EvolDir

July 1, 2014

Month in Review

Foreword

This listing is intended to aid researchers in population genetics and evolution. To add your name to the directory listing, to change anything regarding this listing or to complain please send me mail at Golding@McMaster.CA.

Listing in this directory is neither limited nor censored and is solely to help scientists reach other members in the same field and to serve as a means of communication. Please do not add to the junk e-mail unless necessary. The nature of the messages should be "bulletin board" in nature, if there is a "discussion" style topic that you would like to post please send it to the USENET discussion groups.

Instructions for the EvolDir are listed at the end of this message.

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Conferences

Belfast HGV2014 Sep17-19

Conference: Human Genome Variation and Complex Genome Analysis Meeting (HGV2014) Belfast, Northern Ireland Message:

September 17th V 19th, 2014 Culloden Estate and Spa, Belfast, Northern Ireland

Website: http://hgvmeeting.org Registration Deadlines: 27th June 2014 (with abstract) 27th July 2014 (without abstract)

Please note the new attendance policies: - APPLICANTS NO LONGER NEED SUBMIT AN ABSTRACT TO REGISTER FOR THIS MEETING - MULTIPLE NAMED AUTHORS CAN REGISTER AND SUBMIT THE SAME ABSTRACT

Scientific topics include: - Clinical NGS (including cancer genomics and rare disease diagnosis) - Epigenomic variation (including that found in the single cell) - Large scale population studies of human disease - Stratified and Personalised medicine - Data and knowledge sharing/discovery (including the Global Alliance for Genomics and Health) - Biomedical informatics - Genomic evolution - Genomic technology advances - Human mosaicism & aging

This residential Conference provides the opportunity for you to interact with an unrivalled international faculty in an environment which promotes discussion and consideration of the key technologies and advances that will inform the development of this important discipline over the coming years. We look forward to welcoming you to this state of the art conference in a venue where you will have excellent opportunities to interact with fellow conference participants and invited faculty.

Yours sincerely, HGV2014 Organising Committee

Anthony Brookes, Stephen Chanock, Pui-Yan Kwok, Mark Lawler, Charles Lee, Barbara Wold

“Lancaster, Owen (Dr.)” <ol8@leicester.ac.uk>

Lausanne ESEB Aug10-15 CallForProposals ReminderDeadline

REMINDER: The deadline for submission of symposium proposals for ESEB 2015 (June 30) is fast approaching! The original call for symposia is repeated below with the relevant information.

ESEB 2015 Lausanne CALL FOR SUBMISSION OF SYMPOSIUM PROPOSALS

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

Submissions for symposium proposals are now invited. These will be processed through our website, currently at: http://www3.unil.ch/wpmu/eseb2015/ Information about the symposia can be found at: www3.unil.ch/wpmu/eseb2015/symposium-information

For symposium submission, please go to :

http://www3.unil.ch/wpmu/eseb2015/wpgforms/symposium/ You will be asked to provide:

1. The names and e-mail addresses of one organizer (for all communication) and one co-organizer (as a replacement). Both must be committed to attend the whole meeting.

2. The proposed symposium title.

3. A summary of max 200 words explaining why you think this makes a good subject for the ESEB Congress.

4. The names of one or two invited speakers (please check beforehand whether these people are available). Organizers cannot invite themselves to their own symposium.

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

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

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

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

Check our webpage for updates:

www.unil.ch/eseb2015; or

www3.unil.ch/wpmu/eseb2015/symposium-information.

We look forward to your contributions

The ESEB2015 organizing committee

John Pannell Department of Ecology and Evolution Biophore Building University of Lausanne CH-1015 Lausanne Switzerland

Phone: + 41 (0) 21 692 4170 Fax: + 41 (0) 21 692 4265 web: http://www.unil.ch/dee/page86963_en.html John Pannell <john.pannell@unil.ch>

Lichtenfels CentralEuropeanIUSSI 26-29Mar

IV Central European Meeting of IUSSI 2015 in Lichtenfels

We are pleased to announce the next Central European Meeting of the International Union for the Study of Social Insects held on 26th to 29th March 2015 in Lichtenfels, Germany. We welcome presentations on any aspect of the evolution, ecology, and/or conservation of social insects.

Please visit our website: (http://www.bayceer.unibayreuth.de/IUSSI/de/meeting_of/gru/html.php?id_obj=123377)

Program and Invited Speakers - Audrey Dussutour, University of Toulouse, France - Christoph Grüter, University of Lausanne, Switzerland.

Deadlines Registration will be open From 1st September to 30th November 2014. The deadline for abstract submission of oral and poster presentations is midnight (CET) of 31st December 2014. On 30th January we will announce the detailed program.

Venue We will discuss, eat and sleep at “Schloss Schney”, once a castle now a conference centre run by the Frankenakademie (http://www.franken-akademie.de). Lichtenfels (http://www.lichtenfels-city.de) is a picturesque town in the upper valley of the river Main with a convenient connection to the high-speed ICE train system of the Deutsche Bahn.

Registration fees including accommodation and catering Non-member 320 EUR Full member 290 EUR Student member 260 EUR

We are looking forward to seeing you in Lichtenfels!

Organizing Committee

Heike Feldhaar, University of Bayreuth Simon Tragust, University of Bayreuth Oliver Otti, University of Bayreuth

oliver.otti@uni-bayreuth.de

Lichtenfels CentralEuropeanIUSSI 26-29Mar Corrected

Announcement with the corrected link to our website:

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London AvianSensesEvolution Sep4-5

Invitation from the Royal Society Online version | Mobile version

We are pleased to inform you about a forthcoming Theo Murphy international scientific meeting organised by Dr Hannah Rowland, Professor Innes Cuthill and Dr Tom Pike, which may be of interest:

When senses take flight: the evolution, development, mechanisms and function of avian senses

Thursday 4 V Friday 5 September 2014 The Royal Society at Chicheley Hall, home of the Kavli Royal Society International Centre

This meeting is by invitation only, please visit the meeting webpage to request an invitation.

Please feel free to circulate this information to interested colleagues or students.

Image copyright Professor Tim Birkhead FRS

Event information

Birds are adapted to a diverse range of habitats, and operate within a broad range of dietary niches. This diversity of life histories has resulted in an equally varied suite of adaptations for acquiring mates, finding food, avoiding predators and for navigation. In this meeting, a distinguished list of international researchers encompassing avian vision, taste, olfaction, geo-magnetic sense, nociception (pain), tactile sense, and emotion, will be brought together to discuss new and emerging evidence of the evolution, development, mechanisms and function of avian senses.

This meeting is free to attend but participants must request an invitation before they can register.

For more information please contact Naomi Asantewa-Sechereh atkavli.events@royalsociety.org or on 020 7451 2515.

Hannah Rowland <h.m.rowland@gmail.com>

Marseilles 18thEvolBiol Sep16-19 DeadlineJun30

Dear all the the 18th ebm registration Dead line is june 30 the program will be available the july 3rd

best regards Pierre

18th Evolutionary Biology Meeting at Marseilles http://sites.univ-provence.fr/evol-cgr/

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

Moscow MolecularPhylogenetics Sep23-26

IV Moscow conference ≪Molecular Phylogenetics MolPhy-4≫ Moscow State University, 23-26 September 2014, Russia

The conference primary scope in the field of molecular evolution is phylogenetics and evolutionary genomics, phyloinformatics, reconstruction of the "Tree of Life", and various applications of phylogenetics. The conference aims to gather leading researchers in the field, stimulate cross-disciplinary interactions, and to establish long-term national and international collaborations. Young investigators are encouraged to participate.

The conference mission is to provide a stimulating platform for the exchange of ideas and experiences in contemporary phylogenetics, molecular evolution and bioinformatics, developing methodology, algorithms, and applications for state-of-the-art analyses of molecular genetic data.

Major topics are:

- Evolutionary genomics - Molecular phylogenetics and systematics - Molecular dating, inferring complex scenarios of coevolution, and reconstruction of complex ancestral traits and events in genome evolution - Development and phylogeny (evo-devo) - Models and algorithms for molecular evolution - Molecular ecology, biodiversity, and biogeography - Applied phylogenetics: genotyping and barcoding of biological objects, molecular anthropology, molecular epidemiology, and forensic science

The venue is Moscow State University, one of the top centers for education and science in Russia. Among the conference organizers and sponsors are Moscow State University (Faculty of Biology, Belozersky Institute for Physicochemical Biology, Faculty of Bioengineering and Bioinformatics, Research & Training Center "Evolutionary Genomics and Bioinformatics"), Russian Academy of Sciences (Institute for Information Transmission Problems), Russian Foundation for Basic Research, and Applied Biosystems (Life Technologies).

For important deadlines, contacts and other relevant information please consult www.en.molphy.ru or email at molphy@molphy.ru.

With best regards, the MolPhy committee

roussine@yandex.ru

RBG Edinburgh PlantEvolution Sep8-9

The United Kingdom is home to exceptional evolutionarybiologists. However, compared to the number of evolutionaryzoologists, the number of their botanical counterparts is few. In many cases, U.K. plant evolutionary biologists are in small numbers at any one institution, and such isolation hinders progress.

The Royal Botanic Gardens, Edinburgh will host a conference on 8, 9 September, 2014 to help address this situation. The conference will showcase evolutionary research on plants by UK researchers to foster new collaborations. The conference will also hold a workshop, where discussion will identify challenges faced and suggest strategies to overcome them. We see this as a first step towards developing a longer-terms strategy for strengthening the UK community of plant evolutionary biologists.

The conference will include a poster and networking session, open speaking slots (both standard and "lightning" talks), as well as an exciting lineup of invited speakers.

For more information and to register, please visit the website at:

http://symposium.bio.ed.ac.uk/-ukplantevolution2014/ Invited speakers:

Mating system: Dr. Mario Vallejo-Marin Speciation: Dr. Richard Buggs Ecological Speciation: Dr. Patrik Nosil Evo-Devo: Dr. Beverley Glover Phylogeny: Dr. Toby Pennington Polyploidy: Dr. Barbara Mable Biogeography: Dr. Bill Baker Population Genetics ? (Molecular ecology): Dr. Simon Hiscock Population Genetics (Genomics): Dr. Rob Ness

International Speaker: Dr. Spencer Barrett (University of Toronto)

– The University of Edinburgh is a charitable body, registered in Scotland, with registration number SC005336.

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crispin.jordan@ed.ac.uk

SanDiego PhysiologicalAdaptation Oct5-8

The upcoming Intersociety Meeting in Comparative and Evolutionary Physiology, organized by the American Physiological Society and several sponsoring societies (Society for Experimental Biology, SICB, TCS) will be held in San Diego, CA, October 5-8, 2014.

The Meeting Website is available at: http://www.the-aps.org/mm/Conferences/APS-Conferences/2014-Conferences/Comparative Funds are available to support student and postdoc travel. Several Special Symposia will cover a variety of topics regarding physiological adaptation.

Abstract submissions are due July 9, 2014.

In particular, Professor Guy Charmantier from Université Montpellier, France has organized a special symposium on Physiological Adaptation from Marine to Freshwater Environments. Invited speakers are listed below. Abstract submissions are encouraged to be included in this session:

Invasions of freshwater habitats by marine and brackish organisms have been successfully performed by only a few animal taxa over evolutionary time, and constitute one of the major transitions in the history of life. In addition, recent and rapid colonizations of freshwater areas have resulted from human activities, such as transportation. Invading low salinity environments confronts the animals with serious challenges for maintaining hydromineral balance, mainly in retaining and acquiring ions against adverse gradients, and excreting excess water. Freshwater environments can also be affected by contaminations, either natural or anthropogenic. As natural selection acts on all developmental stages, each must adapt to new conditions before invasion of a novel environment, such as freshwater, can become successful. This symposium addresses various physiological adaptations that have enabled colonizations of fresh water from marine environments over different time scales. Speakers will describe physiological adaptations at multiple hierarchical levels of biological organization, from molecules to organisms and populations, and will discuss several model species or taxa, mainly crustaceans and fish, at different stages of development, from embryos to adults. The talks will explore adaptive responses to challenges imposed by freshwater environments, including the presence of contaminants.

List of Invited Speakers:

Patricia Schulte, University of British Columbia, Canada

Jonathon Stillman, RTC, SFSU, UC-Berkeley, USA

Carol Eunmi Lee, University of Wisconsin, USA

Guy Charmantier, Université Montpellier, France

This session will also include other talks selected from submitted abstracts.

Carol Eunmi Lee, Ph.D. Professor Center of Rapid Evolution (CORE) 430 Lincoln Drive, Birge Hall University of Wisconsin Madison, WI 53706 carollee@wisc.edu

https://mywebspace.wisc.edu/carollee/web/Lee/-Lee.html carollee@wisc.edu

Seoul Korea CopepodEvolution Jul15

A special symposium on Copepod Evolution will be held at Hanyang University, Seoul Korea, at the Copepoda Conference, hosted by Professor Wonchoel Lee.

Special Symposium on Copepod Evolution

Tuesday, July 15, 9:00 am - 12:30 pm

HIT building, Hanyang University, Seoul, Korea

Invited Speakers (30 minute talks)

B. Evolutionary Adaptation to Environmental Change

Carol Eunmi Lee, University of Wisconsin, USA

Without Gills: Rapid evolution of osmoregulatory function in the copepod Eurytemora affinis during habitat invasions

Hans G. Dam, University of Connecticut, USA

Phenotypic plasticity and evolutionary thermal adaptation in the copepod genus Acartia

C. Evolution of Parasitic Copepods

Geoff Boxshall, The Natural History Museum

The evolution of host specificity in parasitic copepods

Frank Nilsen, University of Bergen, Norway

The salmon louse (Lepeophtheirus salmonis) genome: Some evolutionary implications based on the annotated gene-set.

D. Genomic Regulation

Grace Wyngaard, James Madison University, USA

Can the "yolk genome" hypothesis explain the elimination of billions of basepairs during chromatin diminution of Cyclops in nutrient poor lakes?

E. Zooplankton Metagenomics

Ryuji Machida, Academia Sinica, Taiwan

Community-based zooplankton genetic analyses: lessons from microbial studies

Carol Eunmi Lee, Ph.D. Professor Center of Rapid Evolution (CORE) 430 Lincoln Drive, Birge Hall University of Wisconsin Madison, WI 53706 carollee@wisc.edu

https://mywebspace.wisc.edu/carollee/web/Lee/-Lee.html carollee@wisc.edu carollee@wisc.edu

Suzhou China EvolutionaryGenetics Oct8-12

Cold Spring Harbor Asia meeting on

Evolutionary Genetics and Genomics October 8-12, 2014 - Suzhou, China

Evolution is the central theme in biology, but genomic tools allow new insights into the mechanisms and patterns of evolutionary change. This meeting will provide a format for the exchange of ideas and advances in evolutionary biology and genomics. Particular emphases will include the application of genomic approaches to study population diversity, new findings about adaptation and speciation, and our nascent understanding of the role of genetic interactions in the evolutionary process.

Meeting organized by: Brandon Gaut, University of California, Irvine, USA Song Ge, Institute of Botany, CAS, China Chung-I Wu, University of Chicago/Beijing Institute of Genomics, USA/China

Major topics: 1. Population Genomics V Methods 2. Population Genomics V Inferences 3. The Genomic Basis of Adaptation 4. The Genomic Basis of Speciation 5. Epistasis and Interactions 6. The Evolution of Networks 7. The Origin of Genetic Novelty 8. Epigenetics & Evolution

Many talks will be selected from the openly submitted abstracts on the basis of scientific merit and relevance. Social events throughout the conference provide ample opportunity for informal interactions.

FELLOWSHIP AWARDS will be selected from graduate students or postdocs presentations.

Register Now to get the early bird rate!

Cold Spring Harbor Asia Conferences Suzhou Dushu Lake Conference Center, No.299 Qiyue Road,SIP/ Suzhou, China Phone: +86 512 6272 9029 Fax: +86 512 6272 9028 Website: www.csh-asia.org Email: meetings@csh-asia.org

Brandon Gaut <bgaut@uci.edu>

UToronto Mississauga InvasivePlantEvol Aug6-8 AbstDeadline

Terrestrial Invasive Plant Species II: Abstract Deadline / Early Bird Extension

The Terrestrial Invasive Plant Species II meeting will be held at the University of Toronto Mississauga on 6-8 August 2014. We are inviting presentations on the ecology, evolution, impacts, and management of plants invading terrestrial systems, particularly in Ontario and surrounding areas. Please visit our website (https://secure.utm.utoronto.ca/tips2) for details.

Abstracts:

Please note that abstracts are due by 20 June; see our website for abstract formatting and instructions.

We also have extended our early bird deadline until the abstract submission deadline.

Please see https://secure.utm.utoronto.ca/tips2 for online registration and abstract submission information.

Program and Invited Speakers:

A draft schedule is now available on the website (https://secure.utm.utoronto.ca/tips2/tentative-program); we will update it to accomodate the abstracts that we receive. Our keynote speakers are Spencer Barrett from the University of Toronto, and Kirsten Prior from the University of Florida. We also are organizing a special session devoted to biocontrol of invasive plants; confirmed speakers to date include Bernd Blossey (Cornell University), Rob Bourchier (Agriculture and AgriFood Canada), Richard Casagrande (University of Rhode Island), John Gaskin (USDA-ARS), Hariet Hinz (CABI Switzerland), Lindsey Milbrath (USDA-ARS) and Richard Shaw (CABI UK).

Field Trips:

We are offering two pre-conference field trips on August 6, at a modest additional cost: the Carden Plain Alvar, and Rouge Park (https://secure.utm.utoronto.ca/tips2/optional-field-trips). If you would like to participate in one of these trips, please submit your payment with your conference registration; see our registration page for details. If you already have registered, or wish to add a field trip at a later date, please contact Antonia Maughn (antonia.maughn@utoronto.ca) for instructions. There also will be a lunchtime walk from the conference venue into the Credit River valley on August 8.

See you in August!

TIPS II Organizing Committee: Peter Kotanen, University of Toronto Mississauga (lead organizer) Sandy Smith, University of Toronto (St. George) Roberta Fulthorpe, University of Toronto Scarborough Ben Gilbert, University of Toronto (St. George) Marc Cadotte, University of Toronto Scarborough Pedro Antunes, Algoma University Colin Cassin, University of Toronto Mississauga (student member)

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

UToronto Mississauga InvasivePlantEvol Aug6-8 AbstDeadline 2

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Abstract deadline:

The final deadline for abstract submission for posters and oral presentations is June 20; early bird registration ends the same day. Please see https:/-/secure.utm.utoronto.ca/tips2 for on-line registration and abstract submission information.

Program and Invited Speakers:

A draft schedule is now available on the website (https://secure.utm.utoronto.ca/tips2/tentative-program); we will update it to accommodate the abstracts that we receive. Our keynote speakers are Spencer Barrett from the University of Toronto, and Kirsten Prior from the University of Florida. We also are organizing special sessions devoted to biocontrol and microbial interactions involving invasive plants; confirmed speakers to date include Bernd Blossey (Cornell University), Rob Bourchier (Agriculture and AgriFood Canada), Richard Casagrande (University of Rhode Island), John Gaskin (USDA-ARS), Hariet Hinz (CABI Switzerland), Lindsey Milbrath (USDA-ARS) and Richard Shaw (CABI UK).

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Peter M. Kotanen Department of Biology and Department of Ecology & Evolutionary Biology University of Toronto Mississauga 3359 Mississauga Road Mississauga, ON, L5L 1C6 CANADA tel: 905-828-5365; fax: 905-828-3792 lab: 905-828-5304; skype: peter.kotanen e-mail: peter.kotanen@utoronto.ca http:/-/www.utm.utoronto.ca/˜w3pkota/

Peter Kotanen <peter.kotanen@utoronto.ca>

GradStudentPositions

AalborgU Denmark EvolutionaryBiology

At the Faculty of Engineering and Science, Department of Biotechnology, Chemistry and Environmental Engineering, Section of Biology and Environmental Science a PhD stipend is available within the general study programme Biotechnology. The stipend is open for appointment from 1 September 2014. Job description

The interplay between the genotype and the environment governs the phenotype and ultimately the success of populations and species. The aim of the PhD study is to increase our understanding of interactions between the genotype and the environment. Populations of Drosophila and other arthropod model organisms will be investigated under a range of ecologically relevant benign and stressful environmental conditions and their functional and molecular phenotypes, as well genotypes, will be assessed to pinpoint causes and consequences of genotype by environment interactions. A special case of genotype by environment interactions, namely interactions between inbreeding and the environment, in small populations with high rates of inbreeding and genetic drift may have special focus in the proposed project. Results are expected to deepen our understanding of complex associations between genotypes and environments and thus provide answers to pressing questions in conservation and evolutionary biology.

The PhD project is part of a larger project financed trhough a Sapere Aude grant from the Danish Research Council. Applicants for this PhD position should hold a Master's Degree (or equivalent) in Biology, Biotechnology or similar, and have a strong interest in experimental as well as analytical work. Excellent skills in oral and written English are required. The candidate must submit the application including CV, list of publications (if available), official examination certificates and one or more recommendation letters.

You may obtain further information from Professor MSO Torsten Nygaard Kristensen, phone: (+45) 6146 3375 email: tnk@bio.aau.dk concerning the scientific aspects of the stipend. Please also visit this homepage for more information: http://www.stillinger.aau.dk/-vis-stilling/?vacancy=672971 Kind regards

Torsten

Torsten Nygaard Kristensen Biology and Environmental Science

Phone: (+45) 61463375 | Email: tnk@bio.aau.dk | Web: www.bio.aau.dk Aalborg University | Sohngaardsholmsvej 57 | Aalborg I Denmark

Torsten NygÃrd Kristensen <tnk@bio.aau.dk>

AMU Poznan MHCEvolutionGuppy

Graduate position: AMU_Poznan.MHCEvolutionGuppy

PhD position in evolutionary biology is available for four years starting from 1st October 2014 in a project “Testing new MHC allele advantage in semi-natural populations of the guppy, Poecillia reticulata”. This collaborative project is led by Professor Jacek Radwan (Adam Mickiewicz University, Poznan), Dr Cock van Oosterhout (University of East Anglia) and Dr Joanne Cable (Cardiff University, School of Biosciences), and is funded by Polish Science Centre (NCN).

Genes of the Major Histocompatibility Complex (MHC), involved in parasite recognition, are crucial for the adaptive immune response in vertebrates. While theories explaining maintenance of MHC polymorphism have been proposed decades ago, empirical tests of some of the most influential hypotheses are scant. Most notably, predictions about frequency-dependent selection (i.e. the hypothesis that rare MHC alleles should be selected for because fast-evolving parasites will adapt to evade immune recognition by common MHC alleles) have not been rigorously tested. The aim of this project is to test crucial predictions of this hypothesis using semi-natural populations of the guppy, Poecilia reticulata. The project will be based on Tobago and will use mesocosm setups to trace frequencies of MHC alleles, and infection levels associated with them, over several generations.

The PhD student will be mostly responsible for molecular analyses, but help in running the field experiment at Tobago is also possible.

The candidate should hold MSc degree in biological sciences. Applicants should provide the following documents:

1) Application letter 2) Copy of MSc diploma 3) CV 4) Motivation letter including description of scientific interests 5) Information on scientific activities of the candidate, including list of publications, active conference participation, work in scientific societies, honors and awards, national and international internships 6) Transcript of exam result during under graduate and 2nd level studies. 7) Information on language skills 8) Medical certificate stating candidate's suitability to undertake PhD studies in biology 9) Personal questionnaire 10) Two photos 35x45 mm

To: Dziekanat WydziaÅu Biologii Uniwersytet im. Adama Mickiewicza Ul. Umultowska 89 61-614 PoznaÅ by 3rd July; Interviews will be held between 8th and 11th July.

Further information can be obtained from the project leader via email: jradwan@amu.edu.pl

j.w.radwan@gmail.com

BlackHillsStateU SpearfishGenomics

BlackHillsStateU_Spearfish_Integrative_Genomics

The Masters in Science in Integrative Genomics program at Black Hills State University (Spearfish, South Dakota) currently has openings for the Fall 2014 semester. This program exposes students to modern techniques and instrumentation in the laboratory and field and prepares students for success in both academic and other biotechnology-related pursuits.

Graduate Research Assistantships (RAs) are awarded to students and provide a competitive stipend ($16,640/yr) plus funding for research. All RAs receive a reduced tuition rate (1/3 of in-state rate) and assist with instruction of undergraduate-level science labs.

Black Hills State University, located in the heart of the northern Black Hills V Spearfish, SD, offers 75 academic programs at the associate, bachelor, and master degree levels. BHSU, which has over 4,000 students, has earned a reputation for transforming lives through innovative, high-quality academic programs and a dynamic learning community. Our location provides a natural laboratory for Integrative Genomics. We are also close to the Deep Underground Science and Engineering Laboratory (DUSEL) at Homestake Mine, allowing for collaboration with other major universities (to study, for example, the meta-genomics of the unique microbial communities found in extreme environments).

Learn more about the community here:

www.visitspearfish.com www.youtube.com/-watch?v=HTsFzC9vESI www.youtube.com/-watch?v=BrRRHz2TRDs Information about M.S. Integrative Genomics program requirements and application process can be found here:

www.bhsu.edu/Academics/GraduatePrograms/-IntegrativeGenomics/tabid/2164/Default.aspx For further information email: Raeann.Mettler@bhsu.edu

Raeann Mettler <raeann.mettler@gmail.com>

CNR Napoli Italy HumanAdaptation

We are looking for a motivated candidate for a research project described below.

Position is at the Institute of Genetics and Biophysics - National Research Council in Napoli, Italy http://www.igb.cnr.it/ Deadline for applications is 10/07/2014

BACKGROUND - The understanding of genetic variation is essential to decode traces that evolution has left in our genomes and whole-genome sequence data now allow us to do interpret these signals at a resolution never possible before. Adaptive processes in humans have left signature in the genome and information about sites putatively under positive selection in human is now available.Next challenge is to combine this information with functional interpretation to understand the environmental pressure that drove the adaptation and the underlying molecular mechanisms at cellular level.

RESEARCH PROJECT - This project aims to study functional consequences of a mutation in a gene showing evidences for positive selection in Asians and Europeans. This gene is implicated in the formation of the skin lipid barrier and regulated by UV radiation. Alterations of the gene sequence cause severe forms of skin diseases. This project will clarify key molecular mechanisms of interaction of humans with the environment and advance our understanding of the role of environmental adaptation in modern diseases. Project includes both wet laboratory experiments (40%) and bioinformatics analyses (60%) and a mandatory work experience abroad.

ELIGIBILITY - Candidates with a master degree either in biology/medicine or informatics/mathematics/physics/engineer are equally eligible and in each case they should be willing to do both wet laboratory and computational analyses.

SELECTION CRITERIA - The successful applicant will be selected on documented theoretical and experimental knowledge relevant for the area of study, knowledge of scientific theory and method, analytical skills, personal motivation and team working skills. Well-developed English language skills are required. The applicants are encouraged to provide supporting documents that substantiate qualifications, e.g., knowledge, skills, abilities and experience. Experience with programming languages is a plus. References and interviews will be used to assess qualifications of the applicants.

INFORMATION - We encourage to discuss your application before submitting. Please contact vincenza.colonna@igb.cnr.it. For more information visit: http://goo.gl/axpzzw and http://www.igb.cnr.it/

APPLICATIONS Applications should be submitted to vincenza.colonna@igb.cnr.it and should include: 1. Cover letter 2. CV with information about your: a) Degrees and education b) Job experience c) Independent project V Masters project title and brief description d) Language skills e) ReferencesV name and e-mail addresses of 2V3 reference persons 3. Research plan V this should be a personal statement motivating why you are applying for this position (maximum 2 pages) 4. Other documents V other documents you may wish to provide

The deadline for applications is July 10th 2014

would you like to know about the most amazing project ever? http://www.igb.cnr.it/obilab interested in Life Science and/or Mathematics? visit http://www.bmtl.it/ Vincenza Colonna Consiglio Nazionale delle Ricerche Istituto di Genetica e Biofisica “Adriano Buzzati-Traverso” piano 1, stanza 20 via Pietro Castellino 111 - 80131 Napoli - IT

tel +39 081 6132 254 fax +39 081 6132 706 skype enza.colonna email vincenza.colonna@igb.cnr.it

http://www.igb.cnr.it/index.php?id=90&staff_detail=colonna http://scholar.google.co.uk/citations?user=-ufP1EYgAAAAJ&hl=en&oi=ao Visiting Scientist The Wellcome Trust Sanger Institute Wellcome Trust Genome Campus Hinxton Cambs. CB10 1SA UK

email cv1@sanger.ac.uk

vincenza colonna <vincenza.colonna@igb.cnr.it>

HamburgU EcologicalGenomicsBioinformatics

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

*****

Universität Hamburg invites applications for a

Research Associate commencing on August 1st 2014 (earliest starting date).

