 Postdoctoral Scientist Genetics

ianc@txbiomed.org

Trondheim Norway EvolutionaryGenomics

A two-year postdoctoral position in evolutionary genomics funded by a grant from the Norwegian Research Council to Assistant Professor Arild Husby is available at the Centre for Biodiversity Dynamics (CBD), Department of Biology, < http://www.ntnu.edu/biology > NTNU, Norway.

Job description The aim of the project is to examine ecological adaptation at the molecular genetic level using already available SNP genotype data from 4000 individuals genotyped on a 200k SNP array. The data has been collected in a long-term study of a house sparrow model system consisting of insular populations at the coast of Norway, with extensive pedigrees and individual-level data on phenotypic trait values and fitness. The two main goals of the post doc holder will be to use the SNP data to test for signs of selection on the genomic level. This work will be combined with ongoing GWAS work to link signs of selection in the genome to the genetic variants underlying phenotypic traits, thereby providing a link between population genomic approaches and quantitative genetic work. The second aim is to use recently developed statistical methods (Ovaskainen et al. 2011, Genetics 109), Berg & Coop 2014, PLoS Genet 10) to test for polygenic adaption examining correlated changes in allele frequencies in traits known to be under divergent selection on different islands (Holand et al. 2011, Genet Res 93). Hence, the overall aim of the project is to provide insights into the molecular genetic basis of trait variation in natural populations. The successful candidate will have the possibility to develop his/her own ideas to approach the above issues, including opportunities for fieldwork and laboratory work.

The work will be carried out primarily in the research group of Assistant Professor Arild Husby, but will be in close collaboration with Associate Professor Henrik Jensen, and Professor Otso Ovaskainen. Ass. Prof. Husby and Prof. Ovaskainen are jointly based at the Centre for Biodiversity Dynamics (CBD), NTNU, and the Metapopulation Research Centre (MRC), University of Helsinki, whereas Ass. Prof. Jensen is based at CBD. Both CBD and MRC are Centres of excellence in Norway and Finland, respectively.

More information can be found here: www.ntnu.edu/-cbd, and here: http://www.helsinki.fi/science/-metapop/index.htm . The candidate will be employed at CBD (Department of Biology, NTNU) but will be expected to spend considerable time at MRC. The working language at both institutions is English.

For further information about the postdoctoral position please contact Assistant Professor Arild Husby (Arild.Husby@helsinki.fi, phone no. +358294157691). Informal enquiries encouraged!

Required qualifications and personal qualities Candidates must hold a PhD in biology and be able to document expertise in statistical/quantitative genetics and population genomics. Experience with handling data from next-generation sequencing and/or high-density SNP genotyping techniques and statistical analyses of such data is strongly desired and will be considered an advantage. The successful candidate must be able to work efficiently and goal-oriented both when working independently and when collaborating with others. We are looking for a highly motivated and enthusiastic candidate.

What we offer We can offer an exciting postdoctoral research project with focus on fundamental questions in evolutionary biology using state-of-the-art molecular genetic analyses. The postdoctoral researcher will carry out scientifically challenging research with good opportunities for development of her/his expertise. The successful candidate will benefit from a good working environment and the expertise of members in our research groups which span quantitative genetics, statistical genetics/genomics and mathematical modelling.

Preferred starting date is in February 2016 but this is negotiable.The appointment of the Postdoc will be made according to Norwegian guidelines for universities and university colleges and to the general regulations regarding university employees. NTNUÂs personnel policy objective is that the staff must reflect the composition of the population to the greatest possible extent.

The position as Postdoc is remunerated according to the Norwegian State salary scale. There is a 2% deduction for superannuation contribution.

Application The application with CV, pdfs of publications, reference letters and relevant certificates must be submitted electronically through this page. Applications submitted elsewhere will not be considered. Please indicate preferred starting date in your cover letter. The reference number of the position is: NT 84/15

Deadline for applying: January 15, 2016

Apply through this link:

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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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TuftsU AdaptationSpeciation

The Dopman Lab in the Department of Biology at Tufts University is seeking a Postdoctoral Researcher with interests in Speciation or Adaptive Evolution. Current interests and possible postdoctoral projects include phenology and thermotolerance evolution; circadian and seasonal rhythms; adaptation to climate change; "speciation genes" and genomic divergence; sex-chromosome evolution; ecological and behavioral isolating barriers; and parallel evolution. A PhD in evolutionary biology, genetics & genomics, or in a related field is required. Interested individuals should contact Erik Dopman (erik.dopman@tufts.edu) and provide a CV and a brief statement of prior and future research interests. Informal inquiries are welcomed. http://ase.tufts.edu/-biology/labs/dopman/Default.htm FELLOWSHIP INFORMATION

The NIH-funded Postdoctoral Fellowship position is available in the Training in Education and Critical Research Skills Program (TEACRS) at Tufts University. This NIH-funded program is designed to prepare talented postdoctoral trainees with the career skills needed to succeed in academic biological research. Trainees spend on average 75% of their time conducting bench research and 25% of their time in career development activities that will help them manage the multiple demands of a faculty position. Teaching skills are developed through programs involving mentored classroom assignments at minority-serving institutions in the Boston area. The training is supplemented by workshops and seminars on teaching methods, career opportunities in academia, and essential skills such as grant writing, mentoring, lab management and scientific presentations. The training components are sequenced to allow trainees to balance the activities and to build on previous experiences. TEACRS fellows receive up to four years of salary support and a yearly travel and supply allowance.

They will complete our program ready to manage a successful research program, teach, and balance the multi-faceted demands inherent in a career as an academic scientist. http://sackler.tufts.edu/Academics/-TEACRS-Welcome APPLICATION INFORMATION

The application deadline for positions beginning in the fall of 2016 is March 1. Applicants must be U.S. citizens or permanent residents with no more than two years of postdoctoral training at the time of their appointment to the program. Commitment to the goals of the program, strong academic and research credentials and an interest in teaching and mentoring will be important criteria used in the selection process.

WHY BOSTON, MASSACHUSETTS?

Tufts is located in the academic and intellectual hub of Boston, home to more than 60 distinguished colleges and universities. A truly multi-cultural city, it boasts the largest concentration of international students in the world, providing an unparalleled environment for study and research opportunities. In addition to the numerous colleges and universities, many of the world's leading biomedical research institutions and biotech companies have headquarters or branches based in and around Boston. Recreational activities are abundant and range from music, museums, sports, theatre and restaurants. The beaches of Cape Cod and the hiking trails and ski slopes of Maine, New Hampshire, and Vermont are only 2 to 3 hours away. In Boston, you will discover one of America's most cultural, stimulating, and livable cities.

"Erik.Dopman@tufts.edu" <Erik.Dopman@tufts.edu>

UAlgarve Portugal HybridizationPhylogenomics

Post-Doctoral Research Fellowship - 1 vacancy

Fellowship Reference: CCMAR/BPD/0025/2015

The Algarve Centre for Marine Sciences opens a position for a Post-doctoral research fellowship (BPD) within the project EXCL/AAG-GLO/0661/2012, also known as "Extant- Extant or extinct tipping points - climate changes drive genetic diversity and dynamics of range edge populations as evolutionary hotspots." financed by the Portuguese Foundation for Science and Technology - FCT/MCTES (PIDDAC) under the following conditions:

Scientific tasks: to use next generation sequencing (RNA-seq transcriptome) datasets and phylogenomic methods to address questions concerning the occurrence and extent of hybridization within a family of brown algae (Fucacaea, Phaeophyceae).

Scientific Orientation: Ester A. SerrÃ£o, Gareth Pearson, Cymon Cox, JoÃ£o Neiva (Univ. Algarve and CCMAR)

Work Place: The Algarve Centre of Marine Sciences (Faro, Portugal)

Requirements:

1. Must be fluent in spoken and written in English (the latter to be assessed from the motivation letter to be submitted with the application);

2. Must have a PhD and publications in an area related to the work plan.

Evaluation Criteria:

1. Experience in manipulation and analysis of large-scale sequence datasets and/or knowledge of phylogenetic/phylogenomic methodologies - 50%

2. Bioinformatics experience including familiarity with Unix-based systems, programming/scripting languages (e.g., R, perl/python or similar). - 50%

The jury will exercise the right to contact and interview candidates should they require further information or clarification about their application. In the event that the applicants do not have the necessary profile the jury reserves the right to close the call without any recruitment.

During the fellowship and in the event that the fellowship holder should resign, the jury reserves the right, upon convenience and opportunity, to assign the fellowship to the next applicant in accordance to the ranking position.

Grant conditions: The grant will have an initial duration of 5 months, starting in February 2016 eventually renewed for additional periods until the end of the research project and eventually renewed after the project with the financial support of FCT/MEC through national funds and when applicable through cofounding by FEDER, within the Partnership Agreement PT2020. The fellowship must be exclusively according to the Portuguese law 40/2004, of 18 of August (Scientific Research Fellowship holder statutes), Fellowship Regulation of the Portuguese Foundation for Science and Technology in force (www.fct.pt/apoios/bolsas/docs/-RegulamentoBolsasFCT2015.pdf) and the rules of CCMAR research grants http://www.ccmar.ualg.pt/home/-assets/files/Outros/Reg_bolsas.pdf . Monthly Maintenance Allowance: net 1495.00/per month - BPD, tax free (in accordance with the grant amounts set by the Portuguese Foundation for Science and Technology).

Application Period: From 23 December 2015 to 11 January 2016.

Application Documents: Applicants should submit a letter of motivation (written in english, and explaining the experience in each evaluation criteria), a copy of their PhD certificate, a detailed Curriculum Vitae, copies of their national identity card (or passport) and fiscal number, and the contacts (e-mail and phone) of 3 persons who can provide references.

Submmission of applications: Applications should be submitted by email to ccmar@ualg.pt indicating the reference CCMAR/BPD/0025/2015 (note that we can only accept applications sent through this email). You should only consider your application as validated only after receiving by email a confirmation from CCMAR.

Results: The results will be communicated in writing within 30 working days after the application deadline.

Jury responsible for the selection:

Ester A. SerrÃ£o, Gareth Pearson, JoÃ£o Neiva

informal contact: eserrao@ualg.pt

CCMAR's non-discrimination and equal access opportunities policy - No candidate can be privileged, benefited, jeopardised or private of any right or exempt of any claim in regards to descendent, age, gender, sexual orientation, marital status, economic situation, origin, social economy, genetic heritage, disability, chronic disease, nationality, ethnicity, territory of origin, language, religion, politics and ideological beliefs and union membership.

Faro, 7 December 2015

Ester SerrÃ£o <eserrao@ualg.pt>

UBristol MarineEnvDNA

SeaDNA - Assessing marine biodiversity and structure using environmental DNA: from groundtruthing to food web structure and stability.

We are looking for a postdoctoral researcher with interests in evolutionary biology and ecology to take a key role in a new £1M collaborative project studying environmental DNA (eDNA) in marine ecosystems. The overall objective of the project is to test the potential for eDNA as a tool for marine biodiversity assessment. The key aims of the project are to i) establish how long eDNA from fish and invertebrates persists in the marine environment before it is broken down beyond the point of detectability, 2) test the ability of eDNA to be used as a tool in surveying and monitoring marine species, through direct comparisons of eDNA data to those from traditional surveys, 3) use eDNA data for reconstructing food webs, test for stability in food webs over space and time. The project will combine experimental work on eDNA degradation in the laboratory with analyses of eDNA samples collected from European shelf seas and the Southern Ocean. The project is a partnership between the University of Bristol (Martin Genner), Salford University (Stefano Mariani), British Antarctic Survey (Geraint Tarling, Sophie Fielding and Will Goodall-Copestake), the Marine Biological Association (David Sims) and Imperial College (Eoin O'Gorman).