The position is part time (19.5 hours per week) and is remunerated at the 13 TV-L salary level.

The short-term, three-year contract terminates on July 31st 2017 or at a later date, depending on the starting date.* The short-term nature of this contract is based upon §2 of the Academic Short-term Contract Act (WissZeitVG).

The University aims to increase the number of women in research and teaching and explicitly encourages women to apply. Equally qualified female applicants will receive preference in accordance with Hamburg’s Higher Education Act (HmbHG).

Tasks:

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

Area(s) of responsibility:

The group focus on global biodiversity and evolutionary genomics of freshwater zooplankton (Daphnia), using next-generation sequencing data. Bioinformatics tools are used to detect local adaptation patterns in natural populations and experimental cultures will allow assessing the phenotype/genotype correlation. The candidate will be analysing RNAseq data and plan/conduct follow-up studies on candidate genes, in collaboration with another graduate student (focusing on the experimental part). The Next Gen data analysis includes (but is not limited to) differential expression analysis, SNP calling and eQTL analysis. Furthermore, a comparative approach will be used, since the genomes and transcriptomes of other Daphnia species are available.

The candidate is encouraged to develop specific projects of her or his own choice as long as they include mining this data and are conducted in collaboration with other members of the group.

Requirements:

A university degree in a relevant field: Biology, Bioinformatics

The candidate should:

- be familiar with bioinformatics methods, through experience gained while doing the master project, for example.

- have a strong background in evolutionary biology / molecular ecology. In addition, knowledge of population genetics will be advantageous.

- be familiar with at least one of these scripting languages: python, perl, C++, R

- be creative, critical and have conceptual thinking skills.

- have good communication and writing abilities in English.

- be able to work both independently and as part of a multidisciplinary team.

The working language of the group is English, willingness to learn German is necessary to allow a better integration/communication in the institute and in daily life.

Severely disabled applicants will receive preference over equally qualified non-disabled applicants.

Applications should include a letter of application, a detailed curriculum vitae, an abstract of your master thesis, and copies of degree certificate(s), as well as the names of two scientific referees. These documents should be submitted as a single pdf-file in the given order. The deadline for applications is June 30th 2014. Please send applications to: Mathilde Cordellier via the 'Apply' button. For further information, please contact Mathilde Cordellier on 040-428 38 3933 or mathilde.cordellier@uni-hamburg.de. Alternatively, please consult our website

http://www.uni-hamburg.de/biologie/BioZ/zis/meb/-mit/cordellier.html . * In accordance with §§27, 28 of Hamburg's Higher Education Act (HmbHG).

cordellier@biologie.uni-muenchen.de

KF-UGraz Austria FishEvolution

Two PhD Positions in Ecology and Evolution of Fishes

Two PhD positions are being offered at the Department of Zoology, Karl Franzens University Graz, Austria. The positions offer a 3- year salary funded directly through the University under the new collaborative PhD educational program, assigned to the Evolutionary Biology and Molecular Ecology research group (http://zoologie.uni-graz.at/en/forschen/kategorie41/-evolutionsbiologie-und-molekular-oekologie/). The PhD candidates are affiliated to the Doctoral School of Biology of the University of Graz, and are expected to spend some time in the lab of the respective cooperation partners during their PhD studies. A detailed research plan will be adapted with input from the prospective candidates. One PhD position will focus on topics related to salmonid fishes and second to cichlid fishes, both using molecular genetic and genomic approaches.

The research with salmonid fishes will be carried out in cooperation with Ulrich Schliewen at the Natural History Museum in Munich.

The research on cichlid fishes in cooperation with the lab of Prof. Axel Meyer at the Department of Biology of the University of Konstanz.

CVs should be sent to either Steven Weiss (steven.weiss@uni-graz.at) or Christian Sturmbauer (christian.sturmbauer@uni-graz.at) by June 30, 2014. Candidates should expect to start approximately September 1st 2014.

Steven Weiss, Assoc. Prof Dr. Karl-Franzens University Graz Institute of Zoology Universititätsplatz 2 A-8010 Graz, Austria Tel: +43-0316-380-5599 Fax:+43-0376-380-9875

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

LaurentianU AmphibianEvolutionaryEcol

Graduate Position at Laurentian University (ON) and Keyano College (AB) Evolutionary Ecology of Amphibian Emerging Infectious Diseases

We are seeking one MSc/PhD student to join our lab at Laurentian University http://gearg.jimdo.com/- and the Centre for Evolutionary Ecology and Ethical Conservation (http://ceeec.wordpress.com) in the area of Emergent Infectious Diseases in Amphibians (Ranavirus & Chytrid fungus).

These two diseases are causing mass die-offs in amphibian populations but the evolution, ecology, dynamics and effects of the pathogens are still largely unknown. In particular, 2 questions are of interest: -what are the temporal patterns associated with this host-pathogen(s) system? -what role does a community of host species play in the maintenance of the pathogen(s)?

The student will work in this context by combining fieldwork and experiments depending on his/her interests. Good aptitude for fieldwork, molecular ecology skills and some herpetological knowledge are expected as well as good communication skills.

Starting date: Candidates are expected to commence their studies in January 2015.

Funding: Full funding of approximately $17,000/year is guaranteed for 2 years through a combination of TAships and RAships. Additional scholarships will be available by competition.

How to apply: Interested students should contact us via email, including a cover letter describing background and interests (including specific interests in our lab), cv, transcripts (unofficial is fine).

Dr. David Lesbarrères (dlesbarreres@laurentian.ca) Dr. Danna Schock (danna.schock@keyano.ca)

“It takes all the running you can do to keep in the same place.”

Dr. David Lesbarrères, Associate Professor Director, School of Graduate Studies

Genetic & Ecology of Amphibians Research Group (GEARG) Department of Biology - Laurentian University, http://gearg.jimdo.com/ Ramsey Lake Road, Sudbury, Ontario P3E 2C6, Canada phone: (705)675-1151 ext. 3232/2275 - Fax: (705)671-3840

dlesbarreres@laurentian.ca

LeibnizInst ImmunogeneticDiverstiy

Advertisement of vacancy

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

The Department of Wildlife Diseases offers (beginning 1st September 2014) a PhD-Position on “Measuring immunogenetic diversity during the Pleistocene”(Reference number 20/2014)

This project will utilize novel next generation sequencing approaches to characterize the evolution of immunogenetic loci over a ca. 50,000 year time span in species with contrasting demographic histories (extinct woolly mammoths and muskoxen). We expect to determine the rate of evolution, persistence and replacement of Toll-Like Receptor (TLR) and Major Histocompatibility locus (MHC) alleles for both species which will provide a better understanding of the evolutionary dynamics of the loci that cannot be obtained from examination of modern DNA.

Specific tasks include

- Development of hybridization capture assays coupled with next generation sequencing for the MHC and TLRs - Bioinformatic and evolutionary genetic analysis of generated data - Logistical coordination of work between Canada, Denmark and Germany

Requirements

- Diploma or Master of Science in Biology or related fields; - Strong background in evolutionary biology and phylogenetics; - Preference will be given to candidates with ancient DNA or forensic DNA experience; - Preference will also be given to candidates with next generation sequencing experience; - A background in statistics and bioinformatics would be advantageous; - Organizational skills and ability to work in a team; - Part of the project will take place in Canada. Thus, proficiency in English (speaking and writing) is required

The position is initially limited to two years, beginning September 1, 2014, with the possibility for extension to a maximum of three years. Salary takes place according to TVöD (65%). The IZW is determined to increase the proportion of women in successful scientific careers and particularly encourages female scientists to apply.

For further information please contact Prof. Alex Greenwood (e-mail greenwood@izw-berlin.de). Applicants should submit a letter explaining their interests in and particular skills for this position, a CV, copies of relevant degrees and contact details of two people who can provide a reference, as one single PDF-file before July 11th , 2014.

Applications should be sent to:

Leibniz-Institut für Zoo- und Wildtierforschung im Forschungsverbund Berlin e.V., Personalabteilung, Frau Stephanie Vollberg, (personal@izw-berlin.de), Postfach 70 04 30, 10324 Berlin, www.izw-berlin.de Best wishes Stephanie

Stephanie Vollberg Personal IZW Tel. 030- 5168 107 Fax. 030-5126 104 vollberg@izw-berlin.de

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

Marseilles MarinePopulationGenetics

topic : URGENT PhD in Marseilles-France, marine population genetics/metabarcoding

We seek a highly motivated and well ranked PhD student to study the biodiversity of (marine) coralligenous habitats, at both the community and intraspecific levels, from data that will be mostly obtained using genetic tools including Next-Generation Sequencing, and analyzed taking into account ecological factors and marine currents (at both the local and Mediterranean scales).

The scientific interest relies in comparing diversity at the community level, assessed by metabarcoding and compared with traditional taxonomical methods, and diversity at the intraspecific level (population genetics or genomics), providing ways of testing hypotheses such as the neutral biodiversity one, for instance. The implicated goal± is to gain knowledge on these habitats, which provide important services and are very species rich, in order to propose new, efficient and cost-effective indicators of their ecological status, based on intra-specific and/or inter-specific diversity (to be tested).

The team working on this topic, financed by two European projects is locally composed of a post-doctoral fellow (starting in autumn 2014), a PhD student on coralligenous Socio-ecosystem (starting autumn 2014) and an engineer to help with meta-barcoding (to be hired before the end of 2014), a last-year PhD student (diving, ecology, indicators), and several permanent researchers plus the diving team.

More details are available at: http://www.otmed.fr/-spip.php?article668#SujetChenuil send applications and questions to Anne Chenuil anne.chenuil@imbe.fr

Anne CHENUIL

Email: <anne.chenuil@imbe.fr>

UMR 7263 (CNRS) - IMBE Institut Mditerranen de Biodiversit et d’Ecologie Marine et continentale (IMBE) (Aix-Marseille Universit) Station Marine d’Endoume Chemin de la Batterie des Lions 13007 MARSEILLE

Tel.: +33 (0)4 91 04 16 17 Fax: +33 (0)4 91 04 16 35

Anne Chenuil <anne.chenuil@imbe.fr>

MasseyU 4 EvolCellBiol

Graduate Assistantships in Mathematics, Statistics, Chemistry and Cell Biology

The Institute of Fundamental Sciences has four Graduate Assistant positions available for students wishing to study for a PhD at Massey University < http://www.massey.ac.nz/ > in Palmerston North, New Zealand. One Graduate Assistant position will be appointed in each of the subject areas Mathematics, Statistics, Chemistry and Cell Biology. These are salaried teaching positions in which the appointee will be undertaking full-time PhD studies. Each appointee will be required to contribute up to 360 hours of undergraduate teaching effort in the subject area each year. The positions are for a three-year fixed term to cover the expected duration of PhD research. A successful candidate must meet all the requirements of a suitable match in teaching duties, eligibility to undertake and maintain PhD studies at Massey University, a research area strategic for the Institute, together with an enthusiasm to undertake research in that area.

Note that the GA in Cell Biology will contribute to our first year Biology of Cells paper, but may have research interests in Biochemistry, Biomedicine, Genetics, Plant or Microbial Science, or Evolution.

Interested candidates should visit the Institute website < http://www.massey.ac.nz/massey/learning/colleges/college-of-sciences/research/fundamental-sciences-research/fundamental-sciences-research_home.cfm > to identify a potential PhD supervisor and contact that person to discuss research possibilities.

To apply, please visit: http://jobs.massey.ac.nz/PositionDetail.aspx?p=3D8342 Jennifer A. Tate, Ph.D. Senior Lecturer in Plant Systematics and Evolution Curator, Dame Ella Campbell Herbarium (MPN) Associate Editor, Systematic Botany

Massey University Institute of Fundamental Sciences Private Bag 11222 Palmerston North New Zealand

Phone: 64-6-350-5515 ext. 84718 FAX: 64-6-350-5682

http://www.massey.ac.nz/ ~ jtate/index.htm
J.Tate@massey.ac.nz

MaxPlanckInst Jena BeetleGenomics

*Master Thesis Projects in Max Planck Institute for Chemical Ecology - Research Group Insect Symbiosis *

A position is available from July 2014 in Jena, Germany, to carry out either of the projects outlined below.

Beetles in the subfamily Lagriinae live in association to bacteria of the genus /Burkholderia/, a group exhibiting extraordinary ecological and metabolic versatility. The transmission of the symbiotic bacteria from mother to offspring is facilitated by structures, particularly in the larval stage, that are considered unique in terms of location and development.

Project 1: Horizontal transmission of bacterial symbionts in lagriid beetles

Despite a described vertical transmission route, the possibility remains that lagriid beetles occasionally acquire /Burkholderia/ from the environment or from related host species (horizontal transmission), having important implications for the ecology and evolutionary trajectory of the association. The main purpose of the project is to test whether horizontal transmission of bacterial symbionts can occur across two different lagriid species and to describe potential exchange routes, as well as the possibility of infection by multiple bacterial strains.

In order to address these questions, the student will work on manipulative experiments involving bacterial culture, insect collection and lab rearing, DNA extraction, PCR, phylogenetic analyses and Fluorescence in situ hybridization (FISH). We are looking for a highly motivated candidate with a strong background in the areas of ecology, evolutionary biology, entomology or microbiology, to carry out her/his M.Sc. thesis project or an internship for a period of 4-6 months.

*Project 2: Genomics of /Burkholderia/ symbionts of lagriid beetles *

The symbiotic bacteria in the two lagriid hosts investigated until now belong to the species /Burkholderia gladioli/, which is known to be pathogenic on certain plants and fungi, as well as an opportunistic human pathogen. The lagriid-associated strains possess a genome of comparable size lacking evident signs of gene erosion, contrary to other vertically transmitted bacterial symbionts. A M.Sc. thesis project is available to carry out a comparative genomic analysis of the symbiotic strains and closest relatives with a different life style in order to identify genomic traits and/or specific genes that are potentially relevant for the symbiosis.

The M.Sc. student should have experience and/or a solid theoretical knowledge in bioinformatics, genome analysis and biochemistry, as well as a strong interest in evolutionary biology and the ecology of symbiotic interactions. Background in transcriptome analyses is also advantageous.

Please send your applications (including previous research experience and CV) to:

Laura Flórez/Dr. Martin Kaltenpoth

Max Planck Institute for Chemical Ecology Research Group Insect Symbiosis Hans-Knöll-Straße 8, 07745 Jena - Germany

E-mail: lflorez [at] ice.mpg.de or mkaltenpoth [at] ice.mpg.de

Laura Flórez Insect Symbiosis Research Group Max Planck Institute for Chemical Ecology Hans Knoell Str. 8 07745 Jena, Germany

Tel: +49 (0)3641 57 1804 Fax: +49 (0)3641 57 1810

Laura Florez <lflorez@ice.mpg.de>

ParisSudU EukaryoticPhylogenomics

A PhD position on eukaryotic phylogenomics is available at the University Paris-Sud (France) in the DEEM laboratory (Diversity, Ecology and Evolution of Microorganisms: http://www.ese.u-psud.fr/-spip.php?rubrique7&lang=en).

-Scientific context: Despite intense research in recent years, the general phylogeny of eukaryotes remains poorly resolved. The order of divergence of the major eukaryotic phyla and the settlement of essential metabolic and structural features are still insufficiently described. Many extant eukaryotic phyla emerged through the gain or loss of plastids carrying out photosynthesis. Plastid endosymbiosis is accompanied by a massive flow of Endosymbiotic Gene Transfers (EGT) from the symbiont to the host genome. The first plastid endosymbiosis in eukaryotes involved a cyanobacterium and an unknown host and gave rise to the supergroup Archaeplastida (green algae and plants, red algae, and glaucophytes). This initial endosymbiosis was followed by a number of subsequent endosymbioses where various heterotrophic hosts engulfed and converted green and red algae into the secondary plastids found in many eukaryotic phyla today. These, and their heterotrophic relatives, were shaped by secondary endosymbiosis but we still do not know when, how and to what extent.

-Project: The goal of the PhD project is to decipher the role of secondary endosymbiosis in eukaryotic evolution by improving the genome sequence data for underrepresented phyla and providing a rigorous analysis of EGT traces in these genomes. Using next generation sequencing, we are producing high coverage transcriptomes of a variety of photosynthetic and heterotrophic species having strategic positions on the phylogeny of eukaryotes. The PhD will be in charge of analyzing these data by phylogenomic and comparative genomic methods to: 1) Enhance the resolution of the tree of eukaryotes, 2) detect traces of secondary endosymbiosis and attempt to infer when they occurred, 3) take advantage of this new genomic resources to understand the evolution and the settlement of original metabolic features characteristic of these eukaryotic groups.

-Qualifications: Candidates must have an MSc degree and strong interest in early evolution and eukaryotic diversity and phylogeny as well as some experience in computational biology.

-Application: The application should include 1) a motivation letter, 2) a detailed CV with grades/ranks, and 3) the names and contact information for at least two referees. This material has to be sent by e-mail to David Moreira (david.moreira@u-psud.fr) and Philippe Deschamps (philippe.deschamps@u-psud.fr).

david.moreira@u-psud.fr

TennesseeTechU FloralEvolution

PhD Graduate Student Opportunity Pollination biology of Australian Passiflora

A PhD position in the lab of Dr. Shawn Krosnick is available through the School of Environmental Studies at Tennessee Tech University in Cookeville, Tennessee; starting date is January 2015. A Master's degree is required and must be completed prior to starting the PhD at TTU. The project will examine floral morphology, pollinator-plant interactions, and the evolution of self-compatibility in the three native Australian species of Passiflora (passion vines). Additional taxonomic work is possible depending on the interests of the candidate. Extended field studies in Australia will be required, as well as greenhouse experiments and anatomy/microscopy work conducted in the US. Highly motivated candidates with a strong academic record are encouraged to apply. The successful candidate should be comfortable working independently and enjoy field work under a wide range of conditions. The student will be expected to apply for external funding to support aspects of their field research. Financial support and tuition will be provided through a Teaching Assistantship and will be renewable contingent upon satisfactory performance.

Interested students should send a short description of academic background, research interests, and a CV to skrosnick@tntech.edu by August 1, 2014 for full consideration. Screening of applicants will begin immediately.

Shawn Krosnick, Ph.D. Assistant Professor of Biology Curator of the Hollister Herbarium Tennessee Tech University P.O. Box 5063 Cookeville, TN 38505 931-372-6194 skrosnick@tntech.edu Lab webpage < http://sekrosnick.wix.com/krosnicklab >

skrosnick@tntech.edu

UCanterbury NZ DeepSeaPhylogenetics

PhD Scholarship - Deep Sea Community Phylogenetics

A PhD scholarship is being offered for study in the School of Biological Sciences at the University of Canterbury, New Zealand, with Dr Sharyn Goldstien and Dr Travis Horton, in collaboration with Senior Fisheries Scientist from leading research institutes: Dr Ashley Williams (Secretariat of the Pacific Community), Dr Malcolm Clark (NIWA), and Dr Stephen Newman (Western Australia Fisheries).

We seek a high-calibre student to integrate phylogenetics and spatial ecology to be modelled against isoscapes, magnetic field maps and fishing pressure, with the aim to integrate spatial diversity patterns and potential drivers of diversification in deep-sea habitats.

Our research team members have unique access to comprehensive ecological data sets and biological samples throughout the Pacific, including New Zealand, Australia, New Caledonia and the Kingdom of Tonga. Our skill set allows the integration of phylogenetics and molecular ecology with fundamental ecology, biology and fisheries science, essential to the advancement of deep-sea science and comparative biogeography.

This is a chance for a passionate student to join an international team of scientists focused on advancing deep sea science and ensuring sustainable use of these important resources.

Scholarship Details and Application

The scholarship consists of a NZ $20,000 per annum student stipend (i.e., tax free living allowance) and funding to cover course fees and research expenses for three years.

Applications should be sent via e-mail to Nicki Judson (nicki.judson@canterbury.ac.nz), administrative assistant in the School of Biological Sciences,by 9 July 2014, and should include:

1. (i) a full curriculum vitae (including phone contact details), 2. (ii) a copy of your academic record, 3. (iii) a one page statement of your research interests and aspirations, 4. (iv) the names and contact details of three referees who are willing to provide confidential comments on your capacity to undertake a PhD, and 5. (v) an indication of your desired start date.

Successful applicants may be required to submit copies of official documents before being admitted to the PhD program at the University of Canterbury.Questions of an academic nature can be addressed to Dr Sharyn Goldstien, Sharyn.goldstien@canterbury.ac.nz

Thank you Dr Sharyn Goldstien Marine Ecology and Evolution School of Biological Sciences University of Canterbury PB 4800, Christchurch, 8140 New Zealand

Tel: +64 3 3642987 x. 45646 Fax: +64 3 3642590 www.canterbury.ac.nz/people/goldstien.shtml

sharyn.goldstien@canterbury.ac.nz

UGlasgow Adaptation

PhD Studentship, University of Glasgow

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

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

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

Project team:

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

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

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

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

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

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

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

Deadlines: We are still accepting applicants for this position and will do so until we have found a suitable candidate.

Barbara.Mable@glasgow.ac.uk

UGlasgow VirusEvolution

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

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

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

Application deadline: 31 July 2014 Stipend: £13,726 per annum (2013/14 rate) Start date: 1 October 2014

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

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

Eligibility

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

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

You can apply here: http://www.gla.ac.uk/research/opportunities/howtoapplyforaresearchdegree/ Within the application, at the programme of study search field option, please select 'MVLS - BBSRC WestBio DTP Glasgow/Moredun'.

Please note that, in step 6 within the online application process, you are asked to detail supervisor/project title information. Please detail the following information:

Supervisors: Dr Roman Biek; Dr Colin J McInnes; and Dr Alain Kohl Project title: A genomic approach to uncovering the mechanisms driving host restriction and virulence in louping ill virus

Please ensure that all supporting documents are uploaded at point of application:

- Academic ability evidence - CV/Resume - Degree certificate (if you have graduated prior to 1 July 2014) - Language test (if relevant) - Passport - Personal statement (This should provide any other required information in support of the application, such as evidence of previous academic or professional experience that qualifies you for the programme (projects; placements; voluntary work etc). You should state the reasons why you selected this programme and what benefit you hope to achieve through successful

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UHelsinki AncientEvolution

A 4-year PhD position at University of Helsinki in resurrection ecology:

Reconstructing past responses of Eubosmina maritima to anthropogenic environmental changes using the historical archives of the Baltic Sea sediment

A powerful way to reconstruct past responses of populations to human-induced environmental changes is to use the information hidden in the sediment in the form of dormant eggs and subfossils. We investigate how and why the cladoceran zooplankton community has changed in response to human-induced environmental change during the last century, using resurrection ecology, paleolimnology and paleogenomics.

The PhD project will involve reconstructing past responses of Eubosmina maritima to human-induced changes of the Baltic Sea, particularly to eutrophication and changes in the fish fauna. Recorded phenotypic changes will be related to environmental changes to determine whether the population has been able to track changes in the environment. Reaction norm experiments will be performed to investigate the degree of plasticity and the limits of responses. The work will be complemented with genomic work carried out within the research group. This will allow us to determine the genetic underpinning of the phenotypic changes. A detailed research plans will be developed and tailored to match your individual interests and strengths. The work is done in collaboration with the research groups of prof. Dieter Ebert at University of Basel and Dr Luisa Orsini at University of Birmingham. English is the working language.

*Your role: Your work will include the retrieval and hatching of dormant eggs of E. maritima from dated sediments of the Baltic Sea, the cultivation of clonal lineages from these resurrected eggs, and the performance of reaction norm experiments using the clonal lineages, to determine their responses to blooms of toxic cyanobacteria. In addition, microfossils will be measured to record phenotypic changes across time. Depending on your interests and strengths, you can contribute to the genomic work. You will work in close collaboration with two post-docs within the group, and participate in the supervision of undergraduate students and assistants.

*Qualifications: You will have a Masters or equivalent degree in ecology or evolutionary biology (or related fields), and a strong interest in the research questions and a high motivation to pursue a PhD. Excellent written and oral communication skills in English are required, as are the ability to work efficiently, independently as well as in collaboration.

*We offer: The salary will follow the demands level chart for teaching and research personnel in the salary system of Finnish universities, with a salary component based on personal performance. All standard pension benefits and occupational health care are provided for university employees. For information on the University of Helsinki, please visit: http://www.helsinki.fi/university/index.html *Starting date: 1st of September 2014 or as agreed on.

*To apply: Consideration of applications will begin on 15th of June 2014, and will remain open until filled. Please send your application with (1) a statement of research interests and why you have applied for this position, (2) your CV, (3) an authorized copy of your MSc degree (if available at time of application, and (4) contact details of two references to Dr Ulrika Candolin at ulrika.candolin@helsinki.fi

Feel free to address informal inquiries to:

Ulrika Candolin Phone: +358-(0)2941-57800 Email: ulrika.candolin@helsinki.fi http://www.mv.helsinki.fi/home/ucandoli ulrika.candolin@helsinki.fi

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UHelsinki GeneNetworkEvolutionaryBiol

Graduate position for a PhD in the evolutionary biology of gene networks.

1.Job/ project description:

The main objectives of the PhD project is to:

a) Develop mathematical models of the relationship between genetic and phenotypic variation (or genotype-phenotype map)

b) Understand how this relationship and the patterns of phenotypic variation possible by genetic variation in gene networks affect evolution.

c) Develop models about the evolution of gene networks and embryonic development in general.

A core concept of current evolutionary biology is the genotype-phenotype (GP) map, which connects genetic variation to phenotypic variation and to potential for evolutionary change. The aim of the project is to develop or investigate models of the GP map that can be related to specific biological study systems or specific evolutionary questions investigated by the group. There is considerable flexibility as to the exact topics, and the interests of the candidate will be important in defining the study objects.

These models can be abstract or linked to specific biological systems. The biotechnology institute includes a range of experimental biologitst working on several systems. The supervisor of the theoretical aspects will be Dr. Salazar-Ciudad but the PhD would include close collaboration with Jukka Jernvall group and would include collaboration with developmental biologists, bioinformaticians, paleontologists and other evolutionary and systems biologists. The work may also include, optionally, collaboration, and spending some time, in Barcelona.

The modeling can focus on gene network regulation, cell-cell communication, cell mechanical interactions and developmental mechanisms in general and, optionally, artifical in silico evolution.

2. Requirements:

The applicant must be a biologists, preferably with a strong background in either evolutionary biology, developmental biology or theoretical biology. Some knowledge of ecology, zoology, cell and molecular biology are also desirable.

Bioinformaticians, systems biologists or computer biologists that do not have a degree in biology (e.g. Computer scientists, physicists or engineers) would not be considered (not replied).

Programming skills or a willingness to acquire them is required.

The most important requirement is a strong interest and motivation on science, gene networks and evolution. A capacity for creative and critical thinking is also desirable.

Prior experience in evolutionary or developmental biology is an advantage, and the candidate may be required to do some programming (although how much may depend on the exact project).

3. Description of the position:

The fellowship will be for a period of up to 4 years (100% research work: no teaching involved).

The purpose of the fellowship is research training leading to the successful completion of a PhD degree.

Salary according to Finnish PhD student salaries.

4. The application must include:

-Application letter including a statement of interests - CV (summarizing degrees obtained, subjects included in degree and grades, average grade)

-Application should be send to Isaac Salazar-Ciudad by email:

isaac.salazar@helsinki.fi

Foreign applicants are advised to attach an explanation of their University's grading system. Please remember that all documents should be in English.

5. Examples of recent publications by Isaac Salazar-Ciudad group.

-Salazar-Ciudad I1, Marín-Riera M. Adaptive dynamics under development-based genotype-phenotype maps. Nature. 2013 May 16;497(7449):361-4.

-Salazar-Ciudad I, Jernvall J. A computational model of teeth and the developmental origins of morphological variation. Nature. 2010 Mar 25;464(7288):583-6.

6. Interested candidates should check our group webpage:

http://www.biocenter.helsinki.fi/salazar/index.html
The deadline is 15 of August (although candidates may be selected before).

Isaac Salazar-Ciudad: isaac.salazar@helsinki.fi

isalazar@mappi.helsinki.fi

UMainz EvolutionaryBiology

PhD position, University of Mainz, Department of Evolutionary Biology:

"Evolution of ant slavery and the genetic basis of slavemaker and host behavior"

We invite applications for a 3-years PhD position at the JG University of Mainz, Germany. The project aims at understanding the evolution of slavemaking and host defense behavior and its genetic basis. Our model system are /Temnothorax/ ants, in which ant slavery evolved repeatedly and in which parasite pressure led to the evolution of multiple host defense strategies. In this project, we use a RNA-seq approach to study characteristic gene expression patterns in closely related slavemaker and host species and compare different behavioural states within and between species. Moreover, we will use sequence data to detect differentially selected genes between slavemaker and host species with the aim to identify genes involved in slavemaker and host evolution. Our aim is to link slavemaker phenotype to its underlying genotype, as to unravel in future the genetic basis of coevolution in these obligate social parasite-host systems.

The position requires a Diploma or Master degree in Biology (or a related field). The successful candidate should be highly motivated and have a strong background in evolutionary genetics and behavioral ecology. Previous research experiences with genomics, transcriptomics, bioinformatics, behavioral experiments, or social insects are advantageous, but not required. The position is funded by the DFG (65% TV-L E13). Students from every nationality are encouraged to apply. The working language of the laboratory is English.

Our young group offers an international, dynamic and interactive scientific environment and state-of the art, newly equipped laboratories. Information on our scientific work including recent publications can be found under http://www.bio.uni-mainz.de/-zoo/evobio/318_ENG_HTML.php. For more information, please do not hesitate to contact us feldmeye@uni-mainz.deor foitzik@uni-mainz.de. The University of Mainz hosts many excellent scientific institutions (http://www.uni-mainz.de/eng) and Mainz is a historic city located on the River Rhine with many students and a rich social and cultural life (http://www.mainz.de).

Interested candidates should send an application (as a single pdf e-mail attachment) containing a letter of motivation a brief statement of their research experience and interests (max. 1 page), a curriculum vitae (with the grades of their B.Sc and M.Sc), a copy of their Master or Diploma thesis, and the names and email address of 2-3 potential referees to Dr. Barbara Feldmeyer (feldmeye@uni-mainz.de) or Dr. Susanne Foitzik (foitzik@uni-mainz.de).

Barbara Feldmeyer <feldmeye@uni-mainz.de>

UMainz InsectSocialEvolution

**3-years PhD position: "Social immunity in an insect with family life"

We invite applications for a 3-years PhD position at the JG University of Mainz, Germany (Zoological institute, Dpt Evolutionary Biology). The project aims to better understand the importance of social immunity in the early evolution of social life in insects. Our model system is the European earwig, /Forficula auricularia/, a species with non-obligatory forms of maternal care. The PhD student will conduct a series of standardized experiments to investigate how behavioral interactions between family members help individuals fighting against pathogens, as well as to determine the genes involved in the expression of social immunity. The scientific project includes behavioral experiments (mostly), immunity measurements (e.g. PO and PPO) and RNA-seq analyses. Depending on the student interests, the project may also include quantitative genetics, chemical ecology and/or population genetics.

The position requires a recent Diploma or Master degree in Biology (or a related field). The successful candidate should be highly motivated and have strong background in evolutionary biology and behavioral ecology, as well as experience in conducting behavioral experiments. Good skills in biostatistics or a high motivation to improve the statistical knowledge (e.g. R language) are important. Previous experiences with insect immunity and/or RNA-seq are advantageous, but not required. The position is fully-funded by the DFG (65% TV-L E13). People from every nationality are encouraged to apply. The working language of the laboratory is English.

The University of Mainz hosts many excellent scientific institutions (http://www.uni-mainz.de/eng) and Mainz is a historic city located on the River Rhine with many students and a rich social and cultural life (http://www.mainz.de).

Our young group offers an international, dynamic and interactive scientific environment and state-of the art, newly equipped laboratories. Information on our scientific work including recent publications can be found under http://www.bio.uni-mainz.de/zoo/evobio/322_ENG_HTML.php. For more information, please do not hesitate to contact Joël Meunier (meunier@uni-mainz.de).

Interested candidates should send applications (as a single .pdf e-mail attachment) containing a motivation letter (max. 1 page), a curriculum vitae (with the grades of their B.Sc and M.Sc), a copy of their Master or Diploma thesis (if not finished, please send a summary of the project and the expected date of submission), and the names and email address of 2-3 potential referees to Joël Meunier (meunier@uni-mainz.de).

Review of applications will begin *the 30^th of June 2014* and will continue until the position is filled. The ideal starting date for the position is September 2014, but is negotiable.

Joël Meunier <meunier@uni-mainz.de>

UNorthernBritishColumbia BeetleGenomics

Graduate Opportunity (MSc) Spatial Genomic analysis of North American Mountain Pine Beetle Outbreaks

We are recruiting an MSc student to investigate the spatial genomic patterns among outbreak populations of mountain pine beetle across North America. This will involve collaborative work among a number of Canada Universities and Canadian Forest Service conducted under funding to the TRIA project (see www.thetriaproject.ca). The work will build upon previous spatial genetic studies (e.g., Samarasekera et al 2012; Janes et al 2014) by using a genotype-by-sequencing approach to explore genomic differences among outbreak populations and to identify loci under selection. Results of this study will improve our understanding of the genetic differences among mountain pine beetle outbreaks and provide needed information for the management and predictive modeling of future outbreaks.

The qualified student will conduct the majority of their course work and research at the Prince George campus of the University of Northern BC, but will also have the opportunity to engage in courses and meetings involving TRIA members from other Canadian Universities. UNBC is a small, but dynamic research intensive university (www.unbc.ca). The Prince George area offers abundant outdoor recreation activities. Please see our website for more information on the Natural Resources and Environmental Studies Graduate Program including degree requirements and expectations (www.unbc.ca/nres/).

Qualifications: This is a challenging, but rewarding project requiring a range of interests and aptitudes. Preferably, the successful applicant will have a degree in biology or ecology. Previous experience and coursework in insect biology, population genetic and/or molecular ecology are an asset. The student should be willing to work in a collaborative environment with multiple University and Government research partners.

Ideally the MSc will begin in Sept 2014, although later start dates will be considered. We anticipate a competitive stipend (~20,000/year) and full funding to support lab and other research activities.

For further information please contact Dr. Brent Murray (brent.murray@unbc.ca; 1-250-960-5638; http://-web.unbc.ca/~murrayb).

Samarasekera NG, Bartell N, Lindgren BS, Cooke JEK, Davis CS, James PMA, Coltman DW, Mock KE, and Murray BW. (2012) Spatial Genetic Structure of the Mountain Pine Beetle (Dendroctonus ponderosae) Outbreak in Western Canada: Historical patterns and contemporary dispersal. Molecular Ecology, 21:2931-2948.

Janes JK, Li Y, Keeling CI, Yuen MMS, Boone CK, Cooke JEK, Bohlmann J, Huber PW, Murray BW, Coltman DW and Sperling FAH (2014) How the mountain pine beetle (Dendroctonus ponderosae) breached the Canadian Rocky Mountains. Molecular Biology and Evolution advanced press, April 22, 2014; doi: 10.1093/molbev/msu135

Brent Murray <Brent.Murray@unbc.ca>

UNottingham EvolutionAnimalPersonality

THE EVOLUTION OF INDIVIDUAL BEHAVIOURAL VARIATION

A great deal of research in recent years has revealed that animals from a wide range of species display consistent individual behaviours (known as animal personality, behavioural types, temperament), and that this individual variation can have powerful ecological consequences. In this project the student will focus upon unravelling some of the ecological factors important in the evolution of animal personality, using the three-spined stickleback as a model system.

Sticklebacks occupy a range of habitats which vary naturally in their parasite abundance and diversity, predation regime, and resource availability. The project will involve experimental lab-work, characterising individual fish for personality traits and parasite fauna, infection experiments, and also fieldwork to explore natural behavioural variation among and within populations in the adaptive radiation of sticklebacks on the island of North Uist in the Scottish Outer Hebrides, from which longitudinal data is available on parasite abundance and diversity, predation risk, and resource availability. Key questions include: how do parasites, predation and resource availability interact to produce patterns of individual behavioural variation in natural populations? Do fish with different personality types vary in their parasite load, and if so what is the mechanism driving this? What are the fitness outcomes of personality types under divergent ecological conditions? How does do cumented life-history variation, within- and between-populations relate to behavioural variation?

Applicants should have a good degree in a relevant subject, and a strong interest and enthusiasm for evolutionary biology/ecology/animal behaviour. Previous fieldwork or experience working with animal behaviour and/or fish parasites, and a full driving licence would be beneficial but are not essential. The project will be co-supervised by Assoc. Prof. Andrew Maccoll.

Informal enquiries can be made to Ben Chapman: ben.chapman@nottingham.ac.uk.

Applications, with a detailed CV and the names and addresses of 2 referees, should be sent to Dr Ben Chapman, School of Life Sciences, Room B108, Life Sciences Building, University of Nottingham, Nottingham NG7 2UH. Interviews for this studentship are expected to be held mid-July, but the vacancy is open until filled.

Funding Notes: This studentship is available for a period of at least 3 years starting on 1st October 2014 and provides a stipend of £13,863 per annum, and is fully funded for all EU citizens.

Ben Chapman Senior Research Fellow Ecology & Evolution Group Nottingham University

Ben.Chapman@nottingham.ac.uk

UOslo AvianSpermEvolution

A 4 year PhD position is available at the Natural history Museum (NHM), University of Oslo (http://-www.nhm.uio.no).

The subject of the PhD project is “Evolution of sperm form and function in passerine birds”. Passerine birds, and especially the oscine passerines or songbirds, are highly diversified in sexual traits, including their sperm cells. Recent research has documented that post-copulatory sexual selection, mediated by female promiscuity (extrapair copulations), shape sperm phenotypes and lead to longer and/or faster-swimming sperm over evolutionary time scales. The project will examine in more detail how particular sperm structures, especially the size and shape of the sperm head, which contains the acrosome and the nucleus, vary in response to sexual selection across the passerine phylogeny. The project will also study how variation in sperm phenotypes among males in a population is influenced by current selection pressures. NHM holds a large collection of passerine sperm samples, which will be the main source material for analysis, using high-resolution light and electron microscopy. There will also be some field work in Norway and abroad for collecting additional sperm samples.

We seek a person with strong motivation and ability to define his/her own research questions. The candidate must have wide interests in evolution and ecology, and should have good knowledge in avian systematics and practical experience with ornithological field work. Candidates with experience in microscopy techniques of biological material and relevant tools in molecular phylogenetics and comparative methods will be preferred. Applicants must hold a Master's degree or equivalent in evolutionary biology.

The position is affiliated with the Sex and Evolution Research Group (SERG) at NHM (https://www.nhm.uio.no/english/research/groups/serg/). The research team will also include scientists from Finland and Czech Republic.

For further information and instructions on how to apply, see: http://uio.easycruit.com/vacancy/1200029/71922?iso=no. Application deadline: 22 June 2014

Professor Jan T. Lifjeld Natural History Museum University of Oslo P.O. Box 1172 Blindern NO-0318 Oslo

Phone +47-22851726

j.t.lifjeld@nhm.uio.no

UOslo EvolutionaryGenomics

Doctoral Research Fellowship in Evolutionary Genomics/Behavioural Ecology

A 4-year PhD position is available at the Natural History Museum (NHM), University of Oslo (UiO). The PhD project is part of a larger research program on 'Sperm-pathogen interactions and the evolution of ejaculate antimicrobial defences in passerine birds'.

Animals are constantly exposed to pathogens, and the ability of individuals to combat microbial attack is an important component of fitness. Sperm cells are not immune to microbial exposure, and bacteria can cause reductions in sperm quality and compromise male fertility. Moreover, ejaculate-borne pathogens can be transferred during mating (i.e. STDs), with negative consequences for female fertility. Thus, ejaculate-borne bacteria are predicted to generate intense selection for the evolution of antibacterial substances in seminal fluid. This project integrates organismal and molecular approaches to develop an understanding of the role of bacteria in the evolution of avian seminal fluid and factors that minimise bacterial-induced sperm defects and limit the transmission of STDs. The successful candidate will be allowed to focus on either the evolutionary genomics or the behavioural ecology aspects of the larger study (or some combination of these two) as best fits her/his skills and research interests. She/he will also be encouraged to develop additional, complementary avenues of research.

Interested candidates should have a good degree in a relevant subject, such as background in evolutionary biology or behavioural ecology. In addition, an interest in evolutionary genomics and previous fieldwork and bird handling experience would be advantageous. The position is affiliated with the Sex and Evolution Research Group (SERG) at the Natural History Museum (NHM) and the Centre for Ecological and Evolutionary Synthesis (CEES), and may also include a period of time based in the laboratory of Dr Steve Dorus (Syracuse University, USA). The research team will also include scientists from the USA and Germany. The working language will be English. Fieldwork may be conducted at a variety of locations, including Norway and Italy.

Informal enquiries can be made to Melissah Rowe:

melissah.rowe@nhm.uio.no

For more information and how to apply: http://uio.easycruit.com/vacancy/1198865/71922?iso=gb Melissah Rowe Research Fellow Natural History Museum University of Oslo Norway

melissah.rowe@nhm.uio.no

melissah rowe <melissah.rowe@nhm.uio.no>

UOslo GenomicsAvianSpermCompetition

A 4 year PhD position is available at the Natural history Museum (NHM), University of Oslo (http://www.nhm.uio.no).

The subject of the PhD project is "Functional genomics of sperm phenotypes and cryptic female choice in passerine birds". In many passerine bird species, females copulate frequently with extra-pair mates, which implies that sperm from different males compete for the same set of ova and that there might be sperm-female interactions affecting the outcome of sperm competition. This project takes a molecular approach to deepen our understanding of the possible mechanisms involved in this form of sexual selection at the gamete level. The project has two main goals, a) finding molecular markers or genes associated with sperm performance traits, b) test if females obtain good or compatible genes through extrapair mating, in particular immune genes at the Major Histocompatibility Complex. The project will adopt next-generation sequencing approaches for several analyses, and utilize a large sample of already-collected DNA from families of a few intensively studied species (e.g. willow warblers, bluethroats and barn swallows). There will be little or no field work but extensive analysis of molecular data for this project.

We seek a person with strong motivation and ability to define his/her own research questions. The candidate must have wide interests in molecular ecology/genetics and evolutionary biology, and good practical, hands-on experience with relevant DNA methods. Good computing skills and background in bioinformatics will be of advantage, in particular when handling and analyzing large data sets emerging from next-generation sequencing approaches. Applicants must hold a Master's degree or equivalent in biology.

The position is affiliated with the Sex and Evolution Research Group (SERG) at NHM (https://-www.nhm.uio.no/english/research/groups/serg/). The research team will also include scientists from Finland, Czech Republic and USA.

For further information and instructions on how to apply, see: http://uio.easycruit.com/vacancy/1199917/-71922?iso=no Application deadline: 22 June 2014

Professor Jan T. Lifjeld Natural History Museum University of Oslo P.O. Box 1172 Blindern NO-0318 Oslo

Phone: +47-22851726

j.t.lifjeld@nhm.uio.no

UppsalaU 2 EvolutionaryGenomics

Two 4-year Ph.D. positions in Evolutionary Genomics are available at the Molecular Evolution programme, Uppsala University.

Evolutionary genomics of microbial eukaryotes (Project 1, Jan Andersson group): The position is within a research project on diplomonads, a group of eukaryotic microbes that includes human and fish pathogens. In the Ph.D. project you will use bioinformatics tools to study genome sequence data. The overall goal is to understand how genomic processes affect the biology and pathogenicity of these organisms. More information: http://www.icm.uu.se/research/Molecular-Evolution/People/jan-andersson/?languageId=1 Functional and evolutionary genomics of symbiotic bacteria and their animal hosts (Project 2, Lisa Klasson group): The overall aim of the project is to use large-scale sequencing of DNA and RNA in order to study how symbiotic interactions between bacteria and animal hosts affect both partners' genetic material and evolution. More information: http://www.icm.uu.se/-faculty-research/Molecular-Evolution/People/lisa-klasson/?languageId=1 Qualifications: The candidate should have a master degree or equal in biology, biotechnology, or bioinformatics. Previous experience of working with next-generation-sequencing data and bioinformatic analyses is a plus, familiarity with work in a Linux/Unix environment and a scripting language such as Perl is desirable. The candidate needs to be proficient in both written and spoken English.

For more information and how to apply: Project 1: http://www.uu.se/en/jobs/?positionId=38851 Project 2: http://www.uu.se/en/jobs/?positionId=38849 Jan Andersson <jan.andersson@icm.uu.se>

UppsalaU EvolutionaryTheory

A 4-year Ph.D. position in evolutionary theory is available in the research group of Dr. Claus Rueffler at the Evolutionary Biology Centre (http://www.ebc.uu.se/) in Uppsala, Sweden. Starting date 1st of September 2014, or as agreed upon.

Project: Potential projects include: (i) How do ecological and developmental factors affect the potential for division of labor among individuals within groups and among parts within an individual? (ii) How does organismal and environmental complexity affect the potential for the adaptive evolution of biological diversity?

Detailed research plans will be developed in collaboration with the successful candidate, and tailored to match her/his individual interests and strengths.

Qualification: Potential candidates have one of the following backgrounds: (a) a master degree (or your national equivalent) in evolutionary biology with a strong interest in theoretical approaches and a serious willingness to develop their mathematical skills, (b) a master degree in mathematics, theoretical physics or computer science with a serious interest in evolutionary biology. Proficiency in English is a requirement.

Duties: The postgraduate training comprises four years of full time studies. The successful candidate will receive a PhD position, which entitles the holder to full social benefits. The position can be combined with up to 20% of teaching assistantship, which will then prolong the position accordingly.

The environment: The Evolutionary Biology Centre (EBC, http://www.ebc.uu.se/) is one of the world's leading research institutions in evolutionary biology. The working atmosphere is truly international with a regular recruitment of PhD students and post-docs from abroad. The EBC is part of Uppsala University - the oldest university in Scandinavia - which has approximately 40.000 students and has been top ranked among European Universities in the subject of biology (CHE European ranking). Our lab is part of the Department of Ecology and Genetics (http://www.ebc.uu.se/-Research/IEG/) that excels in many aspects of ecology, genetics and evolution and offers an inspiring international atmosphere. Uppsala University also hosts the Center of Interdisciplinary Mathematics (http://-www.math.uu.se/CIM) that supports research in several areas of biomathematics. The city of Uppsala is a vibrant college town less than an hour's train ride away from Stockholm (and even closer to the Arlanda international airport) with beautiful and easy accessible surroundings.

How to apply: The application should include (1) a letter describing your research interests and motivation for PhD studies, (2) a short description of your education, research interests and research experience, (3) a CV and (4) the names and contact information (address, e-mail address, and phone number) of two reference persons. Furthermore, the application should include (5) an authorized copy of your MSc degree (if already available at time of application) and (6) relevant publications (including MSc thesis). The application must be written in English.

You are welcome to submit your application no later than June 30, 2014. Use the link below to access the application form: http://www.uu.se/en/jobs/jobs-detail-page/?positionId=38367 Feel free to address informal inquiries to Claus Rueffler (claus.rueffler[at]ebc.uu.se).

Claus Rueffler Associate Professor

Department of Animal Ecology Evolutionary Biology Centre Uppsala University Norbyvägen 18D 752 36 Uppsala Sweden

Phone: +46-(0)18-471 2639

claus.rueffler@ebc.uu.se

UVigo Spain EvolutionaryBiol

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

http://biology.uvigo.es We are pleased to announce the *Master in Biological Sciences (MBS) of the University of Vigo (Spain)* for the *academic year 2014-2015*. The MBS aims to provide future professionals in biology with the knowledge, skills and insights they will need to take on top science-based positions around the world.

The* official language of the MBS is English*. Non-English speaking students must demonstrate that they have the minimum language skills to study the Master. Personal interviews with members of the Academic Commission might be required before admission.

The MBS teaching staff covers a wide range of areas, and includes renowned researchers, specialists in developing professional skills and practitioners from industry, with long-term teaching experience. For students interested in doing a PhD, there are two PhD programmes linked to the MBS and rated as excellent by the Spanish Ministry of Education.

Master outline

The MSc programme comprises *120 ECTS distributed between 2 academic years *(60 ECTS each). During the 1st year, students will complete a *Basic Module (12 ECTS)* on experimental design and statistical analysis, followed by an *Elective Component (42 ECTS) *where students will choose among four specific tracks:

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

The 2nd year includes a *Mandatory Major Project (48 ECTS)* and a *Master's thesis (12 ECTS)*, to be carried out under the guidance of one of the MBS professors.

ONLINE APPLICATION for academic year 2014-15 (no payment required)

First pre-registration period (2014): *June 27 July 3*

Second pre-registration period (2014): *August 27 September 3*

DOCUMENTS that must accompany the application form:

DNI, NIE or Passport

Bachelors degree diploma

Brief CV

PRICE FOR THE TWO-YEAR MASTER

3,763

COORDINATOR

María JesÃºs Iglesias Briones

*MBS ADDRESS *

Master in Biological Sciences

Facultad de Biología

Campus Lagoas-Marcosende

Universidad de Vigo

36310 Vigo

Spain

*INFORMATION: *biologicalsciences@uvigo.es

Armando Caballero <armando@uvigo.es>

UZurich EvolutionaryTheory

Institute of Evolutionary Biology and Environmental Studies, University of Zurich, Switzerland.

PhD position in Evolutionary theory

** deadline for application: July 20th 2014**

** position open until filled, preferred starting date: September 1st 2014 **

The focus of our research is understanding whether or not the details of the genetic systems underlying phenotypic variation affect the process of adaptation and how such details may be molded by evolutionary forces. We are particularly interested in gene multifunctionality, or pleiotropy, and study both the adaptive consequences (constraints) and the evolution of gene pleiotropy. The context of this project is broad and the details will be worked out with the candidate. There is potential for international collaborations.

Possible topics are: - co-evolution of gene pleiotropy and gene expression, - evolution of the genotype-phenotype map of complex traits, - impact of genetic constraints on the evolution of species' ranges under shifting environments.

Required are a strong motivation to pursue a PhD in evolutionary theory, a strong background in population or quantitative genetics, and documented skills in modelling. The project should mix computational and mathematical approaches. Knowledge of a programing language (esp. C/C++) is required. The lab develops and maintains Nemo, an individual-based simulation platform (http://nemo2.sourceforge.net) that will serve as the basic computational simulation tool for the project.

General requirements are a Diploma/Master degree in a relevant discipline. The ideal candidates will have strong oral and written communication skills in English and the ability to work and share ideas in a collaborative environment. Knowledge of German is not essential but may help with everyday life. The Institute hosts two seminar series with high-caliber international speakers and works in close collaboration with scientists of the neighboring research institutions (ETH, EAWAG, WSL, etc.) The PhD position is within the Zurich Life Science Graduate School's program in Evolutionary Biology (http://www.lifescience-graduateschool.ch/).

Interested students should send their application package to frederic.guillaume@ieu.uzh.ch. The package must include, in one PDF file, 1) a cover letter expressing research interests in accordance with the position, 2) a complete CV, including previous research experiences, and 3) reference letters of min two academic referees. Please also attach low resolution copies of official academic transcripts and degrees (if available), and copies of publications (including MSc thesis). Informal enquiries are welcomed.

Dr. Frederic Guillaume Assistant Professor Institute of Evolutionary Biology and Environmental Studies University of Zurich Winterthurerstrasse 190 CH-8057 Zurich tel: +41 44 635 66 23 office: Y13-G-38 http://www.ieu.uzh.ch/research/-evolbiol/ecoevo.html frederic.guillaume@ieu.uzh.ch frederic.guillaume@ieu.uzh.ch

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UZurich PhD EvolutionaryTheory

Institute of Evolutionary Biology and Environmental Studies, University of Zurich, Switzerland.

PhD position in Evolutionary theory

The focus of our research is understanding whether or not the details of the genetic systems underlying phenotypic variation affect the process of adaptation and how such details may be molded by evolutionary forces. We are particularly interested in gene multifunctionality, or pleiotropy, and study both the adaptive consequences (constraints) and the evolution of gene pleiotropy. The context of this project is broad and the details will be worked out with the candidate. There is potential for international collaborations.

Possible topics are: - co-evolution of gene pleiotropy and gene expression, - evolution of the genotype-phenotype map of complex traits, - impact of genetic constraints on the evolution of species' ranges under shifting environments.

Required are a strong motivation to pursue a PhD in evolutionary theory, a strong background in population or quantitative genetics, and documented skills in modelling. The project should mix computational and mathematical approaches. Knowledge of a programing language (esp. C/C++) is required. The lab develops and maintains Nemo, an individual-based simulation platform (http://nemo2.sourceforge.net) that will serve as the basic computational simulation tool for the project.

General requirements are a Diploma/Master degree in a relevant discipline. The ideal candidates will have strong oral and written communication skills in English and the ability to work and share ideas in a collaborative environment. Knowledge of German is not essential but may help with everyday life. The Institute hosts two seminar series with high-caliber international speakers and works in close collaboration with scientists of the neighboring research institutions (ETH, EAWAG, WSL, etc.) The PhD position is within the Zurich Life Science Graduate School's program in Evolutionary Biology (http://www.lifesciencegraduateschool.ch/).

Interested students should send their application package to frederic.guillaume@ieu.uzh.ch. The package must include, in one PDF file, 1) a cover letter expressing research interests in accordance with the position, 2) a complete CV, including previous research experiences, and 3) reference letters of min two academic referees. Please also attach low resolution copies of official academic transcripts and degrees (if available), and copies of publications (including MSc thesis). Informal enquiries are welcomed.

Dr. Frederic Guillaume Assistant Professor Institute of Evolutionary Biology and Environmental Studies University of Zurich Winterthurerstrasse 190 CH-8057 Zurich tel: +41 44 635 66 23 office: Y13-G-38 http://www.ieu.uzh.ch/research/evolbiol/ecoevo.html frederic.guillaume@ieu.uzh.ch frederic.guillaume@ieu.uzh.ch

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UZurich SouthAfricanFlora

Postgraduate Positions at the Institute of Systematic Botany of the University of Zurich

We are looking for PhD or PostDoc students to investigate the patterns and processes of diversification in the Cape flora of South Africa, using Restionaceae as study group. We are seeking to integrate community ecological data (community assembly, niche filling and niche evolution, and community and pool diversity), with macroevolutionary patterns (variation in diversification models, density-dependent diversification, and key innovations) and population genetic patterns (drift versus selection during genetic divergence). Consequently, students with a knowledge of and an interest in any of the following disciplines will be preferred: population genetics and next generation sequencing, phylogenetics, computational biology / bioinformatics, the Cape flora, macroevolution and macroecology. The research group will be based in the Institute of Systematic Botany of the University of Zurich (http://www.systbot.uzh.ch/index_en.html) and will be led by Peter Linder (http://www.systbot.uzh.ch/Personen/ProfessorenundDozenten/PeterLinder.html), in collaboration with Tanja Stadler (ETHZ), Christian Lexer (Uni Fribourg) and Tony Verboom (University of Cape Town). Interested students should send their CV with a letter detailing their interests and the contact details of two referees to Peter Linder (email: peter.linder@systbot.uzh.ch). The project starts as soon as possible after 1 December 2014, applications should reach me by 15 September 2014.

Peter Linder Institute of Systematic Botany, University of Zurich Zollikerstrasse 107 CH-8008 Zurich Switzerland

Phone: +41 (0) 44 634 8410

Peter Linder <peter.linder@systbot.uzh.ch>

Jobs

BarnardCollege EvolutionaryMicrobiology

Adjunct Assistant Professors in Microbiology and Molecular Biology

(Evolutionary biologists are encouraged to apply)

The Department of Biology at Barnard College, Columbia University, seeks an Adjunct Assistant Professor for the Fall 2014 semester to teach one or both of following: (i) a lecture in microbiology (twice weekly) and (ii) a laboratory course in molecular biology (once weekly). The appointment would begin in August 2014. A Ph.D. and relevant teaching experience are required. Applicants should apply online through the Barnard College Human Resources website. If interested in both positions, apply for either position and indicate interest and qualifications for both positions in a cover letter. Barnard College is an Equal Opportunity Employer. Women and members of under-represented minorities are encouraged to apply.

https://careers.barnard.edu/postings/search – *Sarah Boorsma* Department Administrator SI Coordinator Department of Biology Barnard College 3009 Broadway New York, NY 10027

Phone: (212)-854-2437 Fax: (212)-854-1950

Sarah Boorsma <snickel@barnard.edu>

CaliforniaStateU Chico AquaticEvolution

Technically this is an ecology position but we are also interested in recruiting candidates with interest in evolutionary ecology, molecular ecology/population genetics etc.