Key roles of will be undertaking experimental work on eDNA degradation in the laboratory, conducting analyses of eDNA samples collected from European shelf seas and the Southern Ocean, liaising closely with partners organisations to ensure project progression, disseminating research through talks and peer reviewed manuscripts, and contributing to project impact through engagement with research end-users. You should have a doctoral degree and should also have an aptitude for experimental design, and enthusiasm for aquarium-based experiments and fieldwork. You should also have experience of molecular laboratory work and knowledge of bioinformatics tools.. There is funding to support this post for 39 months, is Bristol based, and will start on 1 March 2016.

Closing Date 10 January 2014, with interviews in mid-late January. Salary £31656 to £35609 per annum. For the job description and information on how to apply, visit http://www.bris.ac.uk/jobs/find/ using the job reference code: ACAD101769

For informal enquiries please contact Dr Martin Genner (m.genner@bristol.ac.uk)

Dr Martin Genner School of Biological Sciences University of Bristol Bristol Life Sciences Building 24 Tyndall Avenue Bristol BS8 1TQ

Tel: +44 (0) 117 39 41182

M Genner <M.Genner@bristol.ac.uk>

UCalifornia Irvine PopulationGenomics

A postdoctoral scholar position is available in the laboratory of Dr. Kevin Thornton at University of California, Irvine.

Area of research: Population genetics of polygenic adaptation

Description of duties: The postdoc will be part of a project generally focused on the integration of population- and quantitative- genetic models of adaptation, and their implications for how we interpret patterns of standing genetic variation, results of association studies, etc. Within this project, there is room for considerable freedom related to modeling, parameter inference, and data analysis. The data analysis could have a focus on Drosophila and/or human population-genomic data.

Salary: $50,000/year in the first year. Salary is adjusted in subsequent years according to the NIH salary scale.

Required qualifications include a recent PhD in evolution, genetics, bioinformatics or a related field. The ideal candidate would have a background in population- and/or quantitative genetics, with a solid understanding of theory. Additionally, the candidate should have some programming experience. However, consideration will be given to any motivated applicant interested in evolutionary genomics.

Qualified candidates should submit curriculum vitae, the names and contact info of three references, and a cover letter explaining the candidate's interest in the position and overall research aims and accomplishments to the following on-line recruitment URL:

https://recruit.ap.uci.edu/apply/JPF03213 For more information about this position contact Dr. Kevin Thornton krthornt@uci.edu.

The University of California, Irvine is an Equal Opportunity/Affirmative Action Employer advancing inclusive excellence. All qualified applicants will receive consideration for employment without regard to race, color, religion, sex, sexual orientation, gender identity, national origin, disability, age, protected veteran status, or other protected categories covered by the UC nondiscrimination policy.

kevin.thornton.work@gmail.com

UCalifornia LosAngeles Conservation

The UCLA La Kretz Center for California Conservation Science (http://www.environment.ucla.edu/lakretz/) invites applications for its 2016 Postdoctoral Fellowship in California Conservation Science. Consistent with our mission, we seek a postdoctoral scholar who simultaneously conducts innovative research and interfaces with the conservation and management agencies that direct and lead California conservation.

Our emphasis is on biological conservation, and the successful candidate could work in any discipline that provides the scientific underpinnings for the preservation, protection, management, or restoration of at-risk species, environments, or ecological communities in California. We will consider candidates who have recently completed their PhD, or will have completed it by August 2016. We envision hiring at least one Fellow each year, building a team of conservation scientists with a passion for California and its biodiversity.

The La Kretz Fellowship is for two years, subject to review after the first year. Our expected start date is late summer, 2016. The successful applicant will be expected to conduct research that bridges the interests of at least one UCLA faculty member who is also a La Kretz affiliate (http://www.environment.ucla.edu/lakretz/people/affiliates.asp) with priority science concerns of resource management agencies (broadly defined) in California. We also anticipate that the Fellow will also work with Brad Shaffer, Director of the La Kretz Center, to help develop collaborative research projects that further the mission of the Center. The position has an annual salary of approximately $42,000 plus full benefits and modest research support (approximately $5,000/year). Fellow have the option to reside at the newly renovated La Kretz Field Station (http://www.environment.ucla.edu/lakretz/fieldstation/), located in the Santa Monica Mountains about 25 miles from campus, should it fit with their research objectives. Several of our partner agencies have expressed interest in potential join funding for candidates and projects, should such funding be available. Joint funding is neither necessary nor guaranteed, but we encourage candidates to contact relevant partner agencies to explore such options as they develop their proposals. In support of such co-funding opportunities, our partners listed below have expressed interest in co-funding a La Kretz Center fellow :

Institution or Agency Name Email

The Nature Conservancy Sophie Parker sophie_parker@tnc.org

LA Natural History Museum Luis Chiappe lchiappe@nhm.org

U.S. Geological Survey Robert Fisher rfisher@usgs.gov

US Bureau of Land Management Mike Westphal mwestpha@blm.gov

US Fish and Wildlife Service Cat Darst cat_darst@fws.gov

Tejon Ranch Conservancy Mike White mwhite@tejonconservancy.org

Nature Reserve of Orange County Milan Mitrovich mitrovich@naturereserveoc.org

National Park Service Katy Delaney katy_delaney@nps.gov

National Park Service Seth Riley seth_riley@nps.gov

Department of Defense Robert Lovich robert.lovich@navy.mil

Interested candidates should submit a cover letter, CV, a short (1-2 page) description of their research and management accomplishments, a 2 page proposal (single spaced, plus references) description of their proposed research including potential faculty and agency mentor(s), and copies of two publications, all as a single PDF file, by email to Mario Colon, Administrative Assistant, at mario.colon@ucla.edu. You should also have three letters of recommendation, including one from your Ph.D. advisor, sent under separate emails with the subject line 'La Kretz Postdoc letter for XXX (your last name)'. The deadline for completed applications is 4 January 2016. E-mail questions to Mario or to Brad Shaffer (Director of the La Kretz Center) at brad.shaffer@ucla.edu.

Mario Colon I Administrative Assistant I UCLA La Kretz Center for California Conservation Science 818-519-7740 I mario.colon@ucla.edu I http://www.environment.ucla.edu/lakretz/ Mario Colon <mario.colon@ucla.edu>

UCalifornia SanFrancisco MalariaPopGenetics 2

Postdoc Position available in Malaria Population Genetics at UC San Francisco

A postdoctoral position is available in the laboratory of Bryan Greenhouse, MD, MA in the Division of Infectious Diseases at U.C. San Francisco. The current position will focus on analysis of parasite genetics and epidemiologic data to characterize transmission and evolution of malaria parasites. The successful candidate will have the opportunity to work closely with a diverse team of scientists at UCSF and international collaborators on a number of exciting projects. This research includes work in malaria elimination regions, where densely sampled genetic data will be used to construct transmission networks, to studies in areas with higher malaria burden leveraging broader scale spatial variation in genetic diversity. The fellow will be expected to develop and extend computational methods for deriving epidemiologically relevant information on malaria transmission from genetic, spatial, and epidemiologic data, and will be encouraged to develop an independent line of work under the mentorship of Bryan Greenhouse and co-mentorship of Rasmus Nielsen (U.C. Berkeley). Our work is directly connected to on-the-ground malaria control and elimination efforts, and the scientific output from this position is expected to directly affect interventions in the field in addition to leading to academic publications. Competitive salary including full benefits will be provided commensurate with experience and qualifications.

Essential Skills

- PhD in a relevant field (e.g. population genetics, computational biology, infectious disease dynamics)

- Strong background in population genetics

- Strong statistical and computational skills

- Demonstrated ability to produce independent, creative work

- Ability to work well as member of a team

- Strong written and oral communication skills

Helpful Skills

- Experience with geostatistical data analysis

- Experience in analysis/modelling of pathogen dynamics

- Experience with implementing Markov Chain Monte Carlo (MCMC)

- Familiarity with performance and development laboratory genetic/genomic assays and data

To Apply: Please send a CV including publications, brief statement of research/career interests, and contact information for 3 references to Bryan Greenhouse, MD, MA at bryan.greenhouse@ucsf.edu

“Greenhouse, Bryan” <bryan.greenhouse@ucsf.edu>

UCollege London TetrapodEvolution

University College London: Postdoctoral Research Associate in Tetrapod Modularity and Morphological Evolution

We are currently accepting applications for a European Research Council-funded 30-month postdoctoral researcher post (with possibility of extension) to reconstruct morphological evolution and phenotypic modularity across basal amniotes and non-archosauromorph sauropsids, including squamates and parareptiles, using 3-D surface morphometrics. The successful applicant will be employed to work in Dr. Anjali Goswami's lab as part of a large team conducting a extensive quantitative analysis of evolutionary rates, morphological disparity, and phenotypic integration and modularity across tetrapods through deep time. The postdoctoral researcher will focus on basal amniotes and non-archosauromorph sauropsids and will be responsible for building a comprehensive dataset of 3-D images spanning their living and extinct diversity and extracting surface morphometric data for crania, mandibles, and limbs. With these data, they will conduct extensive analyses to reconstruct the patterns and processes underlying ecomorphological evolution and identify the major intrinsic and extrinsic factors shaping clade diversity. Analyses will include evolutionary rates, morphological disparity, and phenotypic modularity, as well as related topics. Further duties will involve supervision of short-term undergraduate and Master's student projects, assistance in field expeditions, and uploading new data to online resources for free dissemination. This post is now open for applications, with a deadline of February 2, 2016. Further details and link to the online application form can be) found at goswamilab.com. Informal enquiries can be directed to Dr. Anjali Goswami (a.goswami@ucl.ac.uk), or speak to Dr. Goswami in person at SICB in Portland.

Dr. Anjali Goswami Reader in Palaeobiology Department of Genetics, Evolution, and Environment and Department of Earth Sciences University College London Darwin Building 218A Gower Street London WC1E 6BT +44 (0)20 7679 2190 www.goswamilab.com “Goswami, Anjali” <a.goswami@ucl.ac.uk>

UCopenhagen AntEvoDevo

Two Postdoctoral Positions in neural development of eusocial insects, Section for Ecology and Evolution, Department of Biology, University of Copenhagen

The Centre for Social Evolution, Department of Biology, University of Copenhagen, is offering two postdoctoral positions starting on 1 May 2016 or as soon as possible thereafter. The positions are for 2 years.

Project description

Research will focus on the ontogeny of gene-regulatory networks during larval development in ants and other eusocial insects, and on environmental factors that epigenetically determine canalized and plastic caste developmental pathways.

The projects will use comparative genomics and transcriptomics tools to investigate gene expression/regulation and will have bioinformatics support from other group members in Copenhagen and at BGI-Shenzhen.

We hope to attract both a developmental biologists and a neurobiologist to cover complementary angles in this 5-year research program, funded by a grant from the Lundbeck Foundation to Dr. Guojie Zhang.