Thanks

Tag

CALIFORNIA STATE UNIVERSITY, CHICO

College Of Natural Sciences invites applications for a full-time, tenure-track faculty position in Aquatic Ecology in the Department of Biological Sciences at the Assistant or Associate Professor level to start January 2015 or August 2015. The position requires a Ph.D. in Aquatic Ecology or related field, (specialization in Ichthyology preferred), potential to establish externally funded research, a strong interest in teaching and mentoring undergraduate and Master's level graduate students. The full position announcement is available at http://www.csuchico.edu/biol/. To ensure consideration application must be received by: July 31, 2014

Tag Engstrom Dept of Biological Sciences CSU Chico 530-898-6748 tengstrom@csuchico.edu

"Engstrom, Tag" <TEngstrom@csuchico.edu>

ColbyCollege ResTech InsectWingEvolution

RESEARCH TECHNICIAN COLBY COLLEGE, DEPARTMENT OF BIOLOGY Waterville, Maine

The Research Technician will be a full-time, temporary benefitted position. The selected candidate will work between 35 and 40 hours per week.

ESSENTIAL FUNCTIONS AND RESPONSIBILITIES: One opening for laboratory technician to assist research into the development biology, genetics and evolution of alternative wing size morphs in an insect. Technician is responsible for overseeing daily workings of the lab, including ordering supplies, maintaining equipment, as well as conducting experiments. Applicants must be willing to work independently and communicate effectively with the principal investigator. Although student workers in the lab will be directly supervised by the principal investigator (faculty member), the technician will be working alongside undergraduate students, and will be expected to assist the PI in delegating tasks. Thus, the technician must have excellent organizational skills and communication skills. Clear attention to detail with accurate record keeping is required. Technician may also have creative input into the research as abilities dictate.

QUALIFICATIONS: Applicants should have a minimum of a bachelor^{1}s degree in biology or a related subject with experience working in a research laboratory setting. Technicians should have knowledge of basic concepts in molecular biology. Proficiency with data analysis in a spreadsheet program (such as Microsoft Excel) is required.

Preferred Qualifications - Comfort working with live insects - Experience with molecular biology procedures such as PCR, DNA cloning, and RNA synthesis - Experience with microinjection - Experience working in a lab performing next-generation sequencing

- Knowledge of insect development or evolution

PHYSICAL ENVIRONMENT/EFFORT: Duties require that employee interacts with faculty and staff, students, and other outside constituencies. Position involves sitting, although frequent movement is necessary. Walking, standing, bending, twisting, and occasional lifting up to 25 pounds required. Computer usage involving repetitive hand/wrist motion also necessary.

Interested candidates should electronically submit a letter of interest, resume and the names and contact information of three professional references to: HR@Colby.edu and addressed to:

Biology Research Technician - Search Committee Human Resources Colby College 5500 Mayflower Hill Waterville, ME 04901-8855

A review of applications will begin immediately and will continue until the position is filled.

Colby College is committed to equality and diversity and is an equal opportunity employer. We encourage Inquiries from candidates who will contribute to the cultural and ethnic diversity of our college. Colby College does not discriminate on the basis of race, gender, sexual orientation, disability, religion, ancestry or national origin, or age in employment or in our educational programs.

For more information about the College, please visit the Colby web site: www.colby.edu < http://www.colby.edu >

Questions can be directed to Dave Angelini <dave.angelini@colby.edu>.

drangeli@colby.edu

ColoradoStateU PopGenomics LabManager

POPULATION GENOMICS LAB TECHNICIAN/MANAGER JOB

We are searching for a Lab Technician/Manager to collect NGS data for three main population genomics projects, plus other projects as they arise. Primary duties include preparation of RAD libraries, including trouble-shooting and optimization; processing data and calling SNP genotypes using bioinformatics pipeline; keeping up to date on advances in new NGS library prep technologies; training new lab members (primarily PhD students and postdocs) in these methods; ordering supplies; and lab maintenance. Below, we detail our three main projects:

(1) Project #1: Island Scrub Jay landscape genomics (funded by The Nature Conservancy): The lab technician will develop RAD libraries and call SNP genotypes for hundreds of Island Scub Jays, a species endemic to Santa Cruz Island off the coast of southern California. The primary goal is to understand the influence of landscape features and habitat type on neutral and adaptive genetic variation.

(2) Project #2: Genomic response of stream insects to flooding (funded by NSF): The lab technician will develop RAD libraries and call SNP genotypes for hundreds of individuals of several different stream insect species from the Colorado Front Range. The goal of this study is to test the effects of a major flood event on genomic variation and community organization in these species.

(3) Project #3: Landscape genomics of pumas (funded by NSF): As part of a larger project to understand disease dynamics in pumas, the lab technician will develop RAD libraries and call SNP genotypes for hundreds of pumas.

Start date and duration: July 15, 2014 (or until filled); One year with annual extensions pending satisfactory performance.

Required qualifications and skills: We are searching for a lab technician/manager with experience preparing DNA libraries for NGS analyses, processing NGS data using bioinformatics pipelines, and keeping a molecular lab organized and well maintained. The candidate should have experience training others in molecular techniques and should work well with other lab members. The candidate should also have a track record of strong technical, analytical, trouble-shooting, organizational, and interpersonal skills. A bachelors degree (BS or BA) in genomics, population genetics, molecular biology, or a related field is required. An advanced degree in one of these fields is preferred.

Applications: Send a 1-page letter describing why you are interested in this job and your relevant experience; your CV; and the names and contact information for three references to Chris Funk. Review of applications will start June 15th and will continue until a strong candidate is hired.

Salary: $35,000-$40,000 the first year depending on experience.

Principle investigator: Dr. W. Chris Funk, Associate Professor, Colorado State University, Chris.Funk@colostate.edu.

URL: http://wp.natsci.colostate.edu/funklab/
"Funk,Chris" <Chris.Funk@colostate.edu>

ColoradoStateU PopGenomics LabManager DeadlineExtended

POPULATION GENOMICS LAB TECHNICIAN/MANAGER JOB - DEADLINE EXTENDED

We are searching for a Lab Technician/Manager to collect NGS data for three main population genomics projects, plus other projects as they arise. Primary duties include preparation of RAD libraries, including trouble-shooting and optimization; processing data and calling SNP genotypes using bioinformatics pipeline; keeping up to date on advances in new NGS library prep technologies; training new lab members (primarily PhD students and postdocs) in these methods; ordering supplies; and lab maintenance. Below, we detail our three main projects:

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(3) Project #3: Landscape genomics of pumas (funded

by NSF): As part of a larger project to understand disease dynamics in pumas, the lab technician will develop RAD libraries and call SNP genotypes for hundreds of pumas.

Start date and duration: August 1, 2014 (or until filled); One year with annual extensions pending satisfactory performance.

Required qualifications and skills: We are searching for a lab technician/manager with experience preparing DNA libraries for NGS analyses, processing NGS data using bioinformatics pipelines, and keeping a molecular lab organized and well maintained. The candidate should have experience training others in molecular techniques and should work well with other lab members. The candidate should also have a track record of strong technical, analytical, trouble-shooting, organizational, and interpersonal skills. A bachelor^{1}s degree (BS or BA) in genomics, population genetics, molecular biology, or a related field is required. An advanced degree in one of these fields is preferred.

Applications: Send a 1-page letter describing why you are interested in this job and your relevant experience; your CV; and the names and contact information for three references to Chris Funk. Review of applications will start JULY 7th and will continue until a strong candidate is hired.

Salary: $35,000-$40,000 the first year depending on experience.

Principle investigator: Dr. W. Chris Funk, Associate Professor, Colorado State University, Chris.Funk@colostate.edu.

URL: http://wp.natsci.colostate.edu/funklab/
“Funk,Chris” <Chris.Funk@colostate.edu>

CornellU PhylogeneticMethods

LECTURER IN ENTOMOLOGY/PHYLOGENETIC METHODS Academic Year Appointment (9 month) September 1, 2014 - May 2016 Department of Entomology College of Agriculture and Life Sciences (CALS) Cornell University

For more than 125 years, our faculty members, staff and students have been working to advance the field of insect biology and apply that knowledge to solve problems and improve lives. As one of the top-ranked entomology programs in the country, our work spans the globe and impacts human lives on many levels, influencing a broad range of disciplines including human and veterinary medicine, farming, biodiversity and genomics.

The Department of Entomology’s mission is threefold: To pursue studies to understand basic and applied aspects of insect biology; to provide a robust and modern curriculum as part of preeminent undergraduate and graduate programs; and to inform and educate the public about the issues related to insects and other arthropods.

The Department is currently searching for a Lecturer to develop a new course in “Model-based phylogenetic methods and hypothesis testing” to be offered in Spring semester 2015 and 2016.

Course description:

Model-based Phylogenetic Methods and and Hypothesis Testing (4000 level; Spring semester; 4 credits) - This course would provide an advanced undergraduate/graduate level introduction to the diverse methods of model-based phylogenetic analysis including maximum likelihood and Bayesian methods. The course would focus heavily on DNA sequence data and issues associated with reconstructing phylogenetic trees from multiple gene loci. In addition, the course would cover how phylogenies can be used in the context of evolutionary hypothesis testing (including fossil-calibrated phylogenies, character mapping, ancestral state reconstruction, community ecology, and historical biogeography) using rigorous statistical methods. The course will include a computer laboratory for performing analyses using real data sets. Beginning skills in R and/or Perl programming would be introduced. The course would be targeted at students from Entomology, E&EB, NB&B, MB&G, Plant Biology, Microbiology, and associated fields.

Required Qualifications: A PhD in evolutionary biology, systematics, entomology or related fields is essential. We seek a candidate with substantial experience with molecular systematics, molecular evolution, and model-based phylogenetics. A strong commitment to expanding and fostering diversity is required.

Preferred Qualifications: Previous teaching experience at the university level is desirable.

Salary: $37,500 for a 9-month appointment.

Benefits: This is a fully benefits eligible 9 month position which is for a limited term with possible continuation dependent on funding.

Application: Interested candidates should send a letter of interest, resume/vitae; copies of transcripts;

and the names (complete with address, telephone number, email address) of at least three recent job-related references in a single pdf file to Bryan Danforth (bnd1@cornell.edu). The deadline for applications will be June 15, 2014 or until a qualified applicant is identified.

Posting on Cornell website: https://cornellu.taleo.net/careersection/10161/jobdetail.ftl?job=24341 Bryan N. Danforth, Professor Department of Entomology 3124 Comstock Hall Cornell University Ithaca, NY 14853-0901 phone: 607-255-3563/FAX: 607-255-0939 email: bnd1@cornell.edu Lab website: http://www.danforthlab.entomology.cornell.edu/ CU Insect Collection website: http://cuic.entomology.cornell.edu/ Northeast Pollinator Partnership: http://www.northeastpollinatorpartnership.org Bryan Nicholas Danforth <bnd1@cornell.edu>

Dryad director

Dryad (www.datadryad.org), the non-profit organization that operates the Dryad Digital Repository (which is widely used by evolutionary biologists), is searching for a new Executive Director. The job advertisement is pasted below.

Dryad seeks an energetic and enthusiastic Executive Director, ideally with experience in scientific or biomedical research, librarianship, or publishing, to oversee development and operation of the organisation during a period of rapid growth and transformation. The role reports to the Board of Directors. Externally, the postholder will be responsible for building relationships with stakeholders, customers and users of the Dryad Digital Repository < www.datadryad.org >. Internally, key responsibilities include organisational leadership and ensuring Dryad meets its objectives through sound financial management and oversight of day-to-day operations, with the support of a small but growing staff.

The Dryad Digital Repository is a curated resource that makes the data underlying scientific publications discoverable, freely reusable, and citable. Dryad provides a general-purpose home for a wide diversity of data types. Dryad is governed by a nonprofit membership organization and operates from a base in Durham, North Carolina. Membership is open to any stakeholder organization, including but not limited to journals, scientific societies, publishers, research institutions, libraries, and funding organizations.

What Dryad has to offer: Dryad is a leading data repository helping to shape the discourse on policies and reuse of research data at a time when data archiving is rapidly gaining importance. The organization has an exciting and innovative sustainability model with potential for very rapid growth. The Executive Director will work with a highly engaged and experienced international Board of Directors. A strong project team, broad support from stakeholders and a proven funding model make Dryad an exciting organization to lead and develop.

Duties of the Executive Director:

1.

Leadership - ensure that the organization makes progress on the goals and priorities in the strategic plan and report on that progress to the Board and stakeholders.

2.

Organizational Management - recruit, support, manage and retain staff hired by Dryad as well as project team members at other institutions and contractors. Cultivate a strong, responsive and accountable team environment.

3.

Financial oversight - with the Board Treasurer, develop budgets and financial reports that enable the Board to make informed fiduciary decisions. Ensure that financial practices and policies align.

4.

Outreach - develop strong recognition for Dryad in the scientific and medical community and represent the organization at meetings, conferences and other events that engage stakeholders.

5.

Membership - recruit and retain members through clear messaging, networking and by ensuring that features for members are developed and supported.

6.

Messaging - ensure that Dryad's public messaging is on target, engaging and clear. Oversee development and implementation of messaging strategies.

7.

Research and analysis - develop, monitor and report on key impact measures. Develop strategies for collecting and acting on feedback from researchers, journals, members and other stakeholders.

8.

Board Liaison - serve as a non-voting officer of the Board and facilitate clear communication between the Board, project team, stakeholders and contractors. Engage the Board and/or Board committees in policy discussions as needed.

Qualifications:

1.

Degrees: bachelors or graduate degree in science, business, or related field.

2.

Preferred: Experience with scientific or biomedical communities, in an academic setting or allied field such as publishing

3.

Preferred: At least 3 years experience in nonprofit leadership or senior management

4.

Must be eligible to work in North Carolina, USA, and available for travel

To apply: Send a letter of interest, CV, and names of 3-5 references todirector@datadryad.org. Review of applications will begin by September 1, 2014 and continue until the position is filled.*

cfox@email.uky.edu

DukeU LabTechnician

Molecular Biology Technician, Tung Lab at Duke University

An Associate in Research/Laboratory Research Analyst position available, starting immediately, in the Tung lab at Duke University. The Tung lab studies the relationship between behavior, the social environment, and genetics and genomics, with a focus on nonhuman primate populations. We combine detailed phenotypic and demographic information with modern genomic data sets on gene regulation and epigenetics. Current projects focus on the gene regulatory mechanisms linking social adversity and health in rhesus macaques, the epigenetic signature of early life ecological and social adversity, and the genomic and phenotypic consequences of hybridization in wild baboons. Duties will include performance of basic molecular biology laboratory techniques, including DNA and RNA sample extraction and sample preparation for high-throughput sequencing, and responsibility for day-to-day logistics, including purchasing, shipping and receiving, and working with trainees in the lab.

Important skills/traits include: aseptic technique, molecular techniques, attention to detail, ability to work independently, careful record keeping.

Requirements: bachelor's degree, 1 V 2 years experience in a research laboratory (not just a lab class), familiarity with fundamentals of molecular biology.

Position is for 40 hrs/week, and will last 12 months, with the possibility of renewal contingent on performance and availability of funding.

For more information about the lab and our work, see http://people.duke.edu/~jt5/tunglab/home.html If interested, email resume, including contact information for two references, to Shauna Morrow, smorrow@duke.edu

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

Jenny Tung Assistant Professor Department of Evolutionary Anthropology and Duke Population Research Institute jt5@duke.edu 919-668-4912

Jenny Tung <jt5@duke.edu>

FieldMuseum Chicago InsectCollectionManager

Collection Manager, Insects - Field Museum of Natural History, Chicago, IL, USA

The Collection Manager is involved in all aspects of care and maintenance of the Field Museum insect collection and collaborates with Curators in management of the collection. This position will also interact with the FMNH Action and Integrative Research Centers, as well as Education and Exhibits.

This position will have the opportunity to conduct research to a limited extent.

Responsibilities - Preparation, identification, care and organization of specimens (and associated material) - Training and supervision of staff and volunteers in their collection related duties - Provide assistance to visitors in their use of collection, and processing recently collected material, as well as outgoing and incoming specimen loans, loan recalls and loan returns - Maintain records relevant to the collection (KE EMu catalog, loan invoices, accession files, field notes) - Provide the public and professional contacts with information they need from the collection (including digitizing specimens) - Develop grant proposals for collections improvements and liaise with Federal and State authorities and other Entomology collectors and researchers - Monitor and maintain collection supplies and equipment - Incorporate new material into collection including sorting and ID-ing, preparing specimens, cataloguing, labeling and installation

Qualifications - Masters in Biology (with an emphasis in Entomology) with at least 3 year's collection experience; PhD. (with an emphasis in Entomology) desirable - A well versed background in Entomology is required, including familiarity with other Entomology collections and researchers - Knowledge of taxonomic principles, and Entomology collection management - Strong organizational skills necessary to keep collection accessible - Familiarity with personal computers, and collection databases - Knowledge of international and domestic regulations for shipment of alcohol-preserved specimens - Supervisory skills necessary for directing collection personnel - Digitization skills highly desirable

Apply online: http://www.fieldmuseum.org/about/-employment Corrie Saux Moreau, Ph.D. MacArthur Associate Curator - Insects Integrative Research Center Department of Science and Education Field Museum of Natural History 1400 South Lake Shore Drive Chicago, IL 60605 USA Office: (312) 665-7743 Fax: (312) 665-7754 Email: cmoreau@fieldmuseum.org Moreau Lab website: www.moreaulab.org FMNH website: http://fieldmuseum.org/users/corrie-moreau Field Museum Women in Science: http://-/fieldmuseum.org/womeninscience Corrie Moreau <cmoreau@fieldmuseum.org>

IGFL Lyon GenomicsGroupLeaders

CALL for NEW RESEARCH GROUP LEADERS, LYON, FRANCE

Deadline Friday 4th of July 2014

The Institut de Génomique Fonctionnelle de Lyon (IGFL) currently hosts 13 research groups (approx. 110 personnel). The Institute has recently moved to a newly commissioned building, within the multidisciplinary campus of Lyon-Gerland, and, in line with its expansion, is hiring additional groups.

Research at the IGFL focuses on the role of the genome in animal physiology, developmental biology and evolution. In addition, the IGFL is actively seeking to strengthen its research in bioinformatics and modelling at the genomic scale.

IGFL groups have full access to state-of-the-art core services, including high throughput sequencing technologies, X-Ray microtomography, 2D and 3D imaging and morphometrics, transgenic animal facilities (mouse, fish, drosophila, etc), bioinformatics, mass spectrometry, proteomics, FACS sorting, histology and electron microscopy.

The IGFL is searching for outstanding young scientists wishing to start their own team as well as established group leaders interested in joining the IGFL.

Group leaders with a strong interest in animal-based research falling within the scientific mission of the Institute - namely physiology and physiopathology, developmental biology and evolutionary sciences - may apply to this call.

Applications (in English) should include curriculum vitae, a short description of achievements and records of self-financing, a proposed research program of 5 to 10(max) pages and contact details for 3 professional references. The deadline for applications is July 4th 2014. Please send as a single PDF named LASTNAME_IGFL_2014.pdf to direction.igfl@ens-lyon.fr. Enquiries should also be directed to this address.

Interviews of shortlisted candidates will be held in Lyon, France in mid October.

http://igfl.ens-lyon.fr The IGFL is run by the Ecole normale supérieure de Lyon, the Centre National de la Recherche Scientifique, Université Lyon 1 and the Institut National de Recherche Agronomique.

fred <Frederic.Brunet@ens-lyon.fr>

ImperialCollege London LabManager EvoDevo

Hello,

A lab manager/senior research assistant position is available in my lab. A brief description is as follows:

Research background

Vertebrates differ in a wide range of traits, including dramatic differences in their skeletons. The objective of the newly established Evolution of Gene Regulation Group headed by Dr. Vahan Indjeian at the MRC Clinical Sciences Centre, Imperial College London, is to uncover the genetic basis of vertebrate traits. The group asks what genes regulate evolutionary changes in morphology? What are the changes in those genes? Are the same genes used when similar traits evolve in many species? We use combination of tools, including comparative genomics and threespine stickleback and mouse experimental models to answer these questions. For more information about our research, please visit http://www.csc.mrc.ac.uk/-Research/Groups/EPI/EGR/ . Job Summary

This post provides an opportunity for a highly motivated individual to participate in the day to day management of lab resources and coordination of key research processes for the group in addition to the supervision and training group members in various scientific procedures and techniques. The post is initially for 2 years to provide technical support for starting up the lab, setting up the stickleback facility, and ongoing research projects within the group. There will be the possibility to extend the post beyond the 2-year lab start up period.

Main duties / key responsibilities

The specific duties of this role are as follows:

- To actively contribute to the smooth running of the laboratory in co- ordination with other members of the group - To form a good working relationship with other members of the group and actively participate in team work - To design and carry out scientific experiments in accordance with the group projects - To analyse, manage and communicate data, ensuring the validity and reliability of the data at all times - To participate in stickleback field work nationally or internationally as appropriate - To organise and participate in stickleback husbandry and day-to-day maintenance at the on-site stickleback facility, and record keeping in a husbandry database. - To organise and participate in mouse husbandry and record keeping. - To generate reagents for the group projects - To maintain organised and accurate records of experimental data - To actively participate in the group's research meetings

Full Job Description and How to Apply:

Please follow this link for full information about the position and the application submission website: http://www.topcareer.jobs/Vacancy/-irc147074_4461.aspx The closing date for applications is 29 June 2014. Please upload your CV alonh with your Cover Letter describing motivation and names and contacts of three scientific references, when saving your documents please quote IRC147074 in the file name. Only online applications will be accepted at the link provided above.

Thanks very much!

Best regards, Vahan

Vahan Indjeian, PhD Head of Evolution of Gene Regulation Group MRC Clinical Sciences Centre - Imperial College London Du Cane Road, London W12 0NN tel. (+44) 020 8383 8241 vahan.indjeian@imperial.ac.uk http://www.csc.mrc.ac.uk/Research/Groups/EPI/-EGR/ vahan.indjeian@csc.mrc.ac.uk

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MaxPlanckInst Rostock HeadEvolutionaryDemography

The Max Planck Institute for Demographic Research seeks a path-breaking recent Ph.D. eager to develop a highly innovative Max Planck Research Group at a frontier of mathematical, biological, historical, social, economic or qualitative demography.

The successful candidate will be given ample resources to establish and direct an independent research program. For this purpose, he or she will be guaranteed funding to recruit and lead a team of researchers, for operating expenses, scientific collaborators, and technical and secretarial support.

The successful candidate will start a five-year contract (with the possibility of a prolongation after positive evaluation) between October and December 2014. The payment corresponds to the W2 level on the German university scale, equivalent to an Assistant or Associate Professor.

Applicants should have completed a doctoral degree in the past decade. They should have an outstanding record - or show exceptional promise - as demographic scholars.

The Max Planck Society is committed to employing more handicapped individuals and to increasing the share of women in areas where they are underrepresented, and therefore expressly encourages applications from such qualified individuals.

The applicant should submit a three to five page description of a research program, along with a work plan, a complete CV, and three personal references.

Please send applications by July 25, 2014 to applmprg@demogr.mpg.de

Thank you very much.

Best regards, Antje

Antje Gosselck

Max Planck Institute for Demographic Research Konrad-Zuse-Str. 1 D-18057 Rostock Germany

http://www.demogr.mpg.de
mailto:gosselck@demogr.mpg.de Tel. +49 (0) 381 / 2081 108 Fax +49 (0) 381 / 2081 408

"Gosselck, Antje" <Gosselck@demogr.mpg.de>

NaturalHistoryMuseum Copenhagen PlantEvolution

The Natural History Museum of Denmark wishes to appoint a Professor of Higher Plants and Curator of the Botanical collections from 1 February 2015 or as soon as possible thereafter, as advertised on Nature Jobs:

http://www.nature.com/naturejobs/science/jobs/-415475-professor-of-higher-plants-and-curator-of-the-botanical-collections . The professor's duties will include research, curating of the botanical collections, obligations with regard to publication/scientific communication and research-based teaching with associated examination obligations.

The research domain of the Professorship is expected to fall within the broad area of Higher Plants, with the successful applicant demonstrating a track record of combining multiple complementary disciplines in order to tackle research questions of broad-scale relevance. It is therefore expected that the Professor will lead a research program at the Museum that is placed at the state-of-the-art of modern botany, synthesizing both traditional techniques such as fieldwork and exploitation of the botanic collections and gardens, with genomic-scale molecular and computational biology. To achieve this, the applicant will be expected to i) collaborate widely both within the Museum and Internationally, ii) build up a dynamic externally-funded research portfolio, iii) create a research team of postdoctoral researchers, PhD students and MSc/BSc students, and iv) curate and be responsible for part of the botanical collections at the Museum.

Applicants are required to have university level teaching experience, documented teaching competencies and must be able to explain and reflect upon own teaching practice and portfolio. Formal pedagogical training or supervision equivalent to the University of Copenhagen teacher training programme for assistant professors is required in order to obtain a permanent position.

Duties include the applicant's own research, development of the field, assessment tasks, grant applications, and research management such as supervision and training of research fellows and other staff. The successful applicant must also teach, supervise, prepare and participate in examinations, and fulfill other tasks requested by the Department.

Assessment of applicants will primarily consider their level of documented, original scientific production at an international level, including contributions to developments in their field, as well as their documented teaching qualifications. Managerial and out-reach qualifications of applicants including ability to attract external funding will also be considered.

For information about the position, please contact prof. Kurt H. KjÃr on tel. (+45) 3058 9730 or e-mail kurtk@snm.ku.dk.

Further information on the Department is linked at www.science.ku.dk/english/about-the-faculty/-departments/ . The position is open from 1 February 2015 or as soon as possible thereafter.

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

Terms of employment The position is covered by the Memorandum on Job Structure for Academic Staff.

Terms of appointment and payment accord to the agreement between the Ministry of Finance and The Danish Confederation of Professional Associations on Academics in the State.

Commencing salary is currently: For Professors - DKK 582,319 including annual supplement (+ pension DKK 99.577)

Negotiation for salary supplement is possible.

The application, in English, must be submitted electronically through the following link:

https://ssl1.peoplexs.com/Peoplexs22/-CandidatesPortalNoLogin/-ApplicationForm.cfm?PortalID=3789&VacatureID=-643159 Please include

- Curriculum vitae including funding ID - Diplomas - Research plan - description of current and future research plans - Description and documentation of teaching experience and qualifications according to university guidelines - Complete publication list - Separate reprints of 5 particularly relevant papers

The deadline for applications is 15 September 2014.

Trial interviews will be held on 15 December 2014.

Please refer to the following no. in future communication in this case: 211-0255.

Tom Gilbert <mtpgilbert@gmail.com>

ReedCollege ComputationalBiology

Please find details on our search for a Computational Biologist at Reed College, below. Features of the position, not necessarily emphasized in the ad, include some aspects of the Reed environment that are surprisingly supportive for research-active faculty (e.g., terrific students, generous start-ups, little to no emphasis on grades [students generally don't see/look at them], you teach what you do, good SRO support, and a junior sabbatical).

You can contact me, or the search chair (contact info below), if you have any specific questions about the position or running a lab at a small liberal arts and science-focused institution.

Thanks, Sarah

Sarah Schaack, PhD Assistant Professor Reed College schaackmobile@gmail.com https://sites.google.com/site/schaackwork/ *BIOLOGY- COMPUTATIONAL BIOLOGY (TT) *The Biology Department at Reed College invites applications for a tenure-track faculty position (preferably at the rank of assistant professor) in computational biology. We seek candidates with demonstrated excellence in developing, integrating or applying computational or quantitative methods to study biological questions. Outstanding applicants in all areas of computational biology will be considered*.* Qualifications include a PhD in biology, computer science or relevant discipline and postdoctoral or professional experience.

Candidates should articulate a plan to establish and maintain a rigorous and competitive research program that incorporates research opportunities for Reed undergraduates. A competitive start-up package and research space will be provided based on the successful applicant's needs, with salary determined according to the applicant's experience.

In addition to advising senior theses, teaching duties will include the development of a new course that introduces students to computational approaches and techniques in biology, as well as an upper level course in the candidate's computational field of expertise. Additional teaching opportunities could include advanced seminar courses. Formal teaching experience at the college level will be viewed favorably but is not required.

Reed is a distinguished liberal arts college with approximately 1400 students that offers a demanding academic program to bright and dedicated undergraduates. The cover letter should address how the applicant's teaching and scholarship are suited to such a liberal arts college environment. The Reed community believes that cultural diversity is essential to the excellence of our academic program. All applicants, therefore, are invited to address how their teaching, scholarship, mentoring, community service, or other activities could support Reed's commitment to diversity and inclusion (see http://www.reed.edu/diversity/).

Application materials (a cover letter, curriculum vitae, research plan, and representative publications) and three letters of recommendation should be sent electronically as PDF (preferred) or Word attachments to <biology.search@reed.edu>*, subject 'Computational Biology Search' by *1 October 2014 *for full consideration. An equal opportunity employer, Reed College encourages applications from members of underrepresented groups. Specific inquiries should be directed to Dr. Suzy Renn (renns@reed.edu), the chair of the search committee.

Sarah Schaack <schaackmobile@gmail.com>

SouthAfrica ResAssist SocialMolerats

Research assistants needed

Cooperative breeding in subterranean Damaraland mole-rats (Fukomys damarensis)

2 Positions for a minimum of 6 months (max 12 months) starting in August 2014;

Field and laboratory researchers are needed to conduct research on a completely subterranean, highly social mole-rat. Our interest is individual variation in cooperative behaviour and the consequences for life-histories and individual fitness in the cooperatively breeding Damaraland mole-rat (Fukomys damarensis). Our second research objective is investigating the hormonal mechanisms underlying cooperative behaviour and social dynamics in mole-rat groups. The study is initiated by Prof. Tim Clutton-Brock, University of Cambridge.

Position 1

We launched a study of permanently marked, wild mole-rats at the < http://www.kalahari-meerkats.com/index.php?id=krr > Kuruman River Reserve (Northern Cape, South Africa). The mole-rats are trapped, marked and measurements such as blood samples, urine samples and morphological measurements are taken. Animals in their natural burrow systems will be monitored by identity chips remote sensing. About 50% of the time the research assistant will be conducting field research and the other half of the work would be carrying out behavioural observations of captive mole-rats held in tunnel systems at the research station and assisting in conducting behavioural experiment in captive colonies.

Position 2

This position entails assisting in a study on hormonal manipulations of subordinate and dominant mole-rats. We are interested in the organisational and activational effects of steroid hormones on social behaviour and the development of juvenile mole rats. The research assistant holding this position will be involved in all steps of the experiments and will mainly work in the laboratory with our captive mole-rats. The responsibilities include behavioural observations, hormonal measures (blood sampling, urine sampling) and hormonal manipulations (implants).

Applicants for both positions should be enthusiastic, willing to work hard and keen to get involved in a research project in the African bush. Research assistants are expected to stay in the field over night when trapping mole-rats or work night time when observations require night shifts. Research assistants need to be physically fit as capturing mole-rats requires a fair amount of digging. Applicants must be holders of a driving license (Position 1). A zoology related degree and/or previous field experience will be considered an asset.

The successful applicants will work in a small team of 5-6 persons working on mole-rats.

The research station is also the home of several other projects studying meerkats (www.kalahari-meerkats.com), pied babblers, forktailed drongos and hornbills resulting in a stimulating scientific environment. Around 20-30 research assistants are based at the station year round. Research assistants will learn a range of skills such as remote sensing of behaviour, endocrine sampling techniques, capture-mark-recapture techniques, behavioural observations, data handling and management.

Accommodation is provided, and research assistants are paid a monthly allowance to cover their food. A contribution to their travel costs can be provided at the end of their stay.

Applications received until the 27th of June will receive full consideration. Later applications may be considered.

To apply (CV + cover letter) or enquire further information contact:

Dr Markus Zöttl

Research associate

University of Cambridge

Mz338@cam.ac.uk

Specific questions concerning Position 2 contact Philippe Vullioud: philippe.vullioud@gmail.com

Markus Zöttl <mz338@cam.ac.uk>

StockholmU PlantPhylogeography

Assistant professor in plant phylogeography at Stockholm university.

Subject description: The subject involves the study of biogeographic patterns of green plants from a phylogenetic perspective and may involve different levels of organization, from populations and species to the entire plant system.

Main tasks: Research and supervision, in addition to some teaching in plant systematics.

Required qualifications: In order to qualify for the position of associate senior lecturer, the applicant must have completed a doctoral degree or an equivalent degree from another country. In the first instance, an applicant should be considered who has received a doctoral degree or equivalent qualifications no more than seven years before the deadline for applications.

All teaching positions at Stockholm University require the ability to collaborate and the general ability and suitability to perform one's duties.

Additional information and application details: http://www.su.se/english/about/vacancies/-lecturers-researchers/assistant-professor-in-plant-phylogeography-1.180093 *Contact details*: peter.hamback@su.se

UBritishColumbia Evolution

Assistant Professor in Evolutionary Biology (Tier 2 Canada Research Chair)

Closing date: September 5, 2014 at 11pm

The Department of Zoology at the University of British Columbia, in Vancouver, invites applications for an Assistant Professor position in Evolutionary Biology (Canada Research Chair Tier 2). This is a tenure track position, with initial appointment to be made at the Assistant Professor level, beginning no earlier than July 1, 2015.

The position requires a Ph.D. degree, postdoctoral experience, and an exceptional research record. We seek an outstanding individual with an innovative and integrative research program. We especially encourage applications from individuals with expertise in genomics examining fundamental questions in evolutionary biology. The research area should complement existing faculty strengths in evolutionary biology and the Zoology Department.

The successful applicant will become a full member of the Department of Zoology and of the Biodiversity Research Centre (www.biodiversity.ubc.ca/) an outstanding group of scientists studying evolution, ecology, systematics, and genetics. The Centre provides exceptional opportunities to contribute to an interactive research community, develop strength in genomics research and teaching, study and contribute to our physical collections, and to contribute to the Beaty Biodiversity Museum's community and outreach efforts. The candidate will also actively interact with the broadly based group of biologists in the Zoology Department. The Department includes more than 44 principal investigators and vigorously promotes integrative research in biology. Its faculty and students pursue 21 st-century questions in cell and developmental biology, comparative animal physiology, ecology and evolution. The Department actively participates in several interdisciplinary programs, including the graduate programs in genetics, neuroscience, applied mathematics, and resource management.

Responsibilities of the position include establishing and conducting an internationally competitive and externally funded research program, excellent teaching at the undergraduate and graduate levels, supervising graduate students, and participating on service committees for the department, university, and academic/scientific community.

Applicants should send a cover letter, curriculum vitae, statement of research, statement of teaching accomplishments and/or interests, and up to four publications to Dr. Dolph Schluter at jobs@zoology.ubc.ca. Letters of support from three referees should be sent to the same address. The deadline for applications is September 5, 2014.

The Canada Research Chair is equally open to individuals of all nationalities. The Chair is subject to review and final approval by the CRC Secretariat. More information about the CRC program can be found at www.chairs.gc.ca. Applicants must meet eligibility requirement for a CRC Tier 2 position, including having received their PhD in 2005 or later, except under special circumstances.

UBC hires on the basis of merit and is committed to employment equity. All qualified persons are encouraged to apply. We especially welcome applications from members of visible minority groups, women, Aboriginal persons, persons with disabilities, persons of minority sexual orientations and gender identities, and others with the skills and knowledge to engage productively with diverse communities.

schluter@zoology.ubc.ca

UGeorgia PlantGenomics

Job Description can be found here: http:/-/jobs.sciencecareers.org/job/331182/assistant-professor-in-quantitative-genomics/ POSITION: This is a 12-month tenure track faculty position with a 80% research and 20% teaching appointment in the Department of Crop and Soil Sciences, The University of Georgia. The position is home based at the University of Georgia Athens campus.

DUTIES AND RESPONSIBILITIES: The person that fills this position will be responsible for developing an internationally recognized program in one or more of the following: genetics based on high-dimensional data analysis, statistical genomics, genome-wide analysis, gene-environment interactions, and/or epigenetics of crop plants. Development of an independent research program that focuses on the application of quantitative/statistical genomics to crop plants is expected. UGA offers a vibrant research environment with potential collaborations with faculty in crop genetics (http://www.plantbreeding.uga.edu), plant sciences (http://plantcenter.uga.edu) and bioinformatics (http://iob.uga.edu). The successful candidate is expected to conduct research that will result in securing extramural funding and publication of manuscripts in peer-reviewed journals. Teaching responsibilities will include instructio n of graduate and/or undergraduate courses and training of graduate students in the areas of quantitative genomics, statistical genetics or plant breeding, as determined by the Department of Crop and Soil Sciences and the Institute for Plant Breeding, Genetics and Genomics and assigned by the Department Head.

BASIC QUALIFICATIONS: A Ph.D. in plant breeding, genetics, quantitative genetics or genomics, or a closely related field is required. Candidates should have demonstrated skills in verbal and written communication, interpersonal relationships, statistical computational systems, and an ability to workwell with students and colleagues.

Application: Electronically send application package to: Scott Jackson atsjackson@uga.edu. Applicants must submit the following documentation: a letter of application, curriculum vita, and names and addresses of four professional references, and any other information that reflects on professional qualifications.

To assure full consideration, applications must be received by 31 August 2014. Anticipated start date is Spring 2015. The University of Georgia is anAffirmative Action/ Equal Opportunity Employer and encourages applicants regardless of gender or ethnic background. Effective January 1, 2008, the Board of Regents has enacted a "background check" policy for new hires in thesystem as a condition of employment. This policy can be found at: http://policies.uga.edu/FA/-nodes/view/1124/Background-investigations .Upon offer of employment, candidate must complete the "Consent for a Background Investigation" form.

sjackson@uga.edu

UGlasgow ResTech ViralEvolution

Vacancy Reference: 008755 University of Glasgow College of Medical, Veterinary and Life Sciences Institute of Infection, Immunity and Inflammation MRC - University of Glasgow Centre for Virus Research (CVR)

Research Technician Grade: Grade 5 Salary: £20,374 - £24,289 Start Date: To be agreed Reporting to: Dr Daniel Streicker Duration: To 31/03/16

The Centre for Virus Research (CVR) and the Institute of Biodiversity, Animal Health and Comparative Medicine (BAHCM) is seeking an experienced Research Technician to join a new viral epidemiology and emergency group. The postholder will contribute to the efficient day-to-day running of the bat virus epidemiology and emergence group, and to execute molecular and serological assays studies examining patterns of infection and exposure to a variety of bat-associated in samples collected from bats, domestic animals and humans in Peru.

Applicants must have an HNC, VQ3, Higher Grades or equivalent in a relevant subject, and will have excellent technical diagnostic laboratory skills including at least cell culture and RT-PCR/PCR. A minimum of three years relevant work experience, or four to five years relevant laboratory experience in a relevant technical/scientific discipline is essential. Excellent and accurate record keeping and the ability to analyse own data are essential criteria for this post.

Informal enquiries should be directed to Dr Daniel Streicker (Daniel.Streicker@glasgow.ac.uk)

Apply online at www.glasgow.ac.uk/jobs Closing date: 20th July 2014

Daniel Streicker <Daniel.Streicker@glasgow.ac.uk>

ULausanne EvolutionBehavior

The Faculty of Biology and Medicine (FBM) and the Faculty of Business and Economics (HEC) of the University of Lausanne, Switzerland invite applications for the following position:

Full Professor Director of the Programme in Behavior, Economics, and Evolution

The Department of Ecology and Evolution of FBM and the Departments of Economics, Organizational Behavior, and Information Systems of HEC have developed a new interdisciplinary Master of Science major in Behavior, Economics, and Evolution. This major can be taken by students enrolled in the Master of Science programmes in Economics or in Management (in HEC), as well as students in the Master in Behavior, Evolution and Conservation (in FBM). The programme intends to develop teaching and research connections between evolutionary biology and behavioral economics.

We therefore seek an outstanding researcher as full professor and director of the programme with a track record in Sociobiology, Social Evolution, Human Behavioral Ecology, Evolutionary Psychology, Biological Psychology, Neuroeconomics, Evolutionary Economics, or Behavioral Economics (or related areas). The position requires a record of scientific excellence, administrative experience, the motivation to lead a MSc programme, as well as a scientific interest in both evolution and economics.

The Professor is expected to lead the programme and an internationally competitive research programme on proximate and/or ultimate questions pertaining to social decision-making and behavior. She/he is expected to attract external funding and to promote an interactive and synergistic research environment between the Faculty of Business and Economics, and the Faculty of Biology and Medicine.

A start-up package, a state-of-the-art research infrastructure as well as a yearly research allowance for positions and consumables will be available within an environment that has a long track record of excellence in research (http://www.unil.ch/dee ; http://www.hec.unil.ch/ob ; http://www.hec.unil.ch/-deep ; www.hec.unil.ch/isi).

The job description is available on the Internet site https://applicationsinter.unil.ch/inter/noauth/-php/Po/pooffres.php?typelc=3D810 or http://-www.unil.ch/fbm/page64812.html . Further information may be obtained from Prof. Andreas Mayer (Andreas.Mayer@unil.ch), Chairman of the search committee.

The application, in English, must include a full CV (indicating previous positions, teaching experience, list of grants received, publication record), a motivation letter, future research interests, and representative publications, as well as names and contact information of three referees. Applications are received electronically at this address: www.unil.ch/iafbm/application. They should be submitted by August 27th, 2014.

Seeking to promote an equitable representation of women and men among its staff, the University

encourages applications from women.

Laurent Keller Department of Ecology and Evolution Biophore University of Lausanne 1015 Lausanne Switzerland

http://www.unil.ch/dee/page7717_en.html Laurent.Keller@unil.ch

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UNevada DirectorLifeSciences

Director, School of Life Sciences

The University of Nevada, Las Vegas seeks an individual with outstanding academic credentials in any field of Biology to serve as Director of the School of Life Sciences. The successful candidate must have proven management and leadership skills, as well as a strong track record of extramurally funded, internationally recognized research commensurate with appointment at the level of Professor and a demonstrated commitment to excellence in teaching and mentoring. Applicants should present a clear vision to build upon Life Sciences' recent growth and strengths in diverse areas of biology. The new director will lead an active and productive school comprised of 27 tenure-track faculty, 6 full-time lecturers and 10 staff. With over 2000 undergraduate majors and over 40 M.S. and Ph.D. students, Life Sciences has the largest enrollment in the College of Sciences.

UNLV is an urban campus in a growing, vibrant, culturally diverse city, set in the Mojave Desert with easy access to numerous national parks, wilderness, and recreational areas. It is the largest research university in the Nevada System of Higher Education, offering more than 200 degree programs to over 27,000 students, and is a Title III and Title V Minority Serving Institution (MSI). The School of Life Sciences has taken advantage of UNLV's location in an EPSCoR and IDeA-eligible state to attract substantial program funding and will continue to play a significant role in advancing UNLV's goal of Carnegie Foundation - Tier 1 designation within the next decade (http://www.unlv.edu/tier1).

For more information and application details, visit http://hr.unlv.edu/jobs or call (702) 895-2894.

If you are interested in applying for this position, please feel free to contact me for more information. You can also go to http://jobs.unlv.edu/faculty.html and look in the Current Openings for announcement 14307.

Allen G. Gibbs Chair, Director Search Committee School of Life Sciences University of Nevada Las Vegas NV 89154 allen.gibbs@unlv.edu sols.unlv.edu/faculty/gibbs.html (702)-895-3203

allen.gibbs@unlv.edu

UOttawa ClimateChangeAdaptation

While the position below advertises Global change/macroecology, those with evolutionary interests/approaches are encouraged to apply.

The Department of Biology of the Faculty of Science at the University of Ottawa invites applications for a Canada Research Chair (Tier 2) in the area of Global Change and Macroecology. The successful candidate will contribute to undergraduate teaching in the Ecology, Evolution and Behaviour option in the Biology program and the Global Change option of the Environmental Sciences Program, as well as teach graduate courses. The Department of Biology conducts prominent research in macroecology and on how global changes will affect biodiversity and ecosystem services.

Applicants must have a Ph.D. in Biology or in a related field with postdoctoral experience and an exceptional track record in research; the successful candidates are expected to develop internationally-recognized research programs. A commitment to teaching and graduate training, and a willingness to contribute to collaborative and collegial research interactions in the department are necessary. Excellent communication skills in either English or French with at least a passive knowledge of the other official language also are required. Preference will be given to candidates who can teach in both English and French.

The University of Ottawa is located at the heart of Canada's capital: a cosmopolitan environment offering many cultural and recreational activities as well as direct access to a large group of government and industrial research laboratories. The University of Ottawa has a proud tradition of 160 years of bilingualism. Through its Official Languages and Bilingualism Institute, the University provides training to staff members in their second official language. At the time of tenure, professors are expected to have the ability to function in a bilingual setting.

For more details and application instructions see: http://www.academiccareers.uottawa.ca/node/763

Howard D. Rundle, Associate Professor & CRC (Tier 2) Department of Biology, 30 Marie-Curie Priv. University of Ottawa, Ottawa, ON, K1N 6N5, CANADA

Ph: +1 613-562-5800 x2835; Fax: +1 613-562-5486; Skype: howarddrundle http://www.science.uottawa.ca/˜hrund050 http://www.evolution.uottawa.ca howard.rundle@uottawa.ca

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Uppsala Sweden Genome assembly expert

Bioinformatician with expertise in genome assembly

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

Uppsala University is an international research university focused on the development of science and education. Our most important assets are all the individuals who with their curiosity and their dedication makes Uppsala University one of Sweden's most exciting work places. Uppsala University has 41,000 students, 6,500 employees and a turnover of SEK 5,900 million.

Bioinformatics Infrastructure for Life Sciences (BILS; http://bils.se) aims at furthering life science research in Sweden by providing support in the field of bioinformatics. Over 45 experts are currently employed at multiple sites in Sweden, supporting projects in a wide array of areas such as genomics, transcriptomics, proteomics, metabolomics, statistics, and more. BILS is working closely together with SciLifeLab (http://www.scilifelab.se), a national resource that facilitates research in molecular biosciences by providing access to advanced technologies and technical know-how. The large amount of resources available makes Sweden one of the best countries in the world to perform life science research, and together with talented Swedish researchers this has placed Sweden at the forefront of fields such as comparative genomics and genome evolution.

BILS is now starting a genome assembly group at Uppsala University in the creative environment of the SciLifeLab Uppsala node "The Hub" and closely related to the already running BILS annotation platform. This group will work in close collaboration with Swedish research groups embarking on genome projects to aid them with de novo assembly of genomes, including validation of assemblies and other related aspects.

Job description: For this new assembly group we are now looking for expert(s) with both a strong expertise in the area of genome assembly as well as an eagerness to be a part of the development of a new and internationally competitive infrastructure. The assembly team will help Swedish genome assembly projects with anything from providing guidance in the setup and running of assembly projects to completely running the genome assembly. Any type of read data from a wide array of organisms can be expected. The position is technical in nature, with a need to set up standard pipelines for quality control, assembly, and assembly validation, and a strong knowledge in scripting and automation of procedures in a Linux environment is a must for a successful applicant.

Qualifications: We seek a candidate with a PhD in bioinformatics, molecular biology, computer science or any related field with a strong competence in genome assembly, but expertise in other related NGS-areas are also of interest. In particular experience from assembly-projects on large eukaryotes is valued highly. Proficiency in one or more scripting languages (e.g. Perl, Python, Ruby) is a necessity, with experience in pipeline-development and/or development in the area of genome assembly considered extra beneficial. The ability to drive projects and work in a collaborative, yet service-minded environment is a must. Excellent communication skills in both written and spoken English are required, since the candidate will collaborate with scientists of very different backgrounds. Emphasis will be placed on personal suitability for the position.

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

You are welcome to submit your application no later than August 11, 2014. UFV-PA 2014/1993. Please see the link below for full details and to access the application form.

http://www.uu.se/en/join-us/jobs-detail-page/-?positionId=3D39909 henrik.lantz@imbim.uu.se

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UppsalaU EvolGeneticsBioinformatician

Bioinformatics position

A bioinformatics position is available in the group of Jochen Wolf at the Evolutionary Biology Centre in Uppsala, Sweden. The position is initially limited to 2-years and after evaluation can be made permanent.

Background. We are a young, growing research group that applies an integrative approach to study evolutionary processes in natural populations. Major research themes include speciation and genome evolution. One of the main question is to understand the evolutionary processes and genetic mechanisms underlying species divergence (e.g. Ellegren et al. 2012, Shafer et al. 2013, Poelstra et al. in press). Using large-scale genetic approaches, as well as field based experiments, we characterize genomic divergence across populations and (sub-)species and assess its relationship to functional phenotypic divergence. In addition, we engage in (macro-evolutionary) comparative approaches to study evolution across larger timescales (e.g. Nabholz et al. 2013) and sometimes get interested in methodology (Mugal et al. 2014, Vijay et al. 2013). Empirical systems currently include birds (swallows and corvids), marine mammals (pinnipeds and killer whales) and the European hemiclonal Pelophylax water frog system.

The position. The successful applicant will be responsible for management of large transcriptome and genome resequencing data sets and engage actively in ongoing research projects. The applicant is familiar with genetic databases and has experience in standard bioinformatic approaches using high throughput sequencing data from Illumina, SOLID, IonTorrent and (increasingly) single molecule sequencing. Common tasks involve data management, genome assembly and annotation of vertebrates (Birds ca. 1.2 Gb, marine mammals: ca. 3Gb), multiple sequence alignments, mapping, genotyping, etc. Proficiency in relevant programming languages (UNIX, Perl, Python, etc.) is naturally assumed. A background in population genomics or comparative genomics is beneficial.

The environment. The Evolutionary Biology Centre (http://www.ebc.uu.se/) is one of the world's leading research institutions in evolutionary biology. It is part of Uppsala University which has been ranked first place among all European Universities in the subject of biology (CHE European ranking) and bridges a broad variety of disciplines. The scientific environment with numerous seminars, journal clubs and social activities offer excellent possibilities for contacts and collaborations. A graduate school currently directed by Jochen Wolf provides a framework for courses and high-profile seminars broadly reflecting the group's research interests (http://www.ebc.uu.se/education/postgrad/-gradschool/Seminars). Our lab is part of the Department of Evolutionary Biology (http://www.ebc.uu.se/-Research/IEG/evbiol/), an active environment addressing fundamental evolutionary questions with a wide range of different approaches. As a member of the Science for Life Laboratory (http://www.scilifelab.se/-) we make extensive use of high performance computing resources (https://www.uppmax.uu.se/uppnex) and extended bioinformatic infrastructure (http://www.scilifelab.se/platforms/bioinformatics/). We also actively interact with research groups of the nearby BioMedicalCentre (http://www.imbim.uu.se/-Research). The lab is situated in the student town of Uppsala, that offers rich opportunities in cultural and outdoor activities. Sweden's capital Stockholm is less than an hour's train ride away.

How to apply. Applicants with a suitable background with and without a PhD degree are encouraged to apply. Applications including a CV, a statement of motivation and the contact details of at least two references should be sent to: http://www2.personalavd.uu.se/jobb/-appform.php?lang=en&case=UFV-PA%202014/1596 The positions remains open until filled. Starting date is flexible. For more information contact jochen.wolf@ebc.uu.se or see http://www.ebc.uu.se/-Research/IEG/evbiol/research/Wolf/ . Literature. Poelstra JW, Vijay N, Bossu CM et al. Wolf JBW (in press) The genomic landscape underlying phenotypic integrity in the face of gene flow in crows. Science

C. F. Mugal, J. B. W. Wolf, I. Kaj, Why Time Matters: Codon Evolution and the Temporal Dynamics of dN/dS, Mol Biol Evol 31, 212–231 (2014).

B. Nabholz, H. Ellegren, J. B. W. Wolf, High Levels of Gene Expression

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USalford UK EvolutionaryBiol

The School of Environment & Life Sciences at Salford University, Manchester, is investing in its expanding profile of research and training in the areas of human health and environment. We are now offering new academic positions, some of which are highly relevant to modern evolutionary biology, such as:

Lecturer in Bioinformatics/Genomics - Salary range: £37,756 - £45,053, see REF: 1410411 Lecturer in Spatial Epidemiology - Salary range: £37,756 - £45,053, see REF: 1409681 Chair in Science Communication & Digital Media - Salary range: Professorial scale, see REF: 1415337

To apply, visit: www.jobs.salford.ac.uk/ Closing date: 8 June 2014 Interviews will take place in the week commencing 23 June 2014.

To discuss these posts informally, please contact Professor Judith Smith, Head of School j.e.smith@salford.ac.uk

S.Mariani@salford.ac.uk

UTexas Arlington ResAssoc Bioinformatics

University of Texas at Arlington Research Engineering Scientist Associate I

To apply: http://www.uta.edu/hr/careers/ (Posting located in the Engineering Job Family)

Hiring Department: Biology, Genomics Core Facility Pay type: Monthly Salary $2631.00 (negotiable depending on qualifications) Hours per week: 40 (8am - 5pm) FLSA status: Exempt Start Date: Staring immediately Location: Arlington, TX Required Application Materials Please include a Resume and List of References (with contact information)

Purpose To provide IT support to the Genomics Core Facility staff and all equipment in the facility; to provide bioinformatics support to faculty related to next generation sequencing data; to carry out a variety of Genomics Core-related tasks as required.

Essential Functions Diagnose and perform intermediate-to-advanced repair of computing hardware, software (with emphasis on Windows operating systems and Microsoft Office software, including PC troubleshooting skills), and network issues in a professional and timely manner. Administer, maintain and update websites & servers. Provide IT support for the Illumina MiSeq next-generation sequencing machine, including managing of data files, and making these available to customers. Provide IT and bioinformatics support to students and faculty to facilitate genomic analysis, including installation and running of bioinformatics software, writing and management of scripts to manipulate data and data formats, and assistance curating and serving large datasets from the server. Proactively and effectively communicate with supervisors, staff and faculty. Carry out a variety of Core-related duties (placing service calls, training new users, meeting with maintenance technicians) as needed. Create and update online documentation and protocols for standards, services and procedures.

Marginal/Incidental Functions Other functions as assigned

Required Qualifications Bachelor's degree in computer science or biology. Ability to multitask and maintain productivity on multiple projects. Strong analytical, prioritizing, interpersonal, and problem-solving skills. Self-motivated with attention to detail, deadlines and reporting. Experience maintaining server and workstation software and hardware, including Windows and Microsoft Office. Proficiency employing bioinformatics software in a linux/unix environment. Sufficient familiarity with common bioinformatics databases and tools to independently design and perform diverse bioinformatics tasks. Applicants must include in their online resume the following information: 1) Employment history: name of company, period employed (from month/year to month/year), job title, summary of job duties and 2) Education: college or college degree, list school name, degree type, major, graduated or not, and hours completed if not graduated. Equivalent combination of relevant education and experience may be substituted as appropriate.

Preferred Qualifications 1+ years of working experience in bioinformatics, computational biology, computer science, biology, or related fields. Excellent written and verbal communication skills. Proficiency in data analysis including: Programming experience in Perl and/or Python. Unix shell scripting experience. Next generation sequencing data analysis. Experience with data visualization, including analysis in R, and/or experience programming in R. Ability to understand biological questions and bioinformatics solutions.

Working Conditions May work around chemical fumes. May work around standard office conditions. May work around biohazards. May work around chemicals. May work around electrical and mechanical hazards. Repetitive use of a keyboard at a workstation. Use of manual dexterity. Lifting and Moving.

jmcastoe@uta.edu

UWashington ViralEvolutionSocialNetworks

UW.ViralEvolutionSocialNetworks

Programmer/Researcher UW.Viral Evolution Social Networks

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

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

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

Requirements:

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

- Ability to read, analyze and write scientific papers

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

- Experience with the C programming language.

- Excellent communication skills

- Willingness to write detailed software documentation for end users.

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

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

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

Joshua Herbeck <herbeck@uw.edu>

WakeForestU LabTech Genomics

Laboratory Research Technician, Molecular Lab Wake Forest University, Winston Salem, NC

The Lotterhos Lab in the Department of Biological Science at Wake Forest University is seeking a full-time genomics technician to manage our new molecular research lab. We use landscape/seascape genomics, field experiments, and modeling to understand how species will adapt and respond to climate change (https://sites.google.com/site/katielotterhos/home). Most of our empirical work is in marine systems, but we also collaborate with terrestrial biologists and theoreticians.