General job description * Independently carry out and publish cutting edge research * Present results in national and international congresses and scientific meetings * Limited participation in teaching and dissemination activities of the Centre

Required qualifications * A PhD degree within developmental biology, neurobiology, molecular biology or related fields * Relevant lab expertise in tissue dissection and molecular biology techniques * A convincing publication track record * Explicit interests in being part of an interdisciplinary team * Fluent spoken and written English * Excellent communication and interpersonal skills

http://employment.ku.dk/faculty/?show=791145 Guojie Zhang, PhD Assistant Professor Department of Biology, University of Copenhagen Universitetsparken 15, 2100 Copenhagen, Denmark Email guojie.zhang@bio.ku.dk Phone: +45 91855431 and Associate Director of National Genbank BGI-Shenzhen, Beishan Industrial Zone, Shenzhen , China Email: zhanggj@genomics.cn Phone: +85 13914140493 Webpage: https://zhanggj.cngb.org/home/ Guojie Zhang <guojie.zhang@bio.ku.dk>

UFlorida CtenoEvoGeno

POSTDOCTORAL POSITION DEEPC: Diversity, Evolution, and EcoPhysiology of Ctenophores

An NSF-funded postdoctoral research position is currently available in the Ryan group at the Whitney Laboratory for Marine Bioscience in Saint Augustine, Florida (part of the University of Florida). The position is part of the NSF-funded Diversity, Evolution, and EcoPhysiology of Ctenophores (DEEPC) project. The goal of the project is to understand evolution and diversification of Ctenophora using cutting-edge genomic analyses and the deep-sea habitat as the generating force of novel adaptations. We are collecting and generating transcriptomes and genomes from many ctenophore species with habitat depths down to 4000 meters below the surface. The postdoctoral associate will use these molecular data in a phylogenetic context to identify specific genetic events that underlie physiological tolerances and adaptations to the unique selective pressures of life in the deep sea.

Candidates should have or be close to obtaining a Ph.D. in bioinformatics, computational biology, genetics, evolutionary biology, ecology, or a closely related field. Skills in programming, phylogenetics, statistical genetics, and/or the application of computational methods to genomic data are desired. Familiarity with detecting episodic diversifying selection using techniques such as branch-site models is highly desirable. Candidates from groups that are traditionally underrepresented in the sciences are strongly encouraged to apply.

Interested applicants should submit a curriculum vitae, a detailed letter of interest, and the names of three potential referees to Joseph Ryan at joseph.ryan@whitney.ufl.edu by January 1, 2016.

Ryan Group: http://ryanlab.whitney.ufl.edu/- Whitney Lab: http://www.whitney.ufl.edu/ "ctenopalooza@whitney.ufl.edu" <ctenopalooza@whitney.ufl.edu>

UFlorida EvolutionAnimalWeapons

Post-doctoral position in the phylogenetics of the Coreidae (leaf-footed bugs)

A post-doc position is available at the University of Florida (Gainesville, Florida) to work with Drs. Christine Miller and Rebecca Kimball on the phylogeny and evolution of the Coreidae. There are more than 2000 species of these insects worldwide, and male hind femurs (a sexually-selected weapon) are impressively diverse in size and shape. Males in many species use their hind legs as weapons to wrestle over access to females and territories. A major goal of this project is to examine the evolutionary interplay between fighting style and weapon diversification.

This project will involve sequence capture and next-generation sequencing of 1000's of loci from morphologically diverse members of the Coreidae, along with morphological differences in limb morphology, and behavioral assays of fighting styles. The phylogeny will then be used to test hypotheses about the evolution of morphological traits. The postdoc will be responsible for helping to develop sequence probes, obtaining specimens for analysis, library construction and sequence capture, sequence capture, phylogenetic analyses, and testing hypotheses about trait evolution. In addition, the postdoc will help in behavioral assays and microevolutionary studies to understand the incipient stages of weapon diversification.

Integration of research and education is an important element of the post-doctoral position. The postdoc will receive training in innovative teaching methods, including bringing authentic research into the classroom through CURE (Classroom-Undergraduate Research Experience) courses. These courses have the potential to engage dozens of undergraduates in the scientific process including data collection and interpretation. The post-doc should expect to co-teach one of these CURE courses each year. Further, the post-doc will engage in broader impact activities including public outreach through Bug Fest at the University of Florida and public speaking in other venues.

Candidates should have completed a PhD (or will very soon) and have a good knowledge of phylogenetic theory, analyses and molecular techniques. Ideal candidates will also have experience in bioinformatics, computational phylogenetics, managing large phylogenetic datasets, comparative methods and/or animal behavior studies.

Questions and applications should be addressed to Christine W. Miller, cwmiller@ufl.edu. Applications should include: 1) a cover letter outlining your research experiences, interests and career goals; 2) a C.V. including the names and contact information for at least 3 references; and 3) copies of up to 3 publications or manuscripts in review. Applications received by December 15, 2015 will receive the highest consideration but applications through January 1, 2016 may also be considered. The position could begin as early as March 1, 2016.

Christine W. Miller | University of Florida

Assistant Professor of Entomology and Nematology

phone: (352) 273-3917 web: www.MillerLab.net facebook: Miller Lab of Evolutionary Ecology

"Miller, Christine W." <cwmiller@ufl.edu>

UHaifa LocalAdaptation

We invite candidates to apply for two postdoctoral fellowships on local adaptation, phenotypic plasticity and gene expression on two closely related species of fire salamanders -Salamandra infraimmaculata in Israel and Salamandra salamandra in Germany (see abstract below). This is a joint project funded by DIP (German-Israeli Project) in collaboration with Leon Blaustein (University of Haifa, Israel), Alan R. Templeton (University of Haifa, Israel), Sebastian Steinfartz (Technical University of Braunschweig), and Arne Nolte (Max Plank Institute for Evolutionary Biology, Plon). The title and abstract of the grant that funds this project is pasted below. The successful candidate(s) will be responsible largely for designing and conducting the ecological experiments and conducting and analyzing gene expression patterns. Ideally, one postdoc will have expertise in experimental and quantitative ecology (experience in amphibian ecology a plus but not essential) and the second postdoc will have expertise in ecological genomics. The work is largely to conduct research in Israel, and the opportunity exists to spend 1-2 months per year in Germany to conduct ecological field experiments and lab work on gene expression. Interested candidates should send a letter explaining research interests and how their background fits to this study, (2) cv and (3) arrange 2-3 letters of recommendation to both Leon Blaustein (leon@research.haifa.ac.il) and Alan Templeton (temple_a@wustl.edu).

Ecological genomics: Analysis of gene expression underlying parallel habitat adaptation in distinct salamander species

Abstract In a continuously changing world, adaptation to new or altering environmental conditions is one of the most elementary and important biological processes. Although we have much data on the consequences of habitat adaptation at the phenotypic and population structure levels, we are currently missing, with a few exceptions, deeper insights into the genetic architecture of habitat-dependent adaptation. The study of parallel adaptive evolution can illuminate underlying processes and mechanisms. Unlike any other vertebrate group, amphibian species can show a fascinating breadth of habitat-specific adaptations to aquatic and terrestrial habitats. The research teams of this proposal have studied parallel ecological adaptation to larval reproductive habitats in two distinct species of fire salamanders - Salamandra salamandra in Germany and Salamandra infraimmaculata in Israel. By integrating a strong ecological context with genomic approaches, this research proposal aims at extending the ecological-genetic framework of parallel habitat adaptation to the level of the transcriptome in order to simultaneously screen a large number of genes for patterns of evolutionary divergence. We will design species-specific oligonucleotide microarrays based on EST sequences of the larval transcriptomes for each species. These microarrays can then be used to analyze gene expression patterns under fully natural conditions and in experimental setups, whereby analyses are inspired by field studies that analyze the ecology of salamander larvae. As salamander larvae are accessible in large numbers and can be easily manipulated in common environment experiments, this study system is suited to explore gene-expression responses to habitat-specific cues or selection pressures in dedicated experiments reflecting distinct larval habitat types and ecological parameters. The resulting data will reveal whether plastic phenotypes contribute to adaptive phenotypic change and whether they are enhanced by the emergence of genetically fixed traits. In addition to traditional computational methods, we shall use a newly developed individual-centered approach, using a new vector-correlation measure to identify genes that are co-expressed in individuals as opposed to differential expression of genes across populations.

Leon Blaustein

Director, Kadas Green Roofs Ecology Center Head, Community Ecology Laboratory Institute of Evolution and Department of Evolutionary & Environmental Biology Faculty of Natural Sciences, University of Haifa 199 Abba Hushi Rd, Haifa, 3498838, Israel Tel. 972-4-8240736 (office); 972-4-9998881 (home) Cell:

054-268-8290; Institute Fax: 972-4-8246554 http://leonblaustein.wikidot.com http://kadasgre.haifa.ac.il Alan R. Templeton Charles Rebstock Professor Emeritus of Biology and Genetics Professor of Evolutionary and Environmental Biology

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

http://pages.wustl.edu/templeton

UIowa InsectEvolution

The Forbes Lab in the Department of Biology at the University of Iowa is seeking a highly motivated evolutionary ecologist with an interest in tropical insect diversity and expertise in population genomics for a 2-3 year postdoctoral position funded by NSF's Dimensions of Biodiversity Program.

Job Summary: The aim of the project is to examine patterns of present day and historical gene flow among species in the tephritid fruit fly genus Blepharoneura and the same for the Bellopius parasitoid wasps that attack Blepharoneura flies. These flies and wasps are highly host-specific, incredibly diverse, and many species often overlap in their apparent niche space. A major goal is to understand why these insects are so diverse. The postdoc will develop and score double-digest RAD markers for several existing fly and wasp collections from across Central and South America, use those data to model gene flow and migration within each fly and wasp species, and collaborate with other project participants to test hypotheses regarding species interactions and the origin of reproductive isolation in these hyper-diverse insect systems. More information about this system can be found in the following two publications:

http://www.sciencemag.org/content/320/5878/928.short http://www.sciencemag.org/content/343/6176/1240.short

Education required: * PhD in evolutionary biology or closely related field

Desirable Qualifications: * Experience developing and working with RAD-based marker system (or similar marker system) in non-model organisms * Strong background in population genetics / genomics * Interest in diversification, insect evolutionary ecology, insect population genomics, or related field * Interest in working as part of a collaborative research team

Preferred Starting date: September 2016 (negotiable)

Application Deadline: April 15th, 2016, or until position is filled

How to apply: send C.V., a letter of inquiry, two representative publications (if available), and contact information for three potential referees to: andrew-forbes@uiowa.edu

"andrew-forbes@uiowa.edu" <andrew-forbes@uiowa.edu>

UKentucky QuantitativeEvolutionEcol

The Van Cleve lab in the Department of Biology (http://vancleve.theoretical.bio) at the University of Kentucky is seeking a Postdoctoral Scholar broadly interested in quantitative approaches to social evolution, evolutionary ecology, and evolutionary genetics. Part of the position is funded by a collaborative grant from the National Academies Keck Futures Initiative to work on new theoretical approaches to social evolution at the molecular genetic and genomic scale; the partners in the collaboration are the Akcay (http://akcay.bio.upenn.edu/) and Linksvayer (http://sites.sas.upenn.edu/linksvayer-lab) labs at the University of Pennsylvania. Specific research projects for the remainder of the position are flexible and can complement the interests of the individual Postdoctoral Scholar.

The successful candidate will have a Ph.D., a strong quantitative and biological background, experience in programming and modeling, and a record of publication that reflects the ability to conduct original and independent research.

The start date is flexible, though a prospective start date sometime in the Spring Semester 2016 is preferred. The position is funded for two years with review after the first year and further renewal contingent on funding. Salary is commensurate with experience and includes benefits.

Interested applicants should submit a statement describing their research interests (Cover Letter) and a CV including contact information for three references (Curriculum Vita).