The ideal candidate will have previous experience with next-generation molecular lab protocols, such as target capture, RNA-seq, RAD-seq, or whole genome low-coverage sequencing. Specific duties will include ordering and maintaining equipment and supplies, processing genetic samples, preparing DNA and RNA libraries for genotyping and next-generation sequencing, organization of tissue samples, performing basic next-gen data analysis, training students, and maintaining a safe laboratory environment. Some knowledge or experience with bioinformatics/computational biology, and the ability to learn these skills, is also desirable.

We are looking for a well-organized, enthusiastic, independent, and productive individual who would fit well into our interdisciplinary work environment. We offer exciting opportunities to be involved in a wide range of ecological and evolutionary projects, and the potential for co-authorship on scientific manuscripts.

Preferred Qualifications - Experience preparing reagents/buffers, gel electrophoresis, and PCR - Experience working in a lab performing next-generation sequencing, particularly on the Illumina platform - Familiarity with scientific computing languages such as R, Python, Perl - Familiarity with alignment and gene annotation of next-gen data - Knowledge of marine biology or evolution - Master's degree or equivalent experience

This is a full-time position for a period of 12 months with good benefits. The desired start date is no later than 15 Aug 2014.

Applications are at: https://wakejobs.silkroad.com/WFU/Employment_Listings.html Tracking Code: 1643-141

The Winston Salem area in North Carolina offers a wide range of recreational activities in the outdoors, music, history, and the arts.

Feel free to contact me with questions:

Katie E. Lotterhos

lotterke@wfu.edu

WhitmanCollege LabTech MolEvol

Seeking a full-time laboratory technician to carry out research on the molecular basis of repeated evolution:

The successful candidate will work with me for one year to design and implement functional tests of candidate genes for the regulation of floral pigmentation in the Chilean monkeyflower (Mimulus). Renewal contingent upon funding and job performance.

Requirements include: - a Bachelor's degree in Biology or a related discipline - research experience in a molecular lab, preferably including qPCR, cloning, and plasmid design and construction - attention to detail and ability to work independently

I run an undergraduate research lab at Whitman College, a selective liberal arts college located in the small but vibrant community of Walla Walla, in eastern Washington. Walla Walla receives numerous awards for quality of life thanks to its music, art, and wine scenes: http://www.wallawalla.org/ .This is a full-time position with benefits, starting at $30,000 annual salary. Starting date is flexible but should be this summer or this fall.

To apply, please visit https://whitmanhr.simplehire.com/postings/1109 and upload: - a cover letter describing your background and reason for being interested in the position - your CV / resume - names and contact information for three references

Questions may be directed to: Dr. Arielle Cooley cooleya@whitman.edu

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Arielle Cooley, Assistant Professor Whitman College Biology Department Walla Walla, WA 99362

cooleya@whitman.edu

Other

AGA student award winners

American Genetic Association Presents the Annual Stephen J. O’Brien Award

The Council of the American Genetic Association has granted the annual Stephen J. O’Brien Award for best student-authored articles published in Journal of Heredity’s 2013 volume. The award honors Dr. Stephen J. O’Brien, who served as Editor-In-Chief for the Journal from 1987-2007.

An Award Committee made up of the current Editor-In-Chief, Scott Baker, an Associate Editor, Jill Pecon-Slattery, and a Council member, David Baum, evaluated 15 eligible articles. Council voted to present this year’s award to two authors for their outstanding papers: Dr. Sara Hanson for her article, “Inventory and Phylogenetic Analysis of Meiotic Genes in Monogonont Rotifers”, Journal of Heredity 2013:104(3):357-370 (supervisor, Dr. John Logsdon), and Dr. Alexander Nater for his article “Marked Population Structure and Recent Migration in the Critically Endangered Sumatran Orangutan (Pongo abelii)”, Journal of Heredity 2013:104(1):2-13 (supervisor, Dr. Michael Krützen).

The Award Committee, in presenting their recommendation to Council, had the following comments:

“The panel had a difficult time choosing a single top paper, as the strongest candidates differed markedly in subject and approaches. One article emphasizes genomics of rotifers, and the other the conservation genetics of Sumatran orangutans. The rotifer paper was refreshingly different from approaches taken by the other papers, examined an interesting evolutionary problem, and featured impressive methodology, including 454 sequencing of 2 genomes and rtPCR experiments for gene expression. The orangutan paper was nicely written and included comprehensive molecular ecology data across the full range of an endangered ape. It illustrated the insights possible by the integration of genetic and behavioral data of critically endangered, long-lived species."

The award includes a $1,500 prize to each author, as well as up to $1,500 reimbursement to attend the AGA Symposium, and a three-year AGA membership and subscription to Journal of Heredity.

The complete announcement and both freely available articles are available at http://jhered.oxfordjournals.org/content/105/4/583.full
We congratulate both emerging researchers on this achievement.

Scott Baker Editor, Journal of Heredity

agajoh@oregonstate.edu

AnnArbor Hackathon Sep15-19

Apply for the Tree-for-All: A hackathon to access OpenTree's global phylogeny resources.

A global 'tree of life' will transform biological research in a broad range of disciplines from ecology to bioengineering. To help facilitate that transformation, the OpenTree < http://opentreeoflife.org > project [1] now provides online access to >4000 published phylogenies, and a newly generated tree covering more than 2.5 million species.

The next step is to build tools to enable the community to use these resources. To meet this aim, OpenTree < http://www.opentreeoflife.org/ >, Arbor < http://www.arborworkflows.com/ > [2] and NESCent's HIP < http://www.evoio.org/wiki/HIP > working groups [3] are staging a week-long hackathon September 15 to 19 at U. Michigan, Ann Arbor. Participants in this 'Tree-for-all' will work in small teams to develop tools that use OpenTree's web services to extract, annotate, or add data in ways useful to the community. Teams also may focus on testing, expanding and documenting the web services.

How could a global phylogeny be useful in your research or teaching? What other data from OpenTree would be valuable? How could OpenTree web services be integrated into familiar workflows and analysis tools? How could we add to the database of published trees, or enrich it with annotations?

If you can imagine using these resources, and you have the skills to work collaboratively to turn those ideas into products (as a coder, or working side-by-side with coders), we invite you to apply for the hackathon. The full call for participation (http://bit.ly/1ioPPMc) provides instructions for how to apply, and how to share your ideas with potential teammates (strongly encouraged prior to applying). Applications are due July 8th. Travel support is provided. Women and underrepresented minorities are especially encouraged to apply.

If you have questions, contact Karen Cranston (karen.cranston@nescent.org, @kcranstn, OpenTree), Arlin Stoltzfus (arlin@umd.edu, HIP), Julie Allen (juliema@illinois.edu, HIP), or Luke Harmon (lukeh@uidaho.edu, Arbor).

[1] http://www.opentreeoflife.org [2] http://www.arborworkflows.com/ [3] http://www.evoio.org/wiki/HIP (Hackathons, Interoperability, Phylogenies)

julieallen34@gmail.com

AustNatlU VolFieldAssist FairyWrenPopulations

Field assistant fairy-wrens Australia

I am looking for a field assistant to help monitor a population of red-winged fairy-wrens in south-west Australia from beginning of October to ~22 January 2015 as part of an on-going study on cooperation and competition. The study is based at Smithbrook Nature Reserve in one of the 35 biodiversity hotspots of the world! Duties include searching for nests, monitoring colour-ringed birds, behavioural observations, mist netting and data entry. Working days are long, start early and consist of lots of hiking through dense forest with occasional encounters with venomous snakes. Applicants must be physically fit and have outstanding hearing and vision, be able to work independently, get along well with others in remote field setting and tolerate hot weather conditions. Enthusiasm, self-motivation, and a strong work ethic are a must. Required qualifications: experience in monitoring colour-ringed birds, nest-searching, mist netting and current drivers licence. Field assistant will get an allowance of AU$7000 for total period. Onsite accommodation is provided, but candidate must pay their own flight to Perth, Australia. Candidate must be Australian citizen or eligible for appropriate visa e.g. subclass 417, 600 or 601. To apply, please email a letter outlining previous relevant field research experience, and a resume including names and contact information for 3 referees to Lyanne Brouwer (lyanne.brouwer@anu.edu.au). Applicants will be considered as they apply until the position is filled.

Lyanne Brouwer ARC DECRA Fellow Evolution, Ecology and Genetics Research School of Biology College of Medicine, Biology & Environment Building 116, Daley Rd The Australian National University Canberra, ACT 0200 Australia T: +61 (0) 2 6125 8057 www.MyScience.eu/lyanne http://scholar.google.com/citations?user=emfCqiIAAAAJ
Lyanne Brouwer <Lyanne.Brouwer@anu.edu.au>

AustNatlU VolFieldAssist FairyWrens

Two motivated and capable volunteer field assistants are needed for a long-term research project studying the evolution cooperative breeding and extra-pair mate choice in the superb fairy-wren by Professor Andrew Cockburn.

Fieldwork will involve:

- assisting with mist-netting of superb fairy-wrens
- searching for nests
- monitoring nests

The fieldwork requires spending 6-8 hours/day, 5 days/week at the field site. You will be part of a team of researchers and students working on the project. The study site is a botanical gardens and adjoining eucalypt woodland, and is very close to the university. We are able to provide up to $12,000 Australian to support the expenses of assistants, which is repayable on receipt. Airfares, food and accommodation expenses are are all refundable.

Ideally, applicants should have some field experience, good observational skills, and be able to work independently. Previous nest searching or mist-netting experience would be a great advantage, but is notessential.

For more information, and to apply, please contact Helen Osmond (helen.osmomd@anu.edu.au). Interested applicants should email a cover letter, a CV and the contact details for two referees (ideally at least one referee who has worked with you in the field) to this address.

Andrew Cockburn <Andrew.Cockburn@anu.edu.au>

Australia VolFieldAssistant Aug2014

Volunteer Field Assistant for study on white-browed scrubwrens Aug - Dec 2014

I am looking for a capable volunteer field assistant to help a PhD student monitor a population of colour-banded white-browed scrubwrens in Canberra, Australia for a study on alarm calling in avian communities. This is a great opportunity for recent biology graduates to gain invaluable experience in field research.

Duration: early August to December 2014 (4 months)

Field assistant duties will include assisting with mist-netting of white-browed scrubwrens, observing colour-banded birds, searching for and monitoring nests.

Applicants should be prepared to work long hours with early mornings. White-browed scrubwren nests are very well hidden, so extended periods of close observation of individual birds will be necessary to find them. The field site is located in the Australian National Botanic Gardens in Canberra, across the road from the Australian National University.

Qualifications: previous experience observing colour-banded birds and nest searching is extremely desirable. Applicants should be physically fit, reliable, hardworking and able to work independently.

The project will provide reimbursement of travel expenses (a basic economy airfare), food and accommodation costs in Canberra upon presentation of receipts.

For more information, please contact Jessica McLachlan (jrm93@cam.ac.uk). To apply, please send a cover letter outlining your relevant field research experience, your CV and the contact information for 2 referees to the address above.

jrm93@cam.ac.uk

Canberra Australia VolunteerFieldAssist Aug15-Oct15

Other: VolunteerFieldAssistant.CanberraAustralia.Aug2014

We are seeking a field assistant for two months (August 15-October 15) to help with a behavioral research on brood parasitism in yellow rumped thornbills. These birds are hosts of cuckoos and my PhD focuses on how they defend from parasitism. I perform field experiments in their nests and do behavioral observations so it would be great for people with interests in ethology. Fieldwork will be in Canberra (Campbell park), biking distance from the center of the city. The main duties are finding nest, monitoring them and performing some simple experiments. Experience finding nests is required. We will provide AUD 1500 per month for accommodation and food, but assistants must cover their trip to Canberra. The work is not physically demanding, but enthusiasm, patience and work ethic are a must.

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

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

CostOfMitochondria RoyalSociety

Royal Society Publishing has just published an issue of Philosophical Transactions B on âWhat cost mitochondria? Maintenance and evolution of mtDNA', edited by Duur Aanen, Johannes Spelbrink and Madeleine Beekman. This issue looks at looks at how mitochondria are costly and why we expect them to be, and the role mitochondria play in certain diseases and ageing. More information, and the content of the issue, can be accessed at http://bit.ly/PTB1646. A print version is available at the reduced price of Â£35.00. You can order online via the above web page (enter special code TB1646 when prompted). For a list of all issues in this area, please visit http://bit.ly/orgissues Felicity Davie Royal Society Publishing

T +44 20 7451 2647

The Royal Society 6-9 Carlton House Terrace London SW1Y 5AG http://royalsocietypublishing.org Registered Charity No 207043

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

Geldoc ThermalCycler Advice

Dear Members,

We would like to purchase Geldoc (from Biostep, Germany), and Thermal cycler (from Benchmark Scientific, USA), and seek your feedback on these brands. Earlier we used to use (BioRad, Eppendorf), but selected ones are cheaper than the previous; however do not want to compromise on quality. Any advice will be highly appreciated. Thank you. Best wishes,

AVIK RAY

SERB-DST-young scientist Ashoka Trust for Research in Ecology and the Environment (ATREE) Srirampura, Royal Encalve, Jakkur Post Bangalore - 64, India, phn: 91-80-23635555 (Office) ext -161, Fax: 91-80-23530070 alternate email: avik.ray@atree.org

avik.ray.kol@gmail.com

KewGardens Cuts Petition

Dear colleague,

Science and conservation at Kew Gardens (http://www.kew.org/) is under threat due to government cuts - Â£5M deficit will lead to a loss of over 120 posts (see http://www.bbc.co.uk/news/uk-england-london-26821046)!

Please help to prevent this, please sign this e-petition: http://bit.ly/save_kew , and please, please forward this message to your colleagues and friends. Every single signature is VERY important¡'

Dr Gerhard PRENNER Senior Researcher in Morphology/Anatomy Royal Botanic Gardens, Kew Jodrell Laboratory Richmond, Surrey, TW9 3DS UK

* ++44(0)20 8332 5316 * g.prenner at kew.org http://www.kew.org/science-conservation/research-data/science-directory/people/prenner-gerhard Gerhard Prenner <G.Prenner@kew.org>

NESCent CallForProposals

Dear colleagues:

I would appreciate if you could please distribute NESCent's call for proposals to your members of your organizations and colleagues. Thank you once again for your help and time.

SHORT-TERM VISITORSHIPS IN EVOLUTIONARY BIOLOGY AND RELATED FIELDS

We are now accepting proposals for Short Term Visitors at The National Evolutionary Synthesis Center (NESCent). Terms at NESCent can be up to 3 months. We are looking to support innovative approaches to outstanding problems in evolutionary science. Proposals are due August 1, 2014. For more information, please see our website at https://www.nescent.org/science/proposals.php. Any questions can be directed at Craig McClain, Assistant Director of Science, at cmcclain@nescent.org

Cheers Craig

Craig R. McClain, Ph.D. Assistant Director of Science National Evolutionary Synthesis Center 2024 W. Main St. Suite A200 Box 104403 Durham, NC 27705 919-668-4590

cmcclain@nescent.org

Associate Editor for Journal of Biogeography: http://www.wiley.com/bw/journal.asp?ref=0305-0270 Deep-Sea News: http://deepseanews.com/ National Evolutionary Synthesis Center: http://www.nescent.org/ Research Homepage: http://craigmcclain.com/ McClain Craig <cmcclain@nescent.org>

Phyloseminar KamilaNaxerova Jun5

Kamila Naxerova Massachusetts General Hospital Phylogenetic analysis of metastatic colon cancer in humans Thursday, June 5, 2014 10:00 AM PDT

Metastasis is the main cause of cancer morbidity and mortality. Despite its clinical significance, several fundamental questions about the metastatic process in humans remain unsolved. Does metastasis occur early or late in cancer progression? Do metastases emanate directly from the primary tumor or give rise to each other? How does heterogeneity in the primary tumor relate to the genetic composition of secondary lesions? Addressing these questions " ideally by examining the genetic makeup of tumor cells in distinct anatomic locations and reconstructing their evolutionary relationships " is crucial to improving our understanding of metastasis. I will give an overview of a simple PCR-based assay that enables the tracing of tumor lineage in patient tissue specimens. The methodology relies on somatic variation in highly mutable polyguanine (poly-G) repeats located in non-coding genomic regions. Poly-G mutations are present in a variety of human cancers. In colon carcinoma, an association exists between patient age at diagnosis and tumor mutational burden, suggesting that poly-G variants accumulate during normal division in colonic stem cells. Poorly differentiated colon carcinomas (which have a worse prognosis) have fewer mutations than well-differentiated tumors, possibly indicating a shorter mitotic history of the founder cell in these cancers. By presenting several patient case studies, I will describe how poly-G fingerprints can be used to construct phylogenetic trees that reflect the evolution of metastatic colon cancer, with an emphasis on how biological considerations inform analysis strategies.

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

Phyloseminar RolandSchwarz Jun19

Roland Schwarz Cambridge Phylogenetic quantification of intra-tumour heterogeneity Thursday, June 19, 2014 9:00 AM PDT

Tumour heterogeneity, i.e. the genomic diversity of cancer cells within a single tumour, is thought to be the source of chemotherapy resistance. In many cancers, this heterogeneity is not limited to point mutations but includes large scale genomic rearrangements and endoreduplications that lead to aberrant copy number (CN) profiles. Reconstruction of the evolutionary tree of cancer within the patient allows us to quantify and understand the aetiology of tumour heterogeneity. In some cancers, such as high-grade serous ovarian cancer (HGSOC), CN profiles predominate. However tree inference is hindered by unknown phasing of major and minor CNs, horizontal dependencies between adjacent genomic loci and the lack of curated CN profile databases to use as a reference for probabilistic inference.

We recently developed MEDICC (Minimum Event Distance for Intra-tumour Copy number Comparisons), an algorithm for phylogenetic reconstruction based on CN profiles. MEDICC uses finite-state transducers (FSTs) to encode a minimum evolution criterion that determines pairwise evolutionary distances between CN profiles. This minimum-event distance computes the smallest number of amplification and deletions of arbitrary length that are necessary to transform one genomic profile into another. The FST-based approach allows us thereby to model dependencies between sites, similar to the problem of modelling indels on trees in traditional phylogenetics. Using this approach we are able to phase major and minor CN profiles to the parental alleles and infer trees and ancestral genomes, while minimizing the overall tree length. The distance measure is formulated such that the resulting matrix of pairwise distances has a direct mapping to a positive semi-definite kernel matrix. This allows us to perform principal component analysis in evolutionary space and use this embedding to numerically quantify tumour heterogeneity and other quantities of interest, such as the degree of clonal expansion, using spatial statistics.

I will talk about the basics of FST-based phylogenetic inference and explain how they can be used to model genomic rearrangement events with horizontal dependencies. I will explain how this approach implicitly maps genomes into a feature space in which we can quantify heterogeneity. Finally, I will present clinical results that show how this quantification of ITH can predict resistance development in the hospital.

For more details please see http://phyloseminar.org/- . – Frederick “Erick” Matsen, Assistant Member Fred Hutchinson Cancer Research Center http://-matsen.fhcrc.org/ Erick Matsen <matsen@fhcrc.org>

Software SMARTPOP PopGeneticsSimulator

Dear all,

SMARTPOP is a new forward-in-time simulator for population genetics. It is free and open source distributed under a GPL v3.0 license. It is subject of ongoing development related to inferences of interaction between population genetics and social system. It can be use to model human communities as well as animal with complex socio-ecological systems.

Its current main features are: - high speed - simulation of explicit individuals and DNA with mutations - possibility to simulate simultaneously sex-linked DNA (mtDNA, X and Y chromosomes) and autosomal loci - complex scenario with demographic changes - outputs diversity estimators or full sequences

For further information (download links, example, manual, etc...), please see the website: http://-smartpop.sourceforge.net A complete description of the software with case studies is also available in: SMARTPOP: inferring the impact of social dynamics on genetic diversity through high speed simulations Elsa G Guillot and Murray P Cox. BMC Bioinformatics 2014, 15:175 http://www.biomedcentral.com/-1471-2105/15/175/ For any question please contact e.guillot@massey.ac.nz

Elsa Guillot, PhD Student, Massey University New Zealand

elza.guillot@gmail.com

SouthAfrica VolunteerFieldAssist SmallMammals

Volunteer opportunity as field assistants for the project:

Evolution and Socio-Ecology of small Mammals in the Succulent Karoo of South Africa

Opportunity: This is a great opportunity for anybody who wants to get more experience in field work relating to eco-physiology, animal behavior, evolution, and ecology before starting an MSc or PhD project.

Project: We study the evolutionary and ecological reasons as well as physiological mechanisms of group living, paternal care, communal nesting and social flexibility in the striped mouse. One focus is on the adaptation to droughts, combining physiological, behavioral, ecological and evolutionary research. As this species is diurnal and the habitat is open, direct behavioral observations in the field are possible.

What kind of people are needed? Biology/zoology/veterinary students are preferred as candidates. Applicants must have an interest in working in the field and with animals. Hard working conditions will await applicants, as the study species gets up with sunrise (between 5 and 6 o‘ clock), and stops its activity with dusk (19 o‘ clock). Work during nights might also be necessary. Work in the field will be done for 5 days a week. Applicants must be able to manage extreme temperatures (below 0 at night in winter, sometimes over 40 C during summer days). Applicants must both be prepared to live for long periods in the loneliness of the field and to be part of a small social group.

Work of volunteer field assistants: Trapping, marking and radio-tracking of striped mice; direct behavioral observations in the field. Volunteers will also see how blood samples are collected for physiological measurements. Volunteers are expected to help with maintenance of the research station (water pump, solar power, etc.).

Confirmation letter: Students get a letter of confirmation about their work and can prepare a report of their own small project to get credit points from their university for their bachelor or masters studies.

Costs: Students have to arrange their transport to the field site themselves. Per month, an amount of Rand 1300 (around 180 US$, 110 Euro) must be paid for accommodation at the research station. Students must buy their own food etc in Springbok (costs of about R 3000, approx. 360 US$ or 250 Euro/month). Including extras (going out for dinner; shopping), you should expect costs of about 600 US$ / 450 Euros per month. Students get an invitation letter which they can use to apply for funding in their home country.

Place: The field site is in the Goegap Nature Reserve near Springbok in the North-West of South Africa. The vegetation consists of Succulent Karoo, which has been recognized as one of 25 hotspots of biodiversity. It is a desert to semi-desert with rain mainly in winter (June to September).

When and how long: At the moment we are looking for one or two volunteers starting in July / August 2014 and for two volunteers starting in December 2014/ January 2015. Volunteers are expected to stay at least three months, but longer periods of up to 6months are preferred.

How to apply? Send a short motivation letter stating why and for which period you are interested and your CV via email to succulent.karooo.research.station@kabelbw.de.

More information under

http://stripedmouse.com/site1_3_5.htm http://www.youtube.com/watch?v=w6rvF5XrVn0&list=UUd12oFYqs5OobiiKMhDnFtw&index=1

Contact via e-mail: succulent.karoo.research.station@kabelbw.de

Succulent Karoo Research Station

a registered South African non-profit organization

Dr. Carsten Schradin (Director)

South Africa

WORKING AS A FIELD ASSISTANT IN GOEGAP NATURE RESERVE

A report by Romy Höppli, student at the University of Zurich, who staid in Goegap June to August 2008

Blue skies without a single cloud for six weeks rocky mountains with little vegetation yellow, orange and pink fields of flowers in whatever direction you look small mammals, lizards and birds in our front yard and Mountain Zebras, Springbok and Ostrich right next door...

This was my time at the Succulent Karoo Research Station in Goegap Nature Reserve in South Africa! During six weeks from the beginning of July until the middle of August I've been living here, studying mice, experiencing nature like never before and being part of a small community where there was always something to laugh and joke about!

After arriving in Goegap, right the next morning my scientific adventure in South Africa began: Setting and checking traps, nest observations and radio-tracking were our daily routine. While I got bitten by the mice quite often in the beginning and my right middle finger was scarred all over, I improved quickly shaking the mice out of the traps, weighing them and checking the number of the ear tag. Other duties like cleaning the cages of

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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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Springer Evolution books

The Applied Evolutionary Epistemology Lab of the Centre for Philosophy of Science of the University of

Lisbon is pleased to announce the publication of the 1st VolumeÂin the New Springer Book Series Interdisciplinary Evolution Research.

THE EVOLUTION OF SOCIAL COMMUNICATION IN PRIMATES: A MULTIDISCIPLINARY APPROACH Edited by Marco Pina & Nathalie Gontier Book Abstract: How did social communication evolve in primates? In this volume, primatologists, linguists, anthropologists, cognitive scientists and philosophers of science systematically analyze how their specific disciplines demarcate the research questions and methodologies involved in the study of the evolutionary origins of social communication in primates in general, and in humans in particular. In the first part of the book, historians and philosophers of science address how the epistemological frameworks associated with primate communication and language evolution studies have changed over time, and how these conceptual changes affect our current studies on the subject matter. In the second part, scholars provide cutting-edge insights into the various means through which primates communicate socially in both natural and experimental settings. They examine the behavioral building blocks by which primates communicate, and they analyze what the cognitive requirements are for displaying communicative acts. Chapters highlight cross-fostering and language experiments with primates, primate mother-infant communication, the display of emotions and expressions, manual gestures and vocal signals, joint attention, intentionality and theory of mind. The primary focus of the third part is on how these various types of communicative behavior possibly evolved, and how they can be understood as evolutionary precursors to human language.Â Leading scholars analyze how both manual and vocal gestures gave way to mimetic and imitational protolanguage, and how the latter possibly transitioned into human language. In the final part, we turn to the hominin lineage, and anthropologists, archeologists and linguists investigate what the necessary neurocognitive, anatomical and behavioral features are in order for human language to evolve, and how language differs from other forms of primate communication.

Table of Contents: http://www.springer.com/life+sciences/evolutionary+%26+developmental+biology/book/978-3-319-02668-8 ABOUT THE SERIES INTERDISCIPLINARY EVOLUTION RESEARCH Website: http://www.springer.com/series/13109 FORTHCOMING ANTHOLOGIES (to appear in Fall & Winter 2014): Macroevolution: Explanation, Interpretation, Evidence, Emanuele Serrelli & Nathalie Gontier (eds)

Reticulate Evolution: Symbiogenesis and Horizontal Gene Transfer, Nathalie Gontier (ed)

Cultural Phylogenetics: Concepts and Applications in Archaeology and Anthropology, Larissa Mendoza Straffon (ed)

INTERESTED IN EDITING AN ANTHOLOGY FOR THE SERIES? Contact Nathalie Gontier at nlgontier@fc.ul.pt. Kindly note that the series does not publish monographs.

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appeelannouncements <appeelannouncements@fc.ul.pt>

PostDocs

AarhusU PrimateGenomics

Population genomics of the X chromosome

A post doc position is available to work in the research group of Mikkel Heide Schierup at the Bioinformatics Research Centre at Aarhus University on comparative evolutionary genomics of the X chromosome (and the Y chromosome) in humans and other great apes. The position is funded by the Danish National Research Council for Independent Research and includes funds for targeted experiments.

We have recently reported that the X chromosome is under strong adaptive evolution (Hvilsom et al. 2012, PNAS 10.1073/pnas.1106877109) and that it has diversity patterns best explained by a large number of very strong selective sweeps, independently occurring in similar places in most great apes species, including humans (Nam et al. 2013 arXiv:1402.5790v2). The candidate will develop models and perform analyses to study this pattern and test different hypotheses, including the possible involvement of X-ampliconic regions. The position will exploit high coverage whole genome sequencing of many individuals of each great apes species and phased trio data from humans. There will also be the opportunity to do expression analysis using RNAseq of testis samples and targeted resequencing of particular difficult regions, such as ampliconic regions. Furthermore, there will be the opportunity to join our participation in international consortia for analysis of primate genomes.

A PhD degree and strong expertise in statistical analysis and population genetics is essential. Analyses will require programming skills and familiarity with high performance computing.

The position is initially for 1 year with possible extension for 1 more year. The starting salary depends on qualifications but is typically in the range of EUR 59,000-65,000 per annum, and there is often reduced taxation for applicants which have not lived and worked in Denmark for the past 3 years.

The working environment is the Bioinformatics Research Center (www.birc.au.dk), which has a strong emphasis on evolutionary analyses and includes the research groups of Drs Thomas Mailund, Thomas Bataillon and Asger Hobolth with whom there are extensive collaborations.

Informal inquiries are welcomed and should be sent to Mikkel Heide Schierup at mheide@birc.au.dk. The application with CV, list of publications and names of three referees should also be sent to mheide@birc.au.dk preferably before July 7. Starting date is negotiable, but the position is available immediately.

Mikkel H. Schierup Bioinformatics Research Center, Aarhus University, CF Mollers Alle Building 1110, 8000 Aarhus C Denmark Ph: +45 8715 6535 http://www.birc.au.dk/ ˜ mheide Mikkel Heide Schierup <mheide@birc.au.dk>

AMU Poznan ModellingMHCEvolution

Evolutionary Biology Group of Professor Jacek Radwan at Adam Mickiewicz University, Poznan, is looking for a Post-Doc in an NCN-funded project investigating evolution of MHC copy number using both empirical and theoretical approaches. The post-doc will perform computer simulations exploring alternative evolutionary mechanisms potentially shaping the number of expressed MHC genes.

The candidate should hold PhD degree in biological sciences, computer sciences or mathematics and should have significant achievements in theoretical modelling of biological processes, documented by publications in international scientific journals. Competence in computer programming is essential.

The employment is offered for up to three years, starting ideally in October 2014, but it is negotiable. Application deadline is 1 September 2014. Further information can be obtained from the project leader via email: jradwan@amu.edu.pl

Prof. Jacek Radwan Institute of Environmental Biology Adam Mickiewicz University ul. Umultowska 89 61-614 Poznan

Jacek Radwan <jradwan@amu.edu.pl>

BiodesignInst Arizona 2 ComparativeGenomics

The Wilson Sayres Lab at Arizona State University in Tempe, AZ is recruiting two Postdoctoral Research Associates in the areas of Comparative Genomics, Statistics, and Bioinformatics to develop methodologies and study evolutionary questions related to sex chromosome evolution and sex biased processes, primarily in mammals, but also other taxa. Successful applicants will join a rapidly growing lab involved in a variety of active research projects and collaborations. Current projects include (1) assessing the magnitude and effect of male mutation bias, (2) simulating patterns of demography and selection on sex chromosomes, (3) determining the timing of recombination suppression on mammalian sex chromosomes, (4) measuring patterns of expression evolution on the active and inactive X chromosomes, (5) identifying signatures of positive selection across mammals proteomes (including sperm proteome), (6) identifying signals of convergent molecular evolution.

The Wilson Sayres Lab is part of the Center for Evolutionary Medicine and Informatics (CEMI), one of 10 research centers in the Arizona State University's Biodesign Institute. Research in the Wilson Sayres Lab covers many different questions in population genetics and molecular evolution, at the interface of biology, statistics, and computer science. Lab members have the opportunity to develop both dry-lab and wet-lab research programs.

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

Desired Qualifications: 1. Experience working with genomes and evolutionary analyses 2. Knowledge of programming languages 3. Knowledge of statistical methodologies 4. Experience parsing and analyzing large datasets (e.g. RNAseq) 5. Understanding of sex chromosome evolution

Application must contain: 1. Curriculum Vitae (max 2 pages) 2. Cover Letter describing your previous research and future research plans (max 1 page) 3. Names, addresses, and phone numbers of three professional references

Applications will continue to be accepted and considered until the job is filled/closed.

For more information see https://sites.google.com/-site/mwilsonsayres/research . To apply, forward one document that includes a cover letter, detailed CV, and names of 3 references to mwilsonsayres@gmail.com. Please put the job title in the subject line of the letter.

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

Sara Brashier <Sara.Brashier@asu.edu>

BrighamYoungU StructuralEvolutionaryGenomics

A postdoctoral position is available at Brigham Young University, Department of Plant and Wildlife Sciences. The postdoctoral person will use data from optical physical mapping technology (BioNanoGenomics) study and quantify the genome relationships of members of the cotton tribe. The postdoc will be required to analyze and interpret physical mapping data within a phylogenetic context and create new methods of comparative analysis for this data. The ideal candidate would have a thorough understanding of High Molecular DNA isolation, a strong foundation in phylogenetics, and skills in bioinformatics. A Ph.D. in plant biology, plant genetics, evolutionary biology or related field is required. Proficient oral communication and proficient writing skills in English are essential. This is a full-time position supported by the NSF Plant Genome Research Program.

*The start date is flexible, but preferably during Fall 2014, and the position is full-time for three years subject to satisfactory performance year-to-year. Salary will be commensurate with experience and skills, and benefits are included. Interested applicants should send a CV, a brief description of research interests and experience, and contact information for three references to Joshua Udall (**jaudall at byu.edu < http://byu.edu >). To receive full consideration, please send all application materials before July 14, 2014.*

Joshua Udall (295 WIDB) Brigham Young University 701 E. University Parkway Plant and Wildlife Science Depart. Provo, UT 84602

Office: 801-422-9307

jaudall1@gmail.com

ChicagoBotanicGarden GenomeAssembly HorizontalGeneTransfer

Postdoctoral Research Associate in Genomics/Bioinformatics at Chicago Botanic Garden

We are hiring a postdoctoral research associate for 2.5 years to lead the genome sequencing efforts of an NSF-funded, Phylogenetic Systematics grant titled “Evaluating the contributions of horizontally transferred bacterial genes and endogenous duplication events to the diversification of diatoms”. This project integrates transcriptomics, phylogenomics, and genome sequencing to understand the role of horizontal gene transfer and whole genome duplication in the diversification of diatoms.

This project is a collaborative NSF research project between Andrew Alverson (University of Arkansas) and Norman Wickett (Chicago Botanic Garden & Northwestern University). The postdoc will be based at the Chicago Botanic Garden, where the genome sequencing, assembly, and annotation efforts will be based.

START DATE: September 1 - October 1, 2014

APPLICATION REVIEW: Begins July 1, 2014

APPLICATION DEADLINE: August 1, 2014

DUTIES AND RESPONSIBLITIES

The postdoc will be responsible for coordinating and conducting the sequencing, assembly, and annotation of several diatom genomes. Additionally, the position includes the analysis of genome content and structure association with the diversification of diatoms, with an emphasis on the detection of horizontal gene transfer and whole genome duplication. Expectations are that postdoc will contribute to the preparation of numerous publications, many of which will be first-authored. Teaching and curriculum development opportunities will be provided through the Graduate Program in Plant Biology and Conservation, a joint program between the Chicago Botanic Garden and Northwestern University. Finally, the position includes involvement in the development of an exhibit on diatom biology to be hosted at the Chicago Botanic Garden.

POSITION REQUIREMENTS

Ph.D. in ecology and evolutionary biology, biology, botany, or a related field. Significant experience in bioinformatics is required, preferably in the area of genome assembly and annotation. Applicants who expect to have completed their PhD by the start date will be preferred.

TO APPLY, Please email a single pdf file that includes a cover letter, CV, and contact information for three references to:

nwickett@chicagobotanic.org

QUESTIONS? Please contact Norman Wickett: nwickett@chicagobotanic.org

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Norman Wickett Conservation Scientist in Genomics and Bioinformatics Chicago Botanic Garden Glencoe, IL 60035 nwickett@chicagobotanic.org http://www.chicagobotanic.org/research/staff/wickett nwickett@chicagobotanic.org

ClemsonU ArthropodBiodiversity

POSTDOC: CLEMSON UNIVERSITY ARTHROPOD BIODIVERSITY

[View this ad online at: https://cubshr9e.clemson.edu/psp/hpprd/EMPLOYEE/HRMS/c/HRS_HRAM.HRS_CE.GBL?Page=HRS_CE_JOB_DTL&Action=A&JobOpeningId=13381&SiteId=1&PostingSeq=1]

The Caterino Arthropod Biodiversity Lab at Clemson University is seeking a postdoctoral associate to conduct integrative research on arthropod biodiversity in the southeastern United States. Projects will analyze patterns of taxonomic or phylogenetic diversity within some arthropod group as they relate to underlying biogeographical, climatic, or anthropogenic factors. For more information on the Caterino Lab, visit: https://sites.google.com/site/caterinolab/home or contact PI Michael Caterino at mcateri@clemson.edu.

POSITION DESCRIPTION: Post Doctoral Fellow

Job Purpose: The Postdoctoral Fellow will conduct and disseminate independent, integrative research resolving evolutionary patterns of arthropod biodiversity in the southeastern United States.

Job Functions: 1) Field and laboratory research and data analysis 2) Prepare publications and proposals 3) Mentor/supervise students conducting related research 4) Prepare research presentations 5) Assist with laboratory management

QUALIFICATIONS: Minimum Qualifications: Ph. D. in Systematic Biology, Entomology, or a closely related field. Candidates must have experience in phylogenetic data analysis.

Preferred Qualifications: Additional desirable expertise includes arthropod taxonomy, entomological fieldwork, and morphological and molecular character development. Ideal candidates will have particular expertise in the systematics of some group of terrestrial or freshwater insects (Coleoptera preferred).

PAY & WORK SCHEDULE: Standard Hrs: 40. Salary commensurate with credentials and experience. The position will run for one year with the possibility of renewal for an additional year.

HOW TO APPLY: To apply, please submit the following: A cover letter, C.V., a two-page proposal of research to be undertaken, and a list of at least three references as a single pdf document titled: your_name_biodiversitypostdoc.pdf to jthoope@clemson.edu. Alternatively, applications can be mailed to: Jennifer Hooper/HR, School of Agricultural, Forest, and Environmental Sciences, Lehotsky Hall, Clemson, SC 29634.

Review of materials will begin immediately and continue until the position is filled. To ensure full consideration, please submit materials by: August 1, 2014

The successful applicant will begin as soon as possible after September 1, 2014.

BENEFITS INFORMATION: Employees who are in time limited positions will earn one and one-quarter days of Annual and Sick Leave per month for a total of thirty (30) days per year. Eligible part-timers will earn days on a pro rata basis.

JOB LOCATION: Poole Agricultural Center - Clemson Main Campus

JEANNE CLERY ACT: The Jeanne Clery Disclosure Act requires institutions of higher education to disclose campus security information including crime statistics for the campus and surrounding areas. As a current or prospective Clemson University employee, you have a right to obtain a copy of this information for this institution. For more information regarding our Employment, Campus Safety and Benefits, please visit the Human Resources - Prospective Employees web page shown below:

http://www.clemson.edu/cao/humanresources/prospective/ CLOSING STATEMENT: Clemson University is an AA/EEO employer and does not discriminate against any person or group on the basis of age, color, disability, gender, pregnancy, national origin, race, religion, sexual orientation, veteran status or genetic information. Clemson University is building a culturally diverse faculty committed to working in a multicultural environment and encourages applications from minorities and women.

Michael S. Caterino John and Suzanne Morse Chair of Arthropod Biodiversity Director, Clemson University Arthropod Collection School of Agricultural, Forest, and Environmental Sciences MAIL: 277 Poole Agricultural Center OFFICE: E-254 Poole Agricultural Center Clemson University Clemson, SC 29634-0310 mcateri@clemson.edu Office phone: (864) 656-3105 https://sites.google.com/site/caterinolab/ mcateri@clemson.edu

CNRS Gif-sur-yvette Demogenetics 2years

A two years postdoctoral position starting in september 2014 in the area of demogenetics is available in Gif-sur-Yvette within the flagship project of BASC labex on the improvement of adaptive capacities of socioecosystems using genetic knowledge.

The researcher will by based in the DEEIT team of CNRS / IRD laboratory LEGS/ BEI in Gif-sur-Yvette, and its activities will be held in collaboration with BASC teams.

Context:

Species distribution and their response to global changes result from both neutral spatial dynamic processes and environmental niche processes. Population genetic data harbor information on both processes and improvements in model based statistical analysis of genetic distributions could help putting them together in order to develop more realistic models of species responses to environment.

Profile: The candidate should have an experience in statistical inference, bayesian or frequentist, and markov chains.

Activities:

The researcher will develop in collaboration with population biologists and biostatisticians of Paris-Saclay IDEX, a bioinformatic tool for the inference of statistical models from genetic and environmental data available on insects, plants, and plant pathogens, in BASC labex teams.

Recruitment: Recruitment will last 2 years and should start in September 2014. Please send CV, motivation letter and recommendation letters before july 15th 2014 to dupas@legs.cnrs-gif.fr and tenaillon@moulon.inra.fr.

Stephane.Dupas@legs.cnrs-gif.fr

CNRS Toulouse ArabidopsisGenomics

POSTDOCTORAL POSITION IN ECOLOGICAL GENOMICS IN ARABIDOPSIS THALIANA

CNRS, TOULOUSE, FRANCE

A post-doctoral position is available for two years on the following project, “Identification of key genes underlying disease resistance to estimate the adaptive potential of natural plant populations in the current climate change”. The postdoctoral researcher will spend 24 months in the research group of Fabrice Roux (http://www6.toulouse.inra.fr/lipm_eng/-Research/Fabrice-Roux) at the Institute of Plant – Microbes Interactions (LIPM) in Toulouse (France; http://www6.toulouse.inra.fr/lipm). This position is available from September 2014 and is funded by the Laboratory of Excellence ’Towards a Unified theory of biotic Interactions: the roLe of environmental Perturbations’(Labex TULIP) and the Région Midi-Pyrénées.

The main goals of the post-doctoral project are (i) to identify genes in the model plant /Arabidopsis thaliana /associated with natural variation of microbiota, and (ii) to identify the signatures of selection acting on those genes. The postdoctoral researcher will be in charge of (i) the characterization of the bacterial and fungal communities (barcoding approach) in 80 natural populations of /A. thaliana /located at different altitudes in the South-West of France, (ii) the genomic characterization of those 80 /A. thaliana/ populations (Pool-Seq approach), (iii) the statistical analyses to map the genes associated with natural variation of microbial communities, and (iv) the genome scan of molecular signatures of natural selection. The post-doctoral researcher will work in close collaboration with the bioinformatic platform (Institute of Plant – Microbes Interactions, LIPM) that will perform the analysis of NGS data. The project offers many opportunities for the postdoctoral researcher to pursue its own ideas using available genomic data.

We are looking for an enthusiastic and motivated evolutionary biologist with a strong background in quantitative genetics and population genomics (with the prerequisite bioinformatic skills to carry out analyses of population genomic data sets) and, if possible, with laboratory experience in molecular methods related to metagenomics.

The Institute of Plant-Microbe Interactions (LIPM) of Toulouse, located on the campus of the French National Institute for Agronomy (INRA) belongs to an institute (FR-AIB) which homes about 350 researchers from INRA, CNRS and University studying Molecular Biology and Evolutionary Ecology in plants. Toulouse, located in the South West of France, near the Pyrenees and the Mediterranean sea, is attractive for its wide variety of food and wines, and is an active area for Plant Research and seed companies.

For application, please send a short CV including a description of past and present research activities, a motivation letter and the contact details of at least two referees. Applicants should not have more than five years experience after they obtained their PhD degree.The salary is about 2200 EUR a month.

Applications or informal enquiries should be sent to:

*Dr Fabrice Roux, Laboratoire des Interactions Plantes-Microorganismes (LIPM), UMR CNRS/INRA 2594, BP 52627, 31326 Castanet-Tolosan cedex, France. Tel : +33 (0)5 61 28 54 59. Fax : +33 (5) 61 28 50 61. E-mail : fabrice.roux@toulouse.inra.fr***

Thanks, Fabrice

Fabrice roux <Fabrice.Roux@toulouse.inra.fr>

DrexelU Bioinformatics

Drexel University hosts two programs in central Africa, the Central African Biodiversity Alliance (www.CABAlliance.org) and the Bioko Biodiversity Protection Program (www.Bioko.org), which operate in Cameroon, Equatorial Guinea and Gabon. We seek a highly qualified and enthusiastic individual to join our team to conduct bioinformatics analyses, develop statistical methods, and analyze population-level genetic data of select animals and plants from Central Africa.

The successful candidate will be expected to analyze and manage genomic sequence from samples collected in central Africa and contribute to the analysis of comprehensive SNP genotypes from wild chimpanzees and an arrowroot plant. The incumbent will be encouraged to develop her/his own research focus on some aspect(s) of the project, which will include examining gene-environment relationships in insects, reptiles and amphibians across an elevational gradient from the Gulf of Guinea rainforest to the Cameroon Highlands. The successful candidate will have demonstrated experience in next generation sequencing analyses as well as strong computational skills, including proficiency in at least one major programming or scripting language (preferably Python, but others apply) and use of a Linux/Unix environment. A good understanding of molecular and evolutionary biology, statistics and proficiency in R is a plus.

The postdoctoral researcher will join the laboratory of Dr. Katy Gonder (http://www.drexel.edu/biology/-contact/facultyDirectory/Gonder/) . The researcher will be expected to collaborate closely with our team of postdoctoral researchers and students at Drexel and in central Africa. The position will also include collaboration with other CABAlliance research groups, including Dr. Tom Smith's group at UCLA and Dr. Nicola Anthony's group at the University of New Orleans.

Inquiries about this position can be directed to Dr. Matthew Mitchell (mwmitchell@drexel.edu) with a subject of Bioinformatics Postdoc. Please apply for this position online at: https://www.drexeljobs.com/-applicants/jsp/shared/frameset/Frameset.jsp?time=-1402452521926 or visit www.drexeljobs.com and search for 'bioinformatics.' The requisition number is 6189.

The position is available from September 1, 2014 for one year with the possibility of renewal for up to three years. Salary will be determined based on experience level.

Dr. Katy Gonder

Associate Professor Department of Biology Drexel University 3245 Chestnut St. Philadelphia, PA 19104

gonder@drexel.edu

GeorgiaTech HumanPopulationGenomics

Postdoctoral position in human population genomics (2015)

The Lachance Lab will open its doors in January as part of Georgia Techs School of Biology. Our lab uses whole genome sequencing and computational approaches to understand how human populations evolve. We are interested in secondary contact between divergent human populations and the interplay between adaptation and hereditary disease.

I am pleased to announce that a postdoctoral position in human population genomics will be available in early 2015. This postdoctoral position will focus on evolutionary models of hereditary disease, and there will be opportunities to develop an independent research program. Georgia Tech is located in the heart of Atlanta, and there will be multiple opportunities for local collaborations (including other researchers in the School of Biology who study molecular evolution and integrative genomics).

The ideal candidate will have a PhD in biology, computer programming ability, strong quantitative skills (e.g. expertise in theoretical population genetics or genetic epidemiology), and multiple first author papers. Previous mentoring experience is also a plus. Funding is available for two years and the start date is flexible (early 2015). Informal inquiries are welcome: send an email containing an updated CV to joseph.lachance@biology.gatech.edu. I will be attending SSEs Evolution 2014 meeting in Raleigh, and would be glad to meet with anyone seeking to join our team. Two PhD student positions are also available.

Joe Lachance Assistant Professor School of Biology Georgia Institute of Technology joseph.lachance@biology.gatech.edu https://sites.google.com/site/lachancelab/home Joseph Lachance <joseph.lachance@biology.gatech.edu>

Gif France Demogenetics

Dear Colleagues,

The flagship project of BASC labex (http://www6.inra.fr/basc) on the improvement of adaptive capacities of socioecosystems is providing a 2 years postdoctoral position starting in september 2014 in the area of demogenetics.

The researcher will be based in the CNRS / IRD laboratory LEGS / BEI in Gif-sur-Yvette (http://www.legs.cnrs-gif.fr/?page_id=1066), and its activities will be held in collaboration with BASC teams.

*Context: *

Species distribution and their response to global changes result from both neutral spatial dynamic processes and environmental niche processes. Population genetic data harbor information on both processes and improvements in model based statistical analysis of genetic distributions could help putting them together in orde'r to develop more realistic models of species responses to environment.

Profile: The candidate should have an experience in statistical inference, bayesian or frequentist, and markov chains.

Activities:

The researcher will develop in collaboration with population biologists and biostatisticians of Paris-Saclay IDEX, a bioinformatic tool for the inference of statistical models from genetic and environmental data available on insects, plants, and plant pathogens, in BASC labex teams.

Recruitment: Recruitment will last 2 years and should start in September 2014. Please send CV, motivation letter and recommendation letters before july 15th 2014 to dupas@legs.cnrs-gif.fr and tenaillon@moulon.inra.fr.

For more information on specific activities to be held, please contact Stéphane Dupas, tel. +33 169823725, dupas@legs.cnrs-gif.fr

Stéphane Dupas

IRD BEI c/o CNRS LEGS 1 av Terrasse 91198 Gif-sur-Yvette France http://www.legs.cnrs-gif.fr/perso.php?id=dupas Tel +33 1 69 82 37 04 Fax +33 1 69 82 44 48

Stéphane Dupas <Stephane.Dupas@legs.cnrs-gif.fr>

GlasgowU BatVirusEmergence

University of Glasgow College of Medical, Veterinary & Life Sciences Institute of Biodiversity Animal Health and Comparative Medicine

Postdoctoral Research Associate: Viral emergence between bats and livestock Ref: 008722 Salary: Grade 7 £32,590 - £36,661 per annum

The Institute of Biodiversity, Animal Health and Comparative Medicine is seeking a postdoctoral researcher with expertise in veterinary/ecological fieldwork and pathogen genomics to join a team working on the ecological and evolutionary drivers of viral emergence between bats and domestic animals.

The successful applicant will play a leading role in this project by establishing a livestock pathogen surveillance network for correlative studies of viral exposure risk and by implementing a bat exclosure experiment to track cross-species between bats and sentinel livestock in real time using metagenomics and molecular diagnostics.

The Research Associate will take the lead on the formulation and submission of research publications and research proposals as well as help manage and direct this complex and challenging project. Fieldwork will be carried out in the Peruvian Andes and Amazon in collaboration with support from local NGO and governmental units. Frequent international travel will be required.

Additional collaborators in the UK include Pablo Murcia (MRC-University of Glasgow Centre for Virus Research, http://www.gla.ac.uk/researchinstitutes/-iii/cvr/) and Roman Biek (Institute of Biodiversity, Animal Health and Comparative Medicine, http:/-/www.gla.ac.uk/researchinstitutes/bahcm/ & Boyd Orr Centre for Population and Ecosystem Health (http://www.gla.ac.uk/researchinstitutes/bahcm/-researchfacilitiesgroups/boydorr/)

The post is initially funded for 3 years with good prospects for extension. Please contact Daniel Streicker with informal inquiries (daniel.streicker@glasgow.ac.uk)

Apply online at www.glasgow.ac.uk/jobs Closing date: 27 July 2014

The University has recently been awarded the Athena SWAN Institutional Bronze Award < http://www.gla.ac.uk/services/humanresources/-equalitydiversity/athenaswan/ > The University is committed to equality of opportunity in employment. The University of Glasgow, charity number SC004401.

Daniel.Streicker@glasgow.ac.uk

HarvardU BioinformaticsComputBiol

POSTDOCTORAL POSITION IN BIOINFORMATICS AND COMPUTATIONAL BIOLOGY

The Lemos laboratory at Harvard University is searching for a postdoctoral fellow in bioinformatics / computational biology interested in pursuing research in epigenomics, population genomics, genotype-environment interaction, and analysis of copy number variation. The fellow should be interested in working with computational data analysis, and be motivated by research that combines experimental genetics, genome analyses, and integration of genome-wide data from a variety of experimental sources. There are plenty of opportunities for individual projects and collaborative work.

The laboratory is housed at the Harvard School of Public Health located within a vibrant research community that includes the Harvard Medical School, and several affiliated hospitals. The school has significant strengths in computational biology, biostatistics, genomics, and engineering that will be all within close reach of the fellow.

Applicants must be extremely curious and motivated by science, be genuinely enthusiastic, and have the ability to work independently within a collegial and collaborative team. Applicants should expect a fun and creative research environment in which I can provide plenty of individual mentoring and support to develop your own interests and ideas.

Applicants must have a PhD at the time of the appointment and have a strong analytical background with proficiency in one or more programming languages. Informal enquires of interested candidates with other backgrounds are also welcome.

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

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

blemos@hsph.harvard.edu

HowardU EvolutionaryMorphology

2-year Postdoctoral Researcher position in the Smith Lab

at Howard University, Washington DC

Applications are invited for a two-year postdoctoral researcher position in the field of evolutionary morphology in the lab of Dr. Nathan Smith in the Department of Biology at Howard University (http://dl.dropboxusercontent.com/u/86743464/-web/smithnd/Home.html). This position is funded by two independent National Science Foundation grants and will require a highly motivated individual with diverse training in phylogenetics, evolutionary morphology, and paleobiology. Projects are focused on: 1) Revising the taxonomy/phylogeny of Caribbean reef corals through integration of morphological/molecular data and fossil taxa; and 2) Illuminating the anatomy, biogeography, and phylogenetic relationships of the Early Jurassic vertebrate fauna of the Central Transantarctic Mountains. Expertise in these taxonomic groups is desirable, but not required. Skills in morphometrics, phylogenetic comparative methods, and the R programming language are highly recommended. The ideal candidate will also have strong writing skills and previous student mentoring experience. Applicants should have completed a Ph.D. in the relevant field and have an established record of research productivity and publications. The appointment is anticipated to begin in Fall 2014 or shortly thereafter. The salary for this position is $45,000 per year with benefits, and funds for research travel and scientific meetings are also available.

Applicants should submit a single PDF file containing: 1) a brief cover letter; 2) CV; 3) a maximum two-page description of research interests and how their skills can contribute to both NSF projects; and 4) contact information for three references; to nathan.smith@howard.edu. Include "Postdoc Application" in the subject line. Applications are due by July 25, 2014 for priority consideration, but will be accepted until the position is filled. Informal inquiries and questions can be directed to: nathan.smith@howard.edu.

Howard University was founded in 1867 in Washington, DC. It is the nation's premier HBCU and has an enrollment of ˜6,600 undergraduate and ˜3,200 graduate and professional students. Howard University does not discriminate on the basis of race, color, national and ethnic origin, sex, marital status, religion or disability.

The Department of Biology (http://biology.howard.edu< http://biology.howard.edu/ >) at Howard University serves ˜700 undergraduate majors and ˜25 M.S. and Ph.D. students. The Department includes 19 faculty members and is actively growing, with 8 new faculty members having joined in the past four years. The Smith lab comprises over 1,000 sq. feet of renovated laboratory and office space, including a dedicated 12x12 window office for a postdoctoral researcher.

Washington, DC is a diverse and vibrant city of 650,000, with 5.8 million residents in the greater DC area. The Nation's capitol is a cultural and scientific center, and home to a variety of top-tier research institutions in the field of evolutionary biology, including the Smithsonian National Museum of Natural History, the National Institutes of Health, and a variety of public and private universities.

Dr. Nathan Smith Department of Biology 415 College Street NW Washington, D.C. 20059

nathan.smith@howard.edu

Nathan D. Smith, Ph.D. Assistant Professor Department of Biology Howard University 415 College Street NW Washington, DC 20059 202-806-6941 nathan.smith@howard.edu Webpage: < http://dl.dropbox.com/u/86743464/web/smithnd/Home.html >

"Smith, Nathan D" <nathan.smith@Howard.edu>

ImperialCollege London CelegansEvolution

A Research Associate position is available to join a newly established group, led by Dr. Michalis Barkoulas in the Department of Life Sciences at the South Kensington Campus of Imperial College London. The group focuses on studying the mechanisms and evolution of phenotypic robustness in C. elegans. The successful applicant will use the C. elegans seam cells as a model and employ genetics, imaging and next-generation sequencing technologies to study questions related to developmental robustness. You will also assist to produce independent and original research within the research interest of the group and submit publications to refereed journals.

The post holder will have a PhD (or equivalent) in development biology or evolutionary genetics. You must be highly motivated, and have the ability to produce work of excellent quality. A strong background in developmental, molecular biology and microscopy techniques and the experience of producing independent and original research are essential. Familiarity with bioinformatics and next generation sequencing data analysis would be a strong advantage. Previous experience in C. elegans genetics and techniques is preferred, but not essential. You must be able to work independently and as part of a team, have the ability to develop and apply new concepts and have a creative approach to problem-solving. You must also have excellent verbal and written communication skills and be able to write clearly and succinctly for publication. This is a fixed term position for 24 months in the first instance with a possibility of extension subject to funding.