Review of applications will begin immediately and will continue until the position is filled. For additional information regarding the position, please contact Jeremy Van Cleve (jvancleve@uky.edu).

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.

– Jeremy Van Cleve

Assistant Professor Department of Biology University of Kentucky E-mail: jvancleve@uky.edu Webpage: http://vancleve.theoretical.bio Phone: (859) 218-3020

"jvancleve@uky.edu" <jvancleve@uky.edu>

ULB Belgium FellowshipsForRefugees

Please find below an announcement for postdoctoral fellowships for refugees at the ULB (Université libre de Bruxelles) in Belgium. Evolutionary biologists fleeing war-torn countries (particularly Iraq and Syria) are welcome to apply.

https://www.ulb.ac.be/solidaire/docs/APPEL-CANDIDATURES.pdf ONE-YEAR (RENEWABLE) POST-DOCTORAL KHALED AL'AS-AD FELLOWSHIPS, FOR REFUGEES HOLDING A PH.D

ELIGIBILITY: The applicant: - must have refugee status or, at the moment they apply for the fellowship, have submitted an application for refugee to the immigration office of a member state of the European Union; - must not have resided or carried out their main activity (work, studies, etc.) in Belgium for more than 24 months in the 3 years immediately preceding recruitment (mobility rule).

APPLICATIONS: Applications must be sent by email to Angélique Greindl (agreindl@ulb.ac.be) by February 15th 2016 at the latest. Applications must include: - A research plan describing the scientific framework, the questions to be addressed and the methodology. - A copy of the PhD diploma or proof that the candidate successfully passed all exams related to the PhD programme. If these documents cannot be provided, applicants will have to provide a clear career description proving that they have at least four years of full-time research experience by the time of the call for applications. - A CV, including a list of publications. - Two letters of reference from scientists working in the same field including, if possible, one from their PhD supervisor. - A letter of acceptance from a member of ULB academic staff confirming that the candidate, if successful, will be welcome in their group and be offered the appropriate scientific environment. - A copy of the applicant's passport, a copy of the document confirming refugee status if this has already been granted, and, if the applicant is already in Belgium, a copy of an official document confirming date of entry to Belgium. In the event of a successful application, the fellowship will be awarded subject to the obtaining of refugee status.

The Research Department (agreindl@ulb.ac.be) and the International Service in the ULB's External Relations Department can help candidates identify and contact members of ULB academic staff working in their field, in order to complete their application and design their research project.

SELECTION PROCEDURE: End February/early March, applications will be submitted to the Board of the Research Council, comprising members of academic staff from the main research domains (Human and Social Sciences, Science and Technology, Life Sciences) (http://www.ulb.ac.be/ulb/greffe/documents/docs/BUREAU-CONSEIL-RECHERCHE.pdf), and expanded to include the Vice-Rector for International Relations and the Vice-Rector in charge of the coordination of the ULB's actions in favour of Syrian and Iraqi refugees. The panel members will receive a copy of all applications at least two weeks before the panel meeting. They will be asked to make their selection by ranking applications on the basis of the following three criteria: the quality of the applicant, the quality of the research project and the quality of the scientific environment.

– Jean-François Flot, Ph.D. Evolutionary Biology & Ecology - C.P. 160/12 Université Libre de Bruxelles Avenue F.D. Roosevelt 50 B-1050 Brussels - Belgium http://ebe.ulb.ac.be/ebe/Flot.html "jflot@ulb.ac.be" <jflot@ulb.ac.be>

UMinnesota EvolQuantGenetics 2

An energetic postdoctoral researcher is sought as a colleague in an NSF-funded project in the field of evolutionary quantitative genetics.

The goal of the research is to evaluate the immediate capacity for ongoing adaptation, as well the extent to which that capacity is realized, within natural plant populations. This study uses quantitative genetic approaches implemented in field experiments in Minnesota and Iowa and focuses on Chamaecrista fasciculata, an annual plant with a native distribution spanning eastern North America.

Qualifications for this position include: Ph.D. in evolutionary biology or related field; strong background in statistics, including experimental design and analysis of data, especially with R; experience with sizeable experiments in the field; evidence of success in completing research through publication. The position is available as early as March 15, 2016, though later start dates can be considered, and has a duration of 2 years with the possibility of extension.

Review of applications is ongoing and will continue until a suitable candidate is found. Interested individuals may contact Ruth Shaw (shawx016@umn.edu) for further information. Applications including C.V., statement of research interests, and names and email addresses of 3 references may be submitted to: http://-www1.umn.edu/ohr/employment/ The position number is 305224.

As an institution committed to demonstrating excellence through diversity, the College of Biological Sciences of the University of Minnesota is committed to hiring diverse faculty and staff, and actively encourages candidates from historically underrepresented groups to apply.

Ruth G. Shaw Professor and Editor in Chief, Evolution Dept of Ecology, Evolution and Behavior 100 Ecology 1987 Upper Buford Circle University of Minnesota St. Paul MN 55108

Ruth Shaw <shawx016@umn.edu>

UNevada Reno MultispeciesMutualisms

A postdoctoral position is available to work in Elizabeth Pringle's lab on the chemical and evolutionary ecology of plant-ant-hemipteran interactions. Our aim is to understand how mutualisms maintained by direct and indirect metabolic exchanges drive eco-evolutionary feedbacks across scales of ecological organization, from organism to ecosystem. To do this, we combine greenhouse and field experiments with chemical and molecular approaches, including evolutionary genetics and metabolomics. A particular area of interest is determining the extent and character of genetic variation in plant phloem chemistry and its effects across multiple trophic levels.

The start date is September 2016, with some flexibility in either direction. Applicants should have a PhD in biology or a related field. The ideal candidate would have training in LC/MS metabolomics and/or evolutionary genetics. A strong interest in the ecology of plants and arthropods is required.

Please contact Beth Pringle (epringle@unr.edu) directly to discuss this position. More details about the lab can be found at www.multimutualism.org . bethpringle@gmail.com

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UNewSouthWales EvolutionGender

We are seeking to appoint a Postdoctoral Research Associate to work on an Australian Research Council Discovery Project titled “On the origins and persistence of gender: combining evolutionary and economic approaches to study sex differences and cultural variations”.

The project is a collaboration between Scientia Professor Rob Brooks (Evolution, School of Biological, Earth and Environmental Sciences UNSW), Associate Professor Pauline Grosjean (Economics, UNSW Business School) and Professor Paul Seabright (Institute of Advanced Studies, Toulouse). Both Brooks and Grosjean are members of UNSW's Evolution & Ecology Research Centre (E&ERC).

This research involves two large field projects; one in the Solomon Islands and another in Australia.

You will be based in Australia and expected to travel to the Solomon Islands for the field project. You will be expected to organise, support and participate in the research concerning sex differences in behavior and gendered behavior at the interface of economics, evolutionary biology and psychology.

* Fixed Term (3 years) * Full Time * Expected commencement in June 2016 (earlier start negotiable)

To be successful in this role you will have:

* PhD in an appropriate field, which may include evolution, economics, anthropology, behavioural ecology and psychology. * Demonstrated research experience with accessible and relevant research across disciplinary

boundaries especially the intersections of economics, evolutionary biology, psychology and anthropology. * Demonstrated quantitative skills. * Experience coordinating teams of employees, students or volunteers. * Preference will be given to candidates with demonstrated experience running and coordinating surveys or field experiments in developing countries, including the supervision of local research assistants.

To Apply

To apply submit your CV along with a cover letter which:

* Systematically addresses the selection criteria * Highlights how your own work fits the project's multi- disciplinary approach * Outlines previous experience running field projects (or how your previous experience in other settings might translate into the field). * The names and contact details of three referees who may be approached.

You may be required to undergo pre-employment checks prior to appointment to this role.

Application close:

7 January 2016

Please direct enquires to rob.brooks@unsw.edu.au or pauline.a.grosjean@gmail.com

"rob.brooks@unsw.edu.au" <rob.brooks@unsw.edu.au>

USouthDakota PhenoscapeProject

Postdoctoral fellow: Bioinformatics, Phenomics

The Phenoscape project (http://phenoscape.org) is recruiting a postdoc with training in bioinformatics and/or developmental biology who is interested in analyzing genomic and developmental data in relation to phenotypic data, with a focus on the vertebrate fin/limb.

The problem of how organismal phenotypes have evolved, are constrained, and acquire novelty, is one of the grand challenges in biology. The Phenoscape group has developed ontology-based methods for representing species phenotypes so that they can be integrated with model organism developmental and genetic data. The projects Knowledgebase (KB; kb.phenoscape.org) contains over 500,000 vertebrate species phenotypes that are linked to ~16,000 genes associated with 320,000+ phenotypes and 37,000 genes with in situ expression data from model organisms (zebrafish, mouse, Xenopus human). These data present a tremendous opportunity for integration with other data types to address questions about the evolution of phenotype.

We are seeking an individual with expertise in developmental biology and/or genomics, to (1) help evaluate results of bioinformatics methods being developed by Phenoscape and (2) leverage the Phenoscape Knowledgebase to study whole-organism phenotype and functional genomics in non-model organisms. The purpose of the methods is to improve prediction of the genetic basis of evolutionarily novel phenotypes by incorporating semantic similarity, homology, and phylogenetic propagation. Vertebrate fin and limb phenotypes and genes are enriched in the KB, and we are thus seeking candidates who ideally have knowledge of genes and networks involved fin/limb development. Further, this position presents a unique opportunity to leverage the linked developmental and genetic data in the Phenoscape KB for large-scale analysis of patterns of phenotypic evolution. a

The postdoc will work under the direction of Paula Mabee (University of South Dakota) in association with Todd Vision (University of North Carolina), as part of a distributed, multidisciplinary team that includes evolutionary and model organism biologists, computer scientists, and bioinformaticists. Ideally the applicant will be based in South Dakota (with opportunities to travel to other sites), but we will consider qualified applicants who are available remotely and/or half-time.

Starting date: This full time postdoctoral position is available to be filled as early as January 2016 (one year with potential to renew).

Required qualifications:

* Ph.D. degree with strong background in bioinformatics; previous experience with ontologies preferred * Experience in functional genomics or developmental biology, with preference for candidates with a background in vertebrate fin and/or limb developmen * Demonstrated communication and writing skills in English * Demonstrated ability to work in a team setting

How to apply: Please contact Dr. Mabee (pmabee@usd.edu) for inquiries. Applications should be directed to Dr. Mabee and include a cover letter, CV, a brief statement detailing your research interests and career goals, and three letters of reference. For more information, please see https://phenoscape.org and http://kb.phenoscape.org/ . "Mabee, Paula" <Paula.Mabee@usd.edu>

UTrento ComparativeAvianCellRecording

Postdoc position on comparative single cell recording in the avian brain

A Postdoc position on single cell recording in the avian brain is available at the Center for Mind/Brain Sciences (University of Trento, Italy) from December 2015. The project focuses on the neural mechanisms underlying numerical capacities and predisposition to detect animacy using the developing domestic chick forebrain as a model. A PhD in neuroscience or related disciplines is required. Experience with single cell recording (not necessarily on the avian brain) is needed. The laboratory is fully equipped and offers an exciting international and interdisciplinary work environment (http://r.unitn.it/en/cimec/abc/abc-team-members). If interested in this job, please send a motivation letter, CV, publications, and e- mail addresses of two academic referees to prof. Giorgio Vallortigara email: giorgio.vallortigara@unitn.it For any question, do not hesitate to contact us: giorgio.vallortigara@unitn.it

Giorgio Vallortigara, Ph.D., FRSB Professor of Neuroscience Center for Mind/Brain Sciences University of Trento Piazza della Manifattura 1, I-38068 Rovereto, Italy Italy E-mail: giorgio.vallortigara@unitn.it Phone: +39 0464-808676 <tel:%2B39%200464-808676> Fax +39 0464 808654 <tel:%2B39%200464%20808654> Mobile: +39 347 1417478 <tel:%2B39%20347%201417478> Personal webpage: http://www.unitn.it/en/cimec/11761/giorgio-vallortigara

UTurku 2 HumanEvolutionaryDemography

1-2 Post-doc Positions in Human Evolutionary Demography

1-2 postdoctoral positions focused on human evolutionary demography will be available in Prof. Virpi Lummaa's research group at the Department of Biology, University of Turku, Finland. The positions are part of Prof. Lummaa's Academy of Finland -funded project to study the evolutionary ecology of human reproductive behavior and longevity across the large demographic and social changes occurring during the past 300 years, and how natural selection has affected human populations at different periods. The group uses longitudinal demographic data from Finland and other countries spanning ~15 generations to investigate how the modern environment of contemporary human populations fuels evolution, and how the recent drastic demographic shifts to low birth and death rates have affected the opportunity for selection or specific trait selection in human populations. We also study how exposure to disease, food shortage or climatic variation is associated with reproduction and longevity. The postdoctoral researcher will have large freedom to develop this research, in collaboration with graduate students and other postdocs involved in the project. The successful candidate will have a PhD in fields such as ecology, evolutionary biology or biological anthropology. Previous experience in analysing longitudinal datasets, strong statistical skills and publication of papers in leading journals in the field is a must. The post could start in January 2016 or as soon as possible thereafter. The post is filled for one year, however thererafter a possible extension for up to four years.

The salary is in accordance with the University salary system (for teaching and research personnel) level 5, where the work specific salary component is 2852 euro/month. In addition, there is a share increase based on the personal performance, which is, at most, 46.3% of the base salary depending on the previous relevant research and teaching experience of the candidate.

Applications must be submitted on December 18, 2015 at latest via the electronic application form of the University of Turku following this link http://www.utu.fi/en/university/university-as-an-employer/open-vacancie s/Pages/home.aspx. Formal applications should include CV (with names and contact details of three referees), a publication list, academic portfolio, and a max. 2 page letter of motivation (describing applicant's research interests, qualifications and reasons for applying). Instructions for preparing an academic portfolio: http://www.utu.fi/en/university/university-as-an-employer/Pages/Coming- to-Work-for-the-University.aspx

For more information, please contact Prof. Virpi Lummaa (v.lummaa(at)sheffield.ac.uk) and Head of Administration Merja Fehlig (merja.fehlig (at)utu.fi).

Virpi Lummaa Department of Animal and Plant Sciences University of Sheffield Sheffield S10 2TN United Kingdom tel. +44 (0)114222 0051 email. v.lummaa@sheffield.ac.uk me: https:/-

/www.sheffield.ac.uk/aps/staff-and-students/-acadstaff/lummaa elephants: http://myanmar-timber-elephant.group.shef.ac.uk/ humans: http://-www.huli.group.shef.ac.uk/index.html Virpi Lummaa <v.lummaa@sheffield.ac.uk>

UTurku EvolutionAsianElephants

Post-doc position on ageing patterns in Asian elephants

A postdoctoral position focused on ageing patterns in Asian elephants will be available in Prof. Virpi Lummaa's research group at the Department of Biology, University of Turku, Finland. The position is part of Prof. Lummaa's ERC-funded project to study the patterns of mortality and reproductive senescence and identify their underlying health correlates, using a large longitudinal dataset on life-histories of a semi-captive population of Asian elephants in Myanmar (Burma). More information about the project is available at http://-myanmar-timber-elephant.group.shef.ac.uk/. The postdoc will take advantage of exceptional lifelong health data recorded for the Myanmar timber elephants combined with newly collected data on a range of correlates of health, condition and reproductive status to conduct a comprehensive study on the links between reproductive investment and proximate correlates of reproductive and survival senescence. The postdoctoral researcher will supervise the digitalisation of bi-monthly health assessments and disease history of the population, and lead research on investigating changes in annual health status and specific disease prevalence of individual elephants, and how these link to growth, physiological measures of health, breeding success across life and longevity. Asian elephants are endangered and both wild and captive populations are predicted to vanish from Myanmar unless the vital rates improve. Understanding health correlates of reproductive and mortality rates thus aids developing management and conservational policies. The successful candidate will have a PhD in fields such as evolutionary biology, epidemiology or veterinary sciences. Strong statistical skills, previous experience in managing and analysing longitudinal datasets and publication of papers in leading journals in the field is a must. The post could start in January 2016 or as soon as possible thereafter with an initial contract for one year, and a possible extension.

The salary is in accordance with the University salary system (for teaching and research personnel) level 5, where the work specific salary component is 2852/month. In addition, there is a share increase based on the personal performance, which is, at most, 46.3% of the base salary depending on the previous relevant research and teaching experience of the candidate.

Applications must be submitted on December 18, 2015 at latest via the electronic application form of the University of Turku following this link http://www.utu.fi/en/university/university-as-an-employer/open-vacancie s/Pages/home.aspx. Formal applications should include CV (with names and contact details of three referees), a list of publications, Academic portfolio, and a max. 2 page letter of motivation (describing applicant's research interests, qualifications and reasons for applying). Instructions for preparing an academic portfolio: http://www.utu.fi/en/university/-university-as-an-employer/Pages/Coming- to-Work-for-the-University.aspx

For more information, please contact Prof. Virpi Lummaa (v.lummaa(at)sheffield.ac.uk).

Virpi Lummaa Department of Animal and Plant Sciences University of Sheffield Sheffield S10 2TN United Kingdom tel. +44 (0)114222 0051 email. v.lummaa@sheffield.ac.uk me: https:/-/www.sheffield.ac.uk/aps/staff-and-students/-acadstaff/lummaa elephants: http://myanmar-timber-elephant.group.shef.ac.uk/ humans: http://-www.huli.group.shef.ac.uk/index.html Virpi Lummaa <v.lummaa@sheffield.ac.uk>

UVirginia Bioinformatics Genomics

Bioinformatics/Genomics Postdoc in Gut Microbiome Studies

Gut microbes play important roles in human health and disease. Central to gut microbial community dynamics is how nutrients flow between community members as well as between the community and its host. The laboratory of Dr. Martin Wu at the Department of Biology University of Virginia is seeking a postdoctoral research associate to work on a project to map and predict metabolic fluxes between gut microbiome and host. Activities will include RNA-Seq, whole genome shotgun metagenomics and 16S RNA sequencing library preparations and next-generation sequencing data analyses. This is a collaborative project funded by NIH. More information about the project can be found at https://grantome.com/grant/NIH/R01-GM108501-02

Applicants must have a Ph.D. in the field of biology, computational biology, or related field by the start date. Molecular biology skills are highly desirable. Applicants should have substantial experience with scripting (e.g. Perl or Python), Linux and bioinformatics tools. Experience with next-generation sequencing data analysis is also required. 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 your background and career interests, and contact information for three (3) references. Search on posting number 0617768. Review of applications will begin December 1, 2015. However, the position will remain open until filled.

Questions regarding this position should be directed to: Dr. Martin Wu (mw4yv@virginia.edu).

Questions regarding the Candidate Profile process or Jobs@UVA should be directed to: Rich 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 Equal Opportunity/Affirmative Action Employer. Women, minorities, veterans and persons with disabilities are encouraged to apply.

“mw4yv@virginia.edu” <mw4yv@virginia.edu>

WashingtonStateU TasmanianDevilsGenomics

POSTDOCTORAL RESEARCHER

Washington State University School of Biological Sciences

We are seeking a postdoctoral researcher to work on landscape genomics and transcriptomics of Tasmanian devils and Tasmanian devil facial tumor disease. This NSF -funded international collaboration builds on over 15 years of research tracking the spread of this unique infectious tumor across Tasmania and consequent endangerment of the iconic Tasmanian devil. Reference genomes are available for both tumor and devil and population genomic data have already been collected for >3500 Tasmanian devil individuals. The successful applicant will have an unprecedented opportunity to analyze thousands of devil genotypes and hundreds of tumor samples taken both before and after epizootics to test for selection throughout both genomes, coevolution, patterns of resistance, etc, across Tasmania. We will then use these data to predict the course of disease in uninfected populations. The position is centered in the lab of Dr. Andrew Storfer (www.wsu.edu/~storfer) at Washington State University, in close collaboration with Dr. Paul Hohenlohe at the nearby University of Idaho (8 miles away). Both universities have genomics core facilities, including the Institute of Bioinformatics and Evolutionary Studies (IBEST;http://www.uidaho.edu/research/ibest) with state-of-of-the art equipment, computational facilities and staff support.

Review of applications will begin on January 5, 2016 and continue until the position is filled. A Ph.D. in Biology or a related discipline, combined with genomics and bioinformatics experience is required. Desired qualities also include a background in population genomics, infectious disease evolution, and/or cancer genomics. Start date is negotiable, but anticipated to be between March and May, 2016. Salary and benefits are competitive. Position is for 1 year, with continuation for an additional year pending satisfactory progress. To apply, please send in pdf format a CV, and names, addresses and email addresses of 3 references, a research statement, and up to 3 representative reprints via email to: Andrew Storfer (astorfer@wsu.edu).

WSU is an Equal Opportunity/Affirmative Action/ADA educator and employer.

Andrew Storfer, PhD Eastlick Distinguished Professor Associate Director for Graduate Studies School of Biological Sciences Washington State University Pullman, WA 99164 USA Phone: (509) 335-7922 Fax: (509) 335-3184 astorfer@wsu.edu www.wsu.edu/~storfer Andrew Storfer <andrew.storfer@gmail.com>

WorkshopsCourses

Barcelona MorphometricsPhylogeny Sep12-16

Dear colleagues,

The 7th edition of the course GEOMETRIC MORPHOMETRICS AND PHYLOGENY has open registration. Basic knowledge of Geometric Morphometrics is required.

GRANTS: Thanks to the donations of former participants, this year there is a place for free at the course for PhD students. If you want to apply please send an e-mail to grants@transmittingscience.org mailto:grants@transmittingscience.org including: 1- Full name and country, 2- Short project (maximum 300 words), 3- Letter of your advisor stating if you have any grant to develop your PhD. Deadline: Marc 31st.

INSTRUCTOR: Prof. Chris Klingenberg (University of Manchester, UK).

DATES: September 12 - 16, 2016.

PLACE: Facilities of the Centre of Restauració i Interpretació Paleontologica, Els Hostalets de Pierola, Barcelona (Spain).

Testimonials of previous editions: http://www.transmittingscience.org/courses/gm/gm-and-phylogeny/#Testimonials PROGRAM,

1. Phylogeny, trees and phylogenetic reasoning.

2. Brief review of geometric morphometrics (Procrustes fit, PCA, etc.).

3. Mapping traits onto phylogenies: squared-change parsimony.

4. Practice: making/editing Nexus files, mapping morphometric data onto the tree (Mesquite, MorphoJ).

5. Phylogenetic signal, morphometric traits and estimating phylogeny.

6. Comparative methods: independent contrasts.

7. Application in morphometrics: evolutionary allometry and size correction.

8. Practice: comparative methods (MorphoJ).

9. Application of comparative methods: morphological integration.

10. Multi-level analyses of integration: inferring evolutionary mechanisms.

11. Application of comparative methods: partial least squares (ecomorphology, etc.).

12. Practice; comparative methods (cont.).

13. Morphometrics, phylogenies and qualitative characters.

14. Disparity and diversification.

15. Presentations of group work.

More information: http://www.transmittingscience.org/courses/gm/gm-and-phylogeny/ or writing to courses@transmittingscience.org mailto:courses@transmittingscience.org

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

Sole

Soledad De Esteban-Trivigno, PhD. Transmitting Science www.transmittingscience.org soledad.esteban@transmittingscience.org

BodegaMarineLab AppliedPhylogenetics

UC Davis

WORKSHOP IN APPLIED PHYLOGENETICS

at Bodega Marine Laboratory, Bodega Bay, California

Sponsored by the

University of California, Davis and Bodega Marine Laboratory

http://treethinkers.org Every spring for the last sixteen years, we have held the Bodega Applied Phylogenetic workshop for graduate students interested in applying phylogenetic methods to diverse topics in biology. For logistical reasons, it is necessary for the course to take a sabbatical in the spring of 2016. The Bodega course return in the spiring of 2017.

We look forward to seeing you next year! Brian Moore & Peter Wainwright Organizers

Brian R Moore <brianmoore@ucdavis.edu>

cE3c Portugal 4 EvolBiol

Subject: Portugal-cE3c-Course: four advanced courses with deadlines January2016 cE3c - Centre for Ecology, Evolution and Environmental Changes is organizing several Advanced Courses: see below the six with closer deadlines.

Additional informations at: http://ce3c.ciencias.ulisboa.pt/training/?cat=1 —–

cE3c - Centre for Ecology, Evolution and Environmental Changes Advanced Course Biodiversity and Plant Evolution organized by Helena Cotrim and Manuela Sim-Sim | 25-30 January 25-30 2016 2016@ Lisbon, Portugal

Objectives: On completion of the course, the students shall have acquired the following knowledge and understanding: - Describe the main evolutionary acquisitions on groups of the plant kingdom and its adaptive significance. - Comprehend the modern plant phylogeny and its sources of information. - Explain the underlying evolutionary mechanisms of diversity and speciation in the plant kingdom. - escribe the variety of pollination syndromes, reproductive systems and population structures present in the plant kingdom, and explain the mechanisms underlying this diversity. - Explain and critically analyse how the genetic diversity and evolutionary potential of plant populations are influenced by phenomena like phenotypic plasticity, seed banks, hybridization, polyploidy and postglacial colonization history. - Formulate hypotheses and propose methods when studying evolutionary phenomena in wild plant species.

Course instructors Helena Cotrim (hmcotrim@fc.ul.pt) Assistant Professor at the Faculty of Sciences of the University of Lisbon, researcher at the Centre for Ecology, Evolution and Environmental Changes (http://ce3c.ciencias.ulisboa.pt/teams/user/?id=206)

Maria Manuela Sim-Sim (msimsim@fc.ul.pt) Assistant Professor at the Faculty of Sciences of the University of Lisbon, coordinator of the NHS research group at the Centre for Ecology, Evolution and Environmental Changes (http://ce3c.ciencias.ulisboa.pt/teams/profile/?id=11)

Intended audience This five days intensive course will be open to a maximum number of 16 participants, being directed to PhD or MSc students in Biology, Evolution, Ecology or related areas, and postdocs and other professionals working in related topics.

Minimum formation: Bachelor in Biology or related area. The course is free for 1st year PhD students in the Doctoral programme in Biology (FCUL), Biodiversity, Genetics and Evolution (UL; UP) and Biology and Ecology of Global Changes (UL, UA). For information of fees for other participants see the programme details (access link below)

Deadline for applications: January 4th, 2016

Candidates should send a short CV and motivation letter to Helena Cotrim (email hmcotrim@fc.ul.pt)

For additional details about the course and to know how to register, click here: http://ce3c.ciencias.ulisboa.pt/training/ver.php?id=4 For more information about the course, please contact: Helena Cotrim (email hmcotrim@fc.ul.pt) or Maria Manuela Sim-Sim (email: msimsim@fc.ul.pt)

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cE3c - Centre for Ecology, Evolution and Environmental Changes Advanced Course Practical Course on Phylogenetics organized by Octavio Paulo| February 1-5 2016 @ Lisbon, Portugal

Objectives: Phylogenetics is one of the scientific areas of Biology that has grown fast and evolved in methodological terms in the last years. Its applications go from the studies of the evolution of species and populations to the least expected, as the study of the origin of the AIDS virus or seasonal cycles of the flu. The course is aimed at students and professionals that intend to get started in phylogenetic analysis as well as researchers already with some experience wanting to deepen or update their knowledge in the field. The course consists of theoretical classes as well as hands-on practical sessions using software. Participants are encouraged to bring their own sequence data for analysis.

. Course instructor Octavio Paulo (octavio.paulo@fc.ul.pt) Professor at the Faculty of Sciences of the University of Lisbon, researcher at the Centre for Ecology, Evolution and Environmental Changes (cE3c - http://ce3c.ciencias.ulisboa.pt/teams/user/?id=3), Coordinator of the Computational Biology & Population Genomics Group (http://ce3c.ciencias.ulisboa.pt/teams/profile/?id=1)

Intended audience This five days intensive course will be open to a maximum number of 20 participants, being directed to PhD or MSc students in Biology, Evolution,

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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

Finland StructuredPops Aug21-28

Dear Colleagues,

We are pleased to announce the 2016 edition of The Helsinki Summer School on Mathematical Ecology and Evolution, an EMS-ESMTB School in Applied Mathematics, which will focus on structured populations. The school will be held between 21 and 28 August 2016 in Turku, Finland. The core program consists of five series of lectures,

Mats Gyllenberg (University of Helsinki): Dynamics of structured populations Hans Metz (University of Leiden): Adaptive dynamics in structured populations Reinhard Bürger (University of Vienna): Population genetics in structured populations Hisashi Inaba (University of Tokyo): Infectious diseases in structured populations André de Roos (University of Amsterdam): Population and community ecology of ontogenetic development

All young researchers working in mathematical ecology 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 31 January 2016. For more details and application, see the school's website at

https://wiki.helsinki.fi/display/BioMath/The+Helsinki+Summer+School+
on+Mathematical+Ecology+and+Evolution+
2016%3A+Structured+Populations

Eva Kisdi, Mats Gyllenberg and Francesca Scarabel

"eva.kisdi@HELSINKI.FI" <eva.kisdi@HELSINKI.FI>

FridayHarbor ComparativeEmbryology Jun13-Jul15

Hello all, Applications are now being accepted for the Comparative Invertebrate Embryology course at the Friday Harbor Labs (June 13 - July 15, 2016).

It is a great course for anyone interested in the evolution of development, developmental mechanisms, animal evolution, or the ecology or physiology of early life stages. The focus of the course is hands-on observation of living embryos and larvae from over a dozen animal phyla. The Friday Harbor Labs gives access to an extraordinary variety of organisms from diverse marine habitats, all in a beautiful setting, and provides opportunities to interact with a broad community of biologists from all over.

I will be co-teaching the course with Dr. Sally Leys, an expert on the development of sponges and the evolution of animal body plans. My own research focuses on the roles of biomechanics in development-environment interactions. In addition, we will have guest lectures from experts on diverse topics and taxa.

For the course description, please see: http://depts.washington.edu/fhl/-studentSummer2016.html#SumA-2 . Be sure to check out some of the other exciting courses offered at the Friday Harbor Labs too.

Please share with students who might be interested.

Thank you.

–Mickey

mvondass@gmail.com

FridayHarborLabs Biodiversity Jun13-Jul15

Friday Harbor Laboratories Marine Invertebrate Zoology June 13 - July 15, 2016

This course will be taught by Dr. Megan Schwartz (University of Washington, Tacoma) and Dr. Kevin Kocot (University of Alabama and Alabama Museum of Natural History). The course takes advantage of the rich marine biota of the Friday Harbor region to teach the principles of animal organization and biodiversity. It emphasizes comparative study of form and function, and of complexity and diversity in phylogenetic and environmental contexts. It focuses on the study of living animals in the laboratory and field in the diverse marine habitats surrounding San Juan Island.

The course reviews the diversity of animal life in an evolutionary and ecological context, focusing on the comparative study of form, function and life history. We will review all animal phyla, and also explore diversity within phyla based on available exemplars.

Biodiversity is one of the most topical subjects in biology, partly because of its accelerating erosion as a result of increasing human pressures and global change. Having a working knowledge of the diversity of life is fundamental to the study of any subject in biology. FHL is arguably the best location in the US for such a course, given the wealth of local diversity and accumulated knowledge of the local fauna built over a century of investigations.

Applications are welcome from advanced undergraduate students, post-baccalaureates, and graduate students. Prior coursework in invertebrate biology or animal diversity will be useful; if in doubt, please contact one of the instructors.

Enrollment is limited to 20 students. No textbook is required for this course.

For more details (including costs and application instructions) please see the course website: http://depts.washington.edu/fhl/-studentSummer2016.html#SumA-1 – Kevin M. Kocot, Ph.D. NSF International Postdoctoral Research Fellow Degnan Lab The University of Queensland School of Biological Sciences 325 Goddard Building 8 St. Lucia, QLD 4072 Australia Ph: +61 0402 488 430

kmkocot@gmail.com

Hungary ConGen May30-Jun10

Course: ConGen2016 - Recent Advances in Conservation Genetics (May 30 - June 10, 2016)

We are pleased to announce the course “ConGen 2016 - Recent Advances in Conservation Genetics.”

The 2016 course will be held at the Lake Balaton Limnological Institute on the shores of this charming freshwater lake in the Transdanubian region of Hungary. The course will be directed by Dr. Stephen J. O’Brien, and taught by renowned scientists in methods, interpretation, and applications of molecular genetic and genomic analyses for conservation of endangered species, who will also share a variety of their personal experiences in this important field.

Information about the course, participating faculty, venue, and registration can be found at the following link:

http://congen2016.com/ Thank you for your help.

Best regards,

Klaus Koepfli

– Klaus-Peter Koepfli, Ph.D. Smithsonian Conservation Biology Institute National Zoological Park 3001 Connecticut Avenue NW Washington, DC 20008 USA Mobile (USA): +1 310 903 0197 E-mail: KoepfliK@si.edu OR klauspeter.koepfli527@gmail.com Theodosius Dobzhansky Center for Genome Bioinformatics Saint Petersburg State University 41A Sredniy Prospekt St. Petersburg 199034 RUSSIA Mobile (Russia): +7 981 105 7785 Skype ID: klauspeter.koepfli

Klaus-Peter Koepfli <klauspeter.koepfli527@gmail.com>

Leicester NGSAssemblyVariantCalling Feb1-3

Leicester NGSAssemblyVariantCalling Feb1-3

BBASH at University of Leicester is pleased to announce that applications for the upcoming Next Generation Sequencing training course are now open.

Deadline for applications: 15th January 2016 Notification of acceptance: 18th January 2016 Course dates: 1st-3rd February 2016

Venue: University of Leicester - College Court Conference Centre, Leicester, UK (http://collegecourt.co.uk/)

Instructors: Richard Badge (BBASH, University of Leicester, UK) Chiara Batini (University of Leicester, UK) Matthew Blades (BBASH, University of Leicester, UK)

Course description

This course will provide an introduction to next generation sequencing (NGS) platforms, data analysis and tools for data quality control, genome assembly and variant calling. The course will be delivered using a mixture of lectures and computer based hands on practical sessions using real data.

This course is aimed at wet-lab biologists who are involved in research projects that will require the handling and analysis of NGS data. A significant proportion of the course will be computer-based using command line tools in the Unix environment, therefore, in order to gain maximum benefit from the course all attendees will be required to have basic Unix skills.

For additional information: https://www2.le.ac.uk/colleges/medbiopsych/facilities-and-services/cbs/bbash/training/workshop-webpages/copy_of_ngs-workshop-2016 The Organisers Chiara Batini (University of Leicester, UK) Matthew Blades (BBASH, University of Leicester, UK)

"cb334@leicester.ac.uk" <cb334@leicester.ac.uk>

Ljubljana Bioinformatics Feb

Genialis is a bioinformatics company that shares the inhouse knowledge by organising bioinformatics courses. BioBash workshops are intensive hands-on trainings where you actually do bioinformatics rather just attend lectures and watch demonstrations. Designed by biologists for biologists, they are ideal for life scientists who are starting to implement bioinformatics into their research as well as those eager to upgrade their data analysis skills. Be it Linux, Python or R, our workshops focus on putting the newly acquired skills immediately into practice.

We have just announced two workshops that will be held in Ljubljana, in February 2016, and registrations are now open -https://www.genialis.com/events/ BioBash R: 1. - 5. February BioBash R Workshop will teach the participants how to efficiently explore their data. Starting from the very beginning, learn how to summarize and reshape data, discover patterns in the data, and create meaningful as well as beautiful graphical summaries. Moreover, a full day introduction into BioConductor will teach you how to analyze next-generation sequencing data with R.

BioBash Essentials: 15. - 19. February BioBash Essentials is aimed at life scientists with little or no knowledge of basic bioinformatic skills. Common and general tools such as Linux command line and regular expressions are explained through practice, and more work is put into building solid programming foundations in Python. The participants learn how to tackle many everyday tasks that come up regardless of their actual scientific question, for example automating repetitive tasks such as querying online databases or extracting information from endless text files. Moreover, a full day introduction into the NGS data analysis will be given, covering in practice the logic behind the filtering, assembly and mapping of short reads.

All our workshops in 2015 were full of enthusiastic trainees who left much better prepared to tackle their data challenges. Let us invite you to read their feedback -https://www.genialis.com/biobash-customer-reviews/ . Here are 5 reasons why our past participants have found our workshops enjoyable and useful:

Designed by biologists for biologists Bioinformatics step-by-step Hands-on workshop Professional execution Competitive price

Who should attend our workshops: Undergraduate and Graduate Students, Post-docs, and Faculty members working with different aspects of bioinformatics.

Still not sure if BioBash is right for you? Read more about the BioBash Workshops online at https://-www.genialis.com/biobash-workshops/, where you can compare detailed agendas of the workshops to find the right workshop for you. We accept only 20 participants on the first-come, first-served basis, so apply soon to avoid disappointment.

Klemen Hrovat

Project Manager

Genialis d.o.o., Ulica Zore Majcnove 4,1000 Ljubljana, Slovenia T:+386 59 054 580|M:+386 40 353 387|E:klemen@genialis.com|W:www.genialis.com klemen@genialis.com klemen@genialis.com

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Lyon France ComparativeGenomics Jan11-22

Dear colleagues,

Registrations for the 2015-2016 edition of the European course on "Comparative Genomics" are open.

The course is aimed at students from the ENS and is open to master and PhD students from European universities.

The course focuses on major discoveries, big challenges, innovative concepts and original approaches in the field of comparative genomics, their applications in biology, medicine and biotechnology, and their impact on society.

This year the course will be held on 11-22 January 2016 at the ENS (Lyon, France).

Registration is free. Lectures are in English.

The preliminary program and registration form are available at:

http://lbbe-dmz.univ-lyon1.fr/spip_cg/ Jean-Nicolas Volff (ENS, Lyon) and Céline Brochier (Univ. Lyon1)

– Pr Céline Brochier-Armanet Université Claude Bernard Lyon 1 Membre de l'Institut Universitaire de France Responsable du master bioinfo@lyon (http://www.bioinfo-lyon.fr) – Laboratoire de Biométrie et Biologie Evolutive UMR CNRS/Lyon 1 5558 43 Bd du 11 Novembre 1918 69622 Villeurbanne, France – Tel: 33 (0)4 26 23 44 76 Mail:celine.brochier-armanet@univ-lyon1.fr Web page:http://www.frangun.org "celine.brochier-armanet@univ-lyon1.fr"

MalhamTarn England R May2-6

"Advancing in statistical modelling using R" Delivered by Dr Luc Bussiere and Dr Tom Houslay This course will run from 2nd - 6th May 2016 at Malham Tarn field station in the Yorkshire Dales National Park, England - http://www.field-studies-council.org/centres/-malhamtarn.aspx This 5 day course costs Â£460 for course only including lunch or Â£655 all inclusive, including all accommodation and meals and minibus connections to and from a local meeting point. The course is designed to bridge the gap between basic R coding and more advanced statistical modelling. It will consist of a series of modules (listed below), each lasting roughly half a day, and designed to either build required skills for future modules or to perform a family of analyses that is frequently encountered in the biological literature. Each module will include practical and self-assessment exercises to help attendees gauge their understanding of the concepts. All course materials (including copies of presentations, practical exercises, self-assessment problems, data files, and example scripts prepared by the instructing team) will be provided electronically to participants. http://prstatistics.co.uk/-advancing-in-r/index.html Course content is as follows Day 1: Module 1 Introduction & data visualization using (graphics) and (ggplot2) Module 2 Univariate regression, diagnostics & plotting fits Day 2: Module 3 Adding additional continuous predictors (multiple regression). Module 4 Adding factorial (categorical) predictors & incorporating interactions (ANCOVA) Day 3: Module 5 Model selection & simplification (likelihood ratio tests, AIC) Module 6 Mixed effects models in theory & practice Day 4: Module 7 Generalised Linear Models (binomial and count data) Module 8 Nonlinear models (polynomial & mechanistic models) Day 5: Module 9 Combining methods (e.g., nonlinear mixed effect (NLME) models & generalised linear mixed effect (GLMM) models) Module 10 Optional free afternoon to cover previous modules and discuss data Please email any inquiries to oliverhooker@prstatistics.co.uk Please feel free to distribute this material anywhere you feel is suitable Upcoming courses; APPLIED BAYESIAN MODELLING FOR ECOLOGISTS AND EPIDEMIOLOGISTS; SPATIAL ANALYSIS OF ECOLOGICAL DATA USING R; INTRODUCTION TO R AND STATISTICS FOR BIOL-

OGISTS; STABLE ISOTOPE MIXING MODELS USING SIAR, SIBER AND MIXSIAR; INTRODUCTION TO PYTHON FOR BIOLOGISTS; TIMES SERIES DATA ANALYSIS FOR ECOLOGISTS AND CLIMATOLOGISTS USING R; MODEL BASED MULTIVARIATE ANALYSIS OF ECOLOGICAL DATA USING R; ADVANCES IN DNA TAXONOMY USING R; GENETIC DATA ANALYSIS USING R. Oliver Hooker PR˜Statistics

"oliverhooker@prstatistics.co.uk"
<oliverhooker@prstatistics.co.uk>

MNHN Paris DNABarcodes Mar7-11

The course "Integrative taxonomy and taxonomic expertise : DNA barcodes in the genomic era" will be from the 7th to the 11th of March, 2016 at the MNHN of Paris, France.

This course is also part of the DEST- Taxonomy training program (http://www.taxonomytraining.eu/).

The course is in English. To register, please fill the form on the website of the course (https://sites.google.com/site/coursbarcode/inscription-1) before the the 3rd of January, 2016.

If you have any question, please contact: Line Le Gall (legall@mnhn.fr) Nicolas Puillandre (puillandre@mnhn.fr) Sarah Samadi (sarah@mnhn.fr)

nicolaspuillandre@gmail.com

MountainLakeBioStation Biodiversity May23-Jul29

Summer 2016 Field Courses

REU Opportunities (NSF Site) Mountain Lake Biological Station mlbs.org/summer2016 < http://www.mlbs.org/summer2016 >

Mountain Lake Biological Station (University of Virginia) announces its 2016 summer program of field-based undergraduate and graduate-level credit courses offered by nationally recruited faculty, and its NSF REU undergraduate research internship program, now in its 24th year.

Summer Courses: mlbs.org/summercourses

********* Plant Diversity and Conservation

********* Field Herpetology

********* Science Writing

********* Field Biology of Fishes

********* Field Biology of Fungi

Financial aid available for undergraduate and graduate students.

Summer REU Internships: mlbs.org/reuprogram

REU participants are recruited from around the country for a unique 10-week learning and living research experience in the southern Appalachian Mountains. Students conduct independent research in field ecology, evolution, behavior and physiology under the supervision of station scientists. REUs are paid internships that include room and board, travel, and a $5,250 stipend.

Program dates: May 23 - July 29

Application deadline February 20.

Please forward this information to colleagues or students you think might be interested. Thanks for your help!

**** Learn all about Mountain Lake at MLBS.org < http://www.mlbs.org/ > ****

Best wishes, happy and safe holidays,

Butch Brodie, Director

Web posting of this announcement: mlbs.org/summer2016 < http://www.mlbs.org/summer2016 >

Portugal cE3c Feb8-12

Subject: Portugal-cE3c-Course Applied Methods in Community Ecology-Feb8-12 2016

cE3c - Centre for Ecology, Evolution and Environmental Changes is organizing the Advanced Course Applied Methods in Community Ecology and Functional Ecology by Paulo A. V. Borges & François Rigal - February 8-12 2016 @ Lisbon, Portugal

Applied Methods in Community Ecology and Functional Ecology

Objectives: This five-days intensive course is mostly a practical course offering an overview on different community ecology and macroecological methods and software

See the PROGRAMME at: http://ce3c.ciencias.ulisboa.pt/training/ver.php?id=2 Course INSTRUCTORS: Paulo A. V. Borges (Assistant Professor at Azores University, researcher at cE3c) (http://www.gba.uac.pt/quem/ver.php?id=4)

& François Rigal (Assistant Professor at Environment and Microbiology Team, MELODY group, University of Pau and external collaborator of cE3c -IBBC, Azorean Biodiversity Group) (http://ce3c.ciencias.ulisboa.pt/teams/user/?id=163)

Intended audience

This five days intensive course will be open to a maximum number of 20 participants, being directed to PhD or MSc students in Ecology, Geography or related areas, and postdocs and other professionals working in related topics.

The course is free for 1st year PhD students in the Doctoral programme in Biology (FCUL), Biodiversity, Genetics and Evolution (BIODIV UL, UP) and Biology and Ecology of Global Changes (BEAG UL, UA). For information of fees for other participants see the programme details.

Deadline for applications: December 6, 2015

For additional details about the course and to know how to register, click here:

http://ce3c.ciencias.ulisboa.pt/training/ver.php?id=2 For more information about the course, please contact:

pborges@uac.pt

Subject: Portugal-cE3c-Course Measuring Biodiversity-Jan4-8 2016

cE3c - Centre for Ecology, Evolution and Environmental Changes is organizing the Advanced Course Measuring Biodiversity by Joaquin Hortal - January 4-8 2016 @ Lisbon, Portugal

Measuring Biodiversity: How to get data, assess its quality and measure different aspects of diversity

Objectives: This five-days intensive course offers an overview of the different ways to measure biodiversity, and provides tips for the stratification of primary biodiversity data and the construction of variables that describe its various facets. It also includes an in-depth review of the different types of data used to measure biodiversity and their problems and limitations.

See the PROGRAMME at: http://ce3c.ciencias.ulisboa.pt/training/ver.php?id=6 Course INSTRUCTORS: Joaquin Hortal (Senior Research Scientist, Museo Nacional de Ciencias Naturales - CSIC, Madrid, Spain)(http://jhortal.com/) & Ana Margarida C. Santos (Marie Curie postdoctoral fellow, Museo Nacional de Ciencias Naturales - CSIC, Madrid, Spain)(http://guidasanto1.wix.com/anamcsantos2)

Intended audience

This five days intensive course will be open to a maximum number of 20 participants, being directed to PhD or MSc students in Ecology, Geography or related areas, and postdocs and other professionals working in related topics.

The course is free for 1st year PhD students in the Doctoral programme in Biology (FCUL), Biodiversity, Genetics and Evolution (BIODIV UL, UP) and Biology and Ecology of Global Changes (BEAG UL, UA). For information of fees for other participants see the programme details.

Deadline for applications: December 11, 2015

For additional details about the course and to know how to register, click here:

http://ce3c.ciencias.ulisboa.pt/training/ver.php?id=6 For more information about the course, please contact:

jhortal@mncn.csic.es

Margarida Matos <mmmatos@fc.ul.pt>

SCENE Glasgow TimeSeries May9-12

TIME SERIS MODELS FOR ECOLOGISTS AND CLIMATOLOGISTS

This course is being delivered by Dr Andrew Parnell, It will run from 9th - 12th of May 2016 at SCENE (the Scottish Centre for Ecology and the Natural Environment), Loch Lomond National Park, Glasgow.

Course overview: This course will cover model-based time series analysis with a particular focus on applications in ecology and climatology. All methods will be illustrated using the free, open-source software package R. Time Series data are ubiquitous in the physical sciences, and models for their behaviour enable scientists to understand temporal dynamics and predict future values. Participants will be taught a wide range of suitable time series models for both discrete and continuous time systems. The course takes a foundational Bayesian approach, which will enable participants to have a deeper understanding of the models being fitted, and to estimate all unknown quantities with uncertainty. Participants are encouraged to bring their own data sets for discussion with the course tutors.

This workshop is aimed at research postgraduates, practicing academics in ecology, climatology, evolution, meteorology, conservation and environmental management, and environmental professionals in government and industry.

The workshop is delivered over 8 half-day sessions (see the detailed curriculum below). The session will consist of Introductory lectures on the concepts and refreshers on R usage. Intermediate-level lectures interspersed with hands-on mini practicals and longer projects. Finally, round-table discussions about the analysis requirements of attendees (optional - bring your own data).

Assumed background: A basic understanding of statistical concepts. Such as regression modelling and generalised linear models. Some understanding of Bayesian Statistics is recommended but will be covered during the introductory sessions. Familiarity with R. Ability to import/export data, manipulate data frames, fit basic statistical models & generate simple exploratory and diagnostic plots.

Curriculum: Day 1: Basic concepts

Class 1: Introduction; some example time series datasets; prediction vs explanation

Class 2: An introduction to Bayesian Statistics.

Class 3: The AR(1) model

Practical: revision on using R to load data, create plots and fit statistical models

Round table discussion: understanding the output from a Bayesian model

Day 2: ARIMA modelling

Class 1: ARMA models for real data

Class 2: ARIMA and sARIMA modelling

Practical: An introduction to the Bayesian modelling language JAGS

Round table discussion: understanding and running a JAGS model

Day 3: Continuous time series

Class 1: Brownian Motion and its application to real data sets

Class 2: An introduction to Stochastic Volatility Modelling

Practical: Fitting continuous time models in JAGS

Round table discussion: Issues of continuous vs discrete time

Day 4: Advanced time series models

Class 1: Multivariate models

Class 2: Fractional differencing and models using differential equations

Practical: Running advanced models in JAGS

Round table discussion: Bring your own data set The cost is Â£450 including lunches and course materials. An all-inclusive option is also available at Â£625; this includes breakfast, lunch, dinner, refreshments, accommodation and course materials. Participants will need a laptop with a recent version of R Please send inquiries to oliverhooker@prstatistics.co.uk or visit the website www.prstatistics.co.uk Please fee free to distribute this information anywhere you think suitable.. http://prstatistics.co.uk/time%20series%20models%20for%20ecologists%20and%20climatologists/index.html Other upcoming courses - GENETIC DATA ANALYSIS USING SIAR; ; APPLIED BAYESIAN MODELLING FOR ECOLOGISTS AND EPIDEMIOLOGISTS; SPATIAL ANALYSIS OF ECOLOGICAL DATA USING R; ADVANCING IN STATISTICAL MODELLING USING R; PYTHON FOR BIOLOGISTS; INTRODUCTION TO

STATISTICS AND R FOR BIOLOGISTS; ADVANCES IN DNA TAXONOMY; BIOINFORMATICS FOR GENETICISTS AND BIOLOGISTS; MULTIVARIATE ANALYSIS OF SPATIAL DATA; MODEL BASE MULTIVARIATE ANALYSIS OF ABUNDANCE DATA; Oliver Hooker PR˜Statistics

"oliverhooker@prstatistics.co.uk"

Scotland SpatialR Apr11-17

"Spatial analysis of ecological data using R"

Delivered by Prof. Jason Matthiopoulos

This course will run from 11th - 17th April 2016 at Mileport Field Station, Isle of Cumbrae, Scotland

The course will cover the concepts and R tools that can be used to analyse spatial data in ecology covering elementary and advanced spatial analysis techniques applicable to both plants and animals. We will investigate analyses appropriate to transect (e.g. line surveys, trapping arrays), grid (e.g. occupancy surveys) and point data (e.g. telemetry). The focal questions will be on deriving species distributions, determining their environmental drivers and quantifying different types of associated uncertainty. Novel methodology for generating predictions will be introduced. We will also address the challenges of applying the results of these methods to wildlife conservation and resource management and communicate the findings to non-experts.

http://prstatistics.co.uk/spatial-analysis-in-R/-index.html Course content is as follows

Day 1: Elementary concepts >Module 1 Introductory lectures and practical; this will cover the key questions in spatial ecology, the main types of data on species distributions, concepts and challenges and different types of environmental data, concepts and challenges; useful concepts from statistics; Generalised Linear Models >Module 2 GIS tools in R: Types and structure of spatial objects in R, generating and manipulating spatial objects, projections and transformations, cropping and masking spatial objects, extracting covariate data and other simple GIS operations in R, optionally plotting simple maps

Day 2: Overview of basic analyses >Module 3 Density estimation, Spatial autocorrelation,Smoothing, Kernel Smoothers, Kriging, Trend-fitting (linear, generalised linear, generalised additive models) >Module 4 Habitat preference, Resource selection functions, MaxEnt: What's it all about? Overview and caveats related to Niche models

Day 3: Challenging problems >Module 5 Analysing grid data, Poisson processes, Occupancy models, Use-availability designs >Module 6 Analysing telemetry data, Presence-only data, Spatial and serial autocorrelation, Partitioning variation by mixed effects models

Day 4: Challenging problems >Module 7 Analysing transect data, Detection functions for point and line transects, Using covariates in transect models. Afternoon for catch up and/or excursion

Day 5: Challenging problems >Module 8 Advanced methods, Generalised Estimation Equations for difficult survey designs, Generalised additive models for habitat preference, Dealing with boundary effects using soap smoothers, Spatial point processes with INLA

Day 6: Delivering advice >Module 9 Prediction, Validation by resampling, Generalised Functional Responses for species distribution, Quantifying uncertainty, Dealing with the effects of population density >Module 10 Applications, Designing protected areas, thinking about critical habitat, Representing uncertainty

Day 7: Hands-on problem solving >Module 11 Round table discussions, About 4 groups, each of 5-10 people working on a particular problem.

This 7 day course costs Â£630 for course only including lunch or Â£965 all inclusive, including all accommodation and meals. Please email any inquiries to oliverhooker@prstatistics.co.uk Please feel free to distribute this material anywhere you feel is suitable

Upcoming courses; ADVANCING IN STATISTICAL MODELLING USING R; INTRODUCTION TO R AND STATISTICS FOR BIOLOGISTS; STABLE ISOTOPE MIXING MODELS USING SIAR, SIBER AND MIXSIAR; INTRODUCTION TO PYTHON FOR BIOLOGISTS; TIMES SERIES DATA ANALYSIS FOR ECOLOGISTS AND CLIMATOLOGISTS USING R; MODEL BASED MULTIVARIATE ANALYSIS OF ECOLOGICAL DATA USING R; ADVANCES IN DNA TAXONOMY USING R; GENETIC DATA ANALYSIS USING R; APPLIED BAYESIAN MODELLING FOR ECOLOGISTS AND EPIDEMIOLOGISTS

Oliver Hooker PR˜Statistics

"oliverhooker@prstatistics.co.uk"
<oliverhooker@prstatistics.co.uk>

Switzerland EvolutionaryBiol Jun21-27

Dear Colleagues

The 2016 edition of the Evolutionary Biology Workshop in the Alps will take place on 21-27June 2016 in Arolla, Switzerland.

Target participants are PhD students in early stages of PhD and advanced Master students - please pass the info to potential participants.

The main goals of this annual workshop, based on a concept developed by Stephen Stearns and John Maynard Smith, are to develop the following skills: - developing your scientific ideas through discussions in groups; - thinking critically and expressing oneself clearly; - turning a general idea into a research project; - writing a research proposal and defending it.

Faculty: Bill Rice (University of California Santa Barbara) Dolph Schluter (University of British Columbia) Tanja Schwander (University of Lausanne) John Pannell (University of Lausanne) Tad Kawecki (University of Lausanne)

It is you, the students, who will be in charge in this course. You will be divided in groups of 4-5 students. In those groups, you will work on your ideas. You, as a group, will decide what the important open questions in broadly defined evolutionary biology are, you will choose one, and attempt to develop a proposal for a research project that will address it. The faculty will visit the groups during the discussions to answer your questions, provide coaching and give you feedback on your projects, but they will generally take the back seat. Additionally, the faculty will give talks about their research and be available for informal discussion with individual students. At the end you will present your projects to other participants, and we will party.

The workshop will take place in the 100-year old hotel Kurhaus http://www.hotel-kurhaus.arolla.com/, located in a small alpine village at an altitude of 2000 m, which will help you to concentrate on the course while giving you also the chance to enjoy the views, small hikes, marmots and the alpine flora.

Fee: CHF 450.- (this covers part of the cost for room and board, the rest being subsidized by the Herbette Foundation).

Participants will receive a course certificate for 3 ETCS credits.

To apply, send a single file (pdf or rtf) containing a short motivation letter including a brief summary of your research interest, a cv, and the name of your scientific advisor to Caroline Betto-Colliard <ecologie-evolution@cuso.ch>, with Cc to tadeusz.kawecki@unil.ch . Please put "Evolutionary workshop" in the subject. Application Deadline: February 14, 2016.

– Tadeusz J. Kawecki Associate Professor Department of Ecology and Evolution University of Lausanne Biophore, office 3111 CH 1015 Lausanne, Switzerland

"tadeusz.kawecki@unil.ch" <tadeusz.kawecki@unil.ch>

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.