For informal enquiries please contact Dr. Michalis Barkoulas (m.barkoulas@imperial.ac.uk). Our preferred method of application is online via our website http://www3.imperial.ac.uk/employment (please select "Job Search" then enter the job title or vacancy reference number including spaces NS 2014 113 ABinto "Keywords"). Please complete and upload an application form as directed. Alternatively, if you are unable to apply online, please contact Hafiza Bibi by email h.bibi@imperial.ac.uk to request an application form. Closing date: 14 July 2014

Michalis Barkoulas Lecturer | Imperial College Department of Life Sciences SAF building office 607 SW7 2AZ, London +44 (0)207 5945227

“Barkoulas, Michalis” <m.barkoulas@imperial.ac.uk>

ImperialCollege London VertebrateEvoDevo

Hello,

A post-doctoral position is available in my lab. A brief description is as follows:

Research background

Vertebrates differ in a wide range of traits, including dramatic differences in their skeletons. The objective of the newly established Evolution of Gene Regulation Group headed by Dr Vahan Indjeian at the MRC Clinical Sciences Centre, Imperial College London, is to uncover the genetic basis of vertebrate traits. The group asks what genes regulate evolutionary changes in morphology? What are the modifications in those genes? Are the same genes used when similar traits evolve in many species? We use a combination of tools, including comparative genomics and three-spine stickleback and mouse experimental models to answer these questions. For more information about our research, please visit http://www.csc.mrc.ac.uk/-Research/Groups/EPI/EGR/ . Available Projects

- To identify and characterise molecular events underpinning adaptive traits in natural stickleback populations.

- To identify and characterise cis-regulatory changes in the human lineage that may explain human-specific traits using mouse models.

- To identify and characterise the genetic basis of repeated evolution of similar traits in many vertebrates.

Job Summary

This post provides an opportunity for a highly motivated individual to participate in a project to investigate the mechanisms and regulation of vertebrate development using three-spine sticklebacks and/or mice as models.

Full Job Description and How to Apply:

Please follow this link for full information about the position and the application submission website:

http://www.topcareer.jobs/Vacancy/-irc147093_4458.aspx The closing date for applications is 29 June. Please submit your CV along with a brief cover letter describing scientific interests and names and contacts of three scientific references, when saving your documents please include IRC147093 in the file name. Only online applications will be accepted at the link provided above.

Thanks very much!

Best regards, Vahan

Vahan Indjeian, PhD Head of Evolution of Gene Regulation Group MRC Clinical Sciences Centre - Imperial College London Du Cane Road, London W12 0NN tel. (+44) 020 8383 8241 vahan.indjeian@imperial.ac.uk http://-www.csc.mrc.ac.uk/Research/Groups/EPI/EGR/ “Indjeian, Vahan” <vahan.indjeian@csc.mrc.ac.uk>

Lyon AlgalVirusBiodiversity

The DECOVIR project (coordinated by Yves Desdevises) aims to determine how environmental factors influence algal virus diversity in marine ecosystems. This project combines recent genomic data with NGS techniques to obtain a precise picture of the actual diversity of a defined virus group, its evolution through time, and its relationships with environmental factors.

We look for a postdoctoral researcher to analyse the data produced during the first two years of the project. The main work consists in developing an analytical method to relate virus abundance and diversity data to environmental variables and host abundance and diversity. This method should permit the use in predictive framework. The following abilities are required: - programming skills - very good level in statistics (particularly multivariate analysis) - experience with high-throughput genomic data would be an advantage

The successful candidate will have a strong written background in English to communicate his/her results in symposia and publications. The position is for one year and will be based in the “Biométrie and Biologie Evolutive” Lab (Université Lyon 1, France, _http://-lbbe.univ-lyon1.fr/_) under the supervision of Stéphane Dray (_http://pbil.univ-lyon1.fr/members/dray/_).

Candidates must be able to start by January 2015 and applications will be evaluated as they are received until the position is filled. Early application is recommended.

To apply, please send CV and publications list, with contact information for a minimum of two professional references to _stephane.dray@univ-lyon1.fr_.

Stéphane DRAY (stephane.dray@univ-lyon1.fr) Laboratoire BBE-CNRS-UMR-5558, Univ. C. Bernard - Lyon I 43, Bd du 11 Novembre 1918, 69622 Villeurbanne Cedex, France Tel: 33 4 72 43 27 57 Fax: 33 4 72 43 13 88 http://pbil.univ-lyon1.fr/members/dray/ Stéphane Dray <stephane.dray@univ-lyon1.fr>

MNHN Paris CricketPhylogenomics

I would like to inform the evolutionary biologists' community of the opportunity to apply for a 2-year post-doctoral position in the Muséum national d'Histoire naturelle, Paris.

The project is entitled "Phylogenomics of cricket communities under environmental pressure in New Caledonia", and supported by the LABex BCDiv (see attached file).

Applications should be sent before 20 june 2014.

Sincerely yours, Laure Desutter

Dr. Laure Desutter-Grandcolas Curator of Ensifera collections Editor-in-chief, Zoosystema ISYEB, UMR 7205 CNRS MNHN UPMC EPHE Muséum national d'Histoire naturelle Département Systématique et Evolution 57 rue Cuvier, CP 50 (Entomologie) 75231 Paris cedex 05, France

Tel +33 (0)1 40 79 34 02 Fax +33 (0)1 40 79 56 79

Laure DESUTTER <desutter@mnhn.fr>

Montpellier StatisticalAnalyses

A 18-months post-doctoral position will be available at CEFE (Montpellier, France) in early 2015 to develop statistical analyses of temporal trajectories of biological communities. The candidate will develop Bayesian methods to analyze existing large datasets in order to study adaptation in fragmented communities of freshwater snails from the West Indies. He/she will be involved in field work and data collection. He/she will have a good training in biostatistics, evolutionary and/or ecological theory, and a PhD in one of these domains. Knowledge of Bayesian methods and R?\programming is a plus. The working environment is the multidisciplinary Gntique et cologie volutive± team at CEFE, and the work will be supervised by P. David (CEFE) and F. Massol (Lille university). Informal inquiries are welcome: send an email containing an updated CV to patrice.david@cefe.cnrs.fr.

Philippe JARNE <philippe.jarne@cefe.cnrs.fr>

Montpellier StatisticalAnalysis

A 18-months post-doctoral position will be available at CEFE (Montpellier, France) in early 2015 to develop statistical analyses of temporal trajectories of biological communities. The candidate will develop Bayesian methods to analyze existing large datasets in order to study adaptation in fragmented communities of freshwater snails from the West Indies. He/she will be involved in field work and data collection. He/she will have a good training in biostatistics, evolutionary and/or ecological theory, and a PhD in one of these domains. Knowledge of Bayesian methods and R?\programming is a plus. The working environment is the multidisciplinary Gntique et cologie volutive± team at CEFE, and the work will be supervised by P. David (CEFE) and F. Massol (Lille university). Informal inquiries are welcome: send an email containing an updated CV to patrice.david@cefe.cnrs.fr.

Philippe JARNE <philippe.jarne@cefe.cnrs.fr>

NorthCarolinaStateU MosquitoePopGenetics

Postdoc: Modeling Population Dynamics and Genetics of Mosquito-vectored diseases

PROJECT DESCRIPTION: Dengue is a mosquito-vectored disease that affects over 100 million people each year. With funding from the NIH and Gates Foundation, we have developed a set of mathematical models ranging from simple to complex, aimed at assisting the design and deployment of novel approaches for suppressing transmission of dengue by its major mosquito vector, Aedes aegypti. We are especially interested in evaluating the potential utility of, as well as risks associated with, using genetically engineered, selfish genetic elements to drive genes into mosquito populations that render them incapable of transmitting dengue fever. Our work also extends to models relevant to suppressing malaria.

Our most detailed model simulates the population dynamics and population genetics of Ae. aegypti in a city on the Amazon river, Iquitos, for which there are rich data sets on both mosquito dynamics and dengue epidemiology. An accompanying epidemiological model is currently under development. Both are coded in C++.

We are just completing a large-scale experiment in Iquitos to both test the model and collect data that can be used to improve the parameterization of all Ae. aegypti models. In the experiment, the mosquito population in one area of the city is suppressed and then allowed to return to normal densities. Although our population dynamics model and many others have been tested to determine if they predict equilibrium dynamics, a much more stringent test is to determine if they can predict response to a perturbation. Following a transition period interfacing with our current postdoc, the new postdoc will assume responsibility for leading the analysis of these data and will further develop the model to examine the dynamic behavior and efficacy of a set of novel transgenic and non-transgenic approaches for manipulating the mosquito population. These innovative technologies and strategies are being developed by our colleagues, so empirical data on small field tests will be available

. We are also building simple spatial and non-spatial, deterministic models as heuristic tools for better understanding basic principles.

In addition to working on model development and analysis, and on comparisons between model and data, the person in this position will collaborate in an interdisciplinary research group composed of mosquito ecologists, disease epidemiologists, molecular biologists, biomathematicians, ethicists, and scientists from disease-endemic countries, in efforts to develop novel transgenic strategies for disease reduction. The person in this position will have the opportunity to spend time in Iquitos to better understand the system being modeled. Desirable skills include the ability to program in C++ or knowledge of a related programming language, statistical experience, particularly in parameter estimation and evaluation of performance of mechanistic models.

For more details on the project see the following publications:

Magori, K., M. Legros, M. Puente, D. A. Focks, T. W. Scott, A. Lloyd, F, Gould. 2009. Skeeter Buster: a stochastic, spatially-explicit modeling tool for studying Aedes aegypti population replacement and population suppression strategies. PLoS Negl Trop Dis 3(9): e508. doi:10.1371/journal.pntd.0000508

Gould, F., Huang, Y., Legros, M., Lloyd, A. L. 2008. A killer-rescue system for self-limiting gene drive of antipathogen constructs. Proc. Royal. Soc. Lond. B. 275:2823-2829.

Xu, C., Legros, M., Gould, F, Lloyd, A. L. 2010.Understanding Uncertainties in Model-Based Predictions of Aedes aegypti Population Dynamics. PLoS Negl. Trop. Dis. 4(9): e830. doi:10.1371/journal.pntd.0000830

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.

Okamoto K. W., M. A. Robert, A. L. Lloyd, F. Gould. 2013. A reduce and replace strategy for suppressing vector-borne diseases: Insights from a stochastic, spatial model. PLoS ONE 8(12): e81860. doi:10.1371/journal.pone.0081860

To apply: email a cover letter and CV to Fred_Gould@ncsu.edu and Alun Lloyd@ncsu.edu

fred_gould@ncsu.edu

Oxford 6 EvolutionaryBiol

All Souls College, Oxford. 5 year Post-Doctoral Research Fellowships

Dear All,

All Souls College is advertising six 5-year Fellowships to be held in Oxford. The on-line application form and further particulars are at:

http://www.all-souls.ox.ac.uk/content/Post-Doctoral_Research_Fellowships In brief, The Fellowships are open to candidates in the Humanities, Social Sciences, Natural Sciences and Mathematics and are intended for early-career researchers seeking to establish an independent programme of research. The

Fellowships provide a generous salary and a research allowance. If the research project is laboratory based, the College will provide additional funds for the Fellow's laboratory consumables, up to a maximum of £5,000 per annum.

Applications close on September 12 2014.

Angela Mclean <angela.mclean@zoo.ox.ac.uk>

Paris6U EvolutionBioinformatics Nov2014

Hello,

Please find below the description of a postdoctoral position to 'Search for common genetic goods in gene families and microbial communities

The theory of genetic public goods recently postulated that genetic sequences can be exploited in various combinations, even by distantly related or unrelated evolving entities, i.e. microbial communities benefiting from the sharing of genes between their members, such as photosynthesis genes between cyanophages and cyanobacteria, or such as drug resistance genes within multispecies biofilm. Yet, the nature, size and diversity of microbial communities sharing such genetic goods remain poorly known. Moreover, the rules of gene sharing also remain to be described.

A wealth of molecular data from metagenomic, single cell metagenomic, and microbial genomes projects is now available to tackle these fundamental issues. Furthermore, sequence similarity networks offer a promising complementary niche to phylogenetic methods to exploit the complexity of these data. These graphs allow for mathematical analyses of genetic diversity and similarities over dozens of millions of sequences, providing novel ways to detect clubs of genomes, which have not necessarily evolved from a single last common ancestor yet exploit some common genetic material. Likewise, these networks allows for the detection of some sets of gene families that exploit common pools of genetic fragments/domains.

To further develop the detection strategies of genetic public goods, our lab is now looking for a post-doctoral fellow in bio-informatics, who will be funded for up to three years by an ERC grant (for a salary of 45,000 euros/year; approximately 2219 euros/ month after taxes). The candidate will take advantage of graph properties and algorithms from the graph theory: - to improve the identification of clubs of genomes /sets of gene and their pool of genetic goods in complex networks with a few millions nodes and dozens of millions of edges; - to analyze domains combinations in genes and gene sharing in communities, using bipartite graphs. - He/she will then analyze the functions of these genetic goods and their distribution across genes and genomes to test what lifestyles favors their sharing.

The candidate will work within a consortium of friendly bioinformaticians (Philippe Lopez), evolutionary biologists (Eric Bapteste), and graph theorists (Michel Habib, Laurent Viennot), and be hosted in the University Pierre and Marie Curie in the center of Paris, France. The current team description and publications can be found at: http://www.evol-net.fr/ Ideally, the candidate should have a good background in bioinformatics, or graph theory and a strong interest for evolutionary biology. The position will start by November 2014, but interested candidates are invited to apply immediately.

Applicants are requested to send a detailed resume, a motivation letter, a pdf copy of their PhDs thesis, and the names of two scientific referees to : eric.bapteste@snv.jussieu.fr

The first round of applications will be closed by July 15, 2014.

Eric Bapteste <epbapteste@gmail.com>

Potsdam Germany TheoreticalCommunityEvolution

Post-Doc for Theoretical Community Ecology at Potsdam, Germany

Pending final approval of funding we offer a full time position for 3 years with a potential second funding period of 3 more years at the department of Ecology/Ecosystem Modelling at Potsdam University (German salary scale E 13, 100%). The position is available within the recently established Priority Programme "Flexibility matters: Interplay between trait diversity and ecological dynamics using aquatic communities as model systems" (www.DynaTrait.de) funded by the German Science Foundation (DFG). We are seeking a highly motivated and productive scientist who is interested and capable of contributing to a modelling team closely interacting with experimentalists conducting laboratory food web experiments. She/he should have strong research interests in community and trait-based ecology (e.g. dynamics of predator-prey and multi-trophic systems), and in the role of adaptability for system dynamics in particular (e.g. via eco-evolutionary dynamics). The work includes developing and analyzing predator-prey and food web models which account for ongoing mutual adaptations of trait values among interacting organisms related to corresponding experiments.

The ideal candidate holds a Ph.D., has an excellent publication record in the field of theoretical ecology and ecological modelling and comprehensive skills in working with systems of differential equations. Prior Post-Doc experience, skills in time-series analysis and interest in co-supervising students is highly welcome. The modelling team, consisting of Post-Docs, Ph.D. and Master students, is supervised by Prof. Dr. Ursula Gaedke and Prof. Dr. Horst Malchow (Univ. Osnabrück) and provides a very stimulating research environment for promoting theoretical ecology by modelling and empirical studies. The position may be suitable to strive for a Habilitation. Fluency in English is essential but gaining some control of the German language is expected. Potsdam (near Berlin, Germany) is an attractive town of about 170,000 inhabitants. It is an UNESCO world heritage and due to its close vicinity to Berlin covers a broad spectrum of all kinds of cultural activities.

For further information please visit http://www.uni-potsdam.de/en/ibb/researchgroups/fullprofessors/-ecology-and-ecosystem-modelling.html or contact U. Gaedke (gaedke@uni-potsdam. de). Applications should include a statement of motivation, a detailed CV with the list of publications, contact details of academic referees and degree certificates. Please send them electronically, if possible as a single file, to U. Gaedke. The position is open until it gets filled. The "12-years-rule" does not apply for this position.

lbecks@evolbio.mpg.de

ReedCollege DrosophilaHostPathogenEvolution

Two postdoc positions are available in Todd Schlenkes lab at Reed College in Portland, Oregon. These positions are funded by an NSF grant to study the genetics and evolution of behavioral immune defenses that fruit flies use to avoid or cure infection by parasitic wasps. Behaviors are increasingly seen as an important component of host defenses against parasitism, and our lab has found that larval flies escape wasp infection and cure infection by utilizing more alcoholic food substrates (Milan 2012 Current Biology), and that adult flies both reduce oviposition (Lefevre 2012 Biology Letters) and oviposit in more alcoholic environments in the presence of wasps (Kacsoh 2013 Science). The aims of the grant are to assess evolutionary tradeoffs between behavioral defenses and cellular defenses, and to further characterize the genetic bases of these behaviors.

Experience with Drosophila, neurobiology, and/or evolutionary genetics is ideal. The positions can be filled immediately. Todd is currently on a visiting associate professor position at Reed through summer of 2015. To apply, please email Todd a CV and contact information for 2-3 references.

Todd Schlenke Reed College Biology Department 503.517.7777 schlenkt@reed.edu

Todd Schlenke <schlenkt@reed.edu>

Smithsonian KudzuEvolutionaryGenomics

POSTDOC - SMITHSONIAN INSTITUTION NATIONAL MUSUEM OF NATURAL HISTORY DEPARTMENT OF BOTANY

A postdoc is available starting September 15, 2014 to work with Dr. Ashley N. Egan in the field of evolutionary genomics. This position is funded by the National Science Foundation and will require a highly motivated individual with diverse training in phylogenetics, population genetics, next-gen sequencing methods, and computational biology. This individual will work with genomic and transcriptomic data to create and collect target enriched data using sequence capture with two-fold aims: i) to create a target gene set useful at the population level for estimating genetic diversity across the native and introduced range of Kudzu (Pueraria montana var. lobata) to determine relative levels of genetic diversity and investigate the evolutionary and introduction history of this highly invasive species; and ii) to create a target gene set useful at the phylogenomic level to create a well-supported and resolved phylogeny at the generic level across phaseoloid/milletioid legumes, a clade of ~250 genera and nearly 4000 species. Expertise in the taxonomic group is desired, but not required. Experience working with next-generation sequencing is highly preferred as is computational scripting skills in perl or another scripting language. Skills in phylogenetics and population genetics data analysis are highly recommended. The ideal candidate will also have strong writing skills and the ability to think and work independently and as part of a team. Applicants should have completed a Ph.D. in the relevant field and have an established record of research productivity and publications. The appointment will start September 15, 2014 and is for one-year with renewal for a second year available upon satisfactory performance. The salary for this position is $40,000 per year with benefits.

Applicants should submit a single PDF file containing: 1) a brief cover letter; 2) CV; 3) a maximum two-'-page description of research interests and how their skills can contribute to project objectives; and 4) contact information for three references; to egana@si.edu . Include "Postdoc Application" in the subject line. Applications are due by July 31, 2014 for priority consideration, but will be accepted until the position is filled. Informal inquiries and questions can be directed to: egana@si.edu.

The Smithsonian Institution has a vibrant research community, bringing together postdocs, graduate students, and researchers from all over the world to study varying topics in the natural sciences (www.si.edu), boasts new state-of-the-art laboratory facilities and offers access to some of the best natural history collections in the world. More information about SI can be found here (www.si.edu) and (www.smithsonianofi.com) and Dr. Ashley N. Egan here (http://botany.si.edu/staff/-staffPage.cfm?ThisName=107&homepage=no).

Washington, DC is a diverse and vibrant city of 650,000, with 5.8 million residents in the greater DC area. The Nation's capitol is a cultural and scientific center, and home to a variety of top-tier research institutions in the field of evolutionary biology, including the Smithsonian National Museum of Natural History, the National Institutes of Health, and a variety of public and private universities.

NOTE: I will be available to meet during the evolution 2014 conference on 23 and 24 June and during the Botany 2014 conference from 26-29 July 2014.

Ashley N. Egan, Ph.D. Research Botanist & Assistant Curator National Museum of Natural History Smithsonian Institution Department of Botany MRC 166 PO Box 37012 Washington DC 20013-7012 Office: 202.633.0902 Fax: 202.786.2563 Egana@si.edu http://botany.si.edu/staff/staffPage.cfm?ThisName=-107&homepage=no "Egan, Ashley" <EganA@si.edu>

Trento Italy InsectEvolutionaryGenomics

Post Doc in "Evolutionary Genomics of insect vectors of apple disease" (151_CRI_IVAD) - deadline June 22, 2014

A postdoc position is available in the Chemical Ecology unit, Sustainable Agro-Ecosystems and Bioresources department of the Research and Innovation Centre (CRI).

The position is related to the project "Scopazzi" funded by the Autonomous Province of Trento (Accordo di Programma) and the Association of Fruit and Vegetable Producers in Trentino (APOT) and aimed at providing new insights into the biology and ecology of the insects vectors of apple proliferation for the development of sustainable control strategies.

The successful candidate will work on genomics and evolution of two insects (hemipterans C. melanoneura and C. picta) which are the main vectors of the "apple proliferation", phytoplasma causing illness in the apple trees. Successful candidate will apply bioinformatics tools to get new insights in the evolution, biology and ecology of these insect vectors.

Please read the position details to understand if you are eligible for the position. In order to apply send your cv and fill the application form. Application and profile are also available at the bottom of the page.

Deadline for application: June 22, 2014.

More info and the full call at: http://www.fmach.it/-Servizi-Generali/Lavora-con-noi/Annunci-lavoro-e-borse-di-studio/Post-Doc-in-Evolutionary-Genomics-of-insect-vectors-of-apple-disease-151_CRI_IVAD-deadline-June-22-2014 Omar Rota-Stabelli PhD Marie Curie - PAT postdoctoral fellow Department of Sustainable Agro-ecosystems and Bioresources, IASMA Research and Innovation Centre, Fondazione Edmund Mach, San Michele all'Adige, (TN), Italy. Phone:+39 0461 615393 Mobile:+39 389 8375091 Fax:+39 0461 615500

Councillor of the Italian Society for Evolutionary Biology Research Associate of the School of Biological Sciences, University of Bristol

Society for Molecular Biology and Evolution www.smbe.org Italian Society for Evolutionary

Biology www.sibe-iseb.it The Systematics Association http://www.systass.org The Willi Hennig Society http://www.cladistics.org Unione Zoologica Italiana www.uzionlus.it Omar's scholar http://scholar.google.it/citations?user=of14yMwAAAAJ Omar Rota-Stabelli <omar.rota@fmach.it>

UBritishColumbia OganismalEvolution

Postdoctoral Research Positions (2): Evolutionary Morphology, Species Discovery, Marine Protistology

Two postdoctoral research positions are available in the Leander Lab at The University of British Columbia, Departments of Zoology and Botany (http://www3.botany.ubc.ca/bleander/index.html). The lab is looking for two broadly trained, self-motivated and enthusiastic individuals excited about species discovery, comparative morphology and the evolution of marine organisms (protistology and invertebrate zoology). The lab is focused on discovering and characterizing diverse groups of (uncultured) marine microbial eukaryotes (free-living protists, meiofuanal animals and parasites) using state-of-the-art approaches that incorporate fieldwork, light microscopy, scanning electron microscopy, transmission electron microscopy and molecular phylogenetics.

The successful applicants must have (1) a PhD in a relevant field, (2) excellent written and oral communication skills, (3) a strong publication record relative to career stage, and (4) expertise in comparative organismal biology, evolutionary biology and systematics. Additional experience with light and electron microscopy is highly desirable. The research will involve routine field collections in nearby habitats, including the Bamfield Marine Sciences Centre (http://www.bms.bc.ca) and potentially the Hakai Research Institute (http://hakai.org).

The successful applicants will be appointed for a minimum of 2-years, contingent on satisfactory progress, and be expected to participate in the UBC Centre for Microbial Diversity and Evolution (http://www.cmde.science.ubc.ca/). The postdoctoral research positions are available in September of 2014, but the actual start dates are negotiable.

If interested in these positions, please email a single PDF containing a short cover letter outlining your research experience and interests, a curriculum vitae, contact information for 3 referees and two representative publications to:

Dr. Brian Leander Department of Zoology bleander@mail.ubc.ca

The closing date for applications is August 17, 2014, but the positions will remain open until filled.

bleander@mail.ubc.ca

UCalifornia Merced AncientDNA

The Blois Paleoecology Lab at UC Merced is recruiting a postdoc to help develop ancient DNA and phylogenetics projects focusing on understanding the dynamic population genetic changes that happened within mammals (particularly small mammals) through the late Quaternary. The postdoc will be responsible for developing original research projects related to the interests and focus of the lab, in addition to contributing to the development and maintenance of the molecular lab. Ongoing projects in the lab use species distribution modeling, community modeling, and paleoecological tools to understand the ecological and evolutionary forces shaping populations, species, and communities across time and space, particularly focusing on fossil small mammal and pollen communities during the late Quaternary. Applications will be reviewed starting June 30th, but the position is open until filled. Please contact Dr. Jessica Blois (*jblois@ucmerced.edu <jblois@ucmerced.edu>*) for additional information.

For more information about the lab, full position information and to apply to the position, please visit the lab website (*www.jessicablois.com < http://www.jessicablois.com >*).

Best, Jessica

Assistant Professor School of Natural Sciences University of California, Merced

Office: Castle #47 Phone: (209) 228-2256 Email: jblois@ucmerced.edu Web: http://jessicablois.com jblois@ucmerced.edu

UCL UNamur Belgium BdelloidRotifers EvolGenomics

_*Postdoctoral position in Evolutionary Genomics and Molecular and Cellular biology *____*(UCL - UNamur, Belgium)*_

**

A 3-year postdoctoral research position is available to investigate the */Molecular and cellular mechanisms of hyper-resistance to stress in the ameiotic bdelloid rotifer /Adineta vaga. *The research will be conducted in the group of Biochemistry, Biophysics and Molecular Genetics of Micro-organisms at the Catholic University of Louvain (UCL, Belgium) to take part in a collaborative ARC research program with the Research Units in Environmental and Evolutionary Biology (URBE) and in Cellular Biology (URBC) at the University of Namur (UNamur, Belgium).

This postdoc position is embedded within the research project entitled: /Asexuality and 'immortality', bdelloid rotifers as an evolutionary 'scandal' and a model system in biology. /This project is funded during 5 years and will start in October 2014.

* PIs of the project:*

*Prof. Bernard Hallet (ISV, UCL), Prof. Karine Van Doninck (URBE, UNamur), *Dr. Florence Debacq-Chainiaux (URBC, UNamur)**

The involved consortium brings together experts in the fields of evolutionary biology and genomics of bdelloid rotifers (K. Van Doninck, URBE, UNamur), DNA recombination and genome plasticity (B. Hallet, ISV, UC) and oxidative stress response (F. Debacq-Chainiaux, URBC, UNamur). The appointed candidate will be expected to share its research time on both sites under the supervision of the three PIs of the consortium. The universities are at a distance of 35km from each other and easily connected by train.

Project:

Bdelloid rotifers are micro-organisms (animals) that have recently attracted much interest in the scientific community because of their ancient asexuality and their extreme resistance to stress, such as desiccation and high doses of ionizing radiation. They are capable to survive when their genome is shattered into small fragments and repair the DNA double strands breaks (DSBs) *(see Hespeels et al., JEB 2014)*. Repeated cycles of chromosomal repair are thought to promote allelic recombination and gene conversion in the absence of meiosis. Moreover desiccation and the induced DNA DSBs are also thought to provide a unique opportunity to acquire horizontally transferred genes, thereby contributing to the adaptive success of these organisms.

In this project, the mechanisms that make bdelloid rotifers unique in terms of evolutionary strategy and hyper-resistance to stress will be investigated based on genomic data recently obtained by our consortium for the bdelloid rotifer /Adineta vaga/ headed by Prof. Karine Van Doninck (*see Flot et al, 2013, Nature 500:453-7*). Genomic approaches will be used to study the dynamics of /A. vaga/ genome during cycles of desiccation/rehydration/radiationand to decipher the genetic expression program that governs the different stages of its life-style. Molecular and cellular approaches will be developed to unveil and characterize the mechanisms that allow /A. vaga/ to repair its shattered chromosomes and generate genetic diversity,as well as its dependence with respect to oxidative stress response. The ultimate prospect of the project is to establish bdelloid rotifers as a new model system for the understanding of fundamental biological processes such as DNA repair, cell survival and senescence.

Contacts:

*Prof. Bernard Hallet, **Bernard.hallet@uclouvain.be

Université Catholique de Louvain. Institut des Sciences de la Vie (ISV)

http://www.uclouvain.be/en-isv.html *Prof. Karine Van Doninck, **karine.vandoninck@unamur.be

University of Namur, Laboartory of Evolutionary Genetics and Ecology (http://www.lege-unamur.be/)

Qualifications:

We are looking for a post-doc with a strong interest and background in evolutionary genomics and molecular and cell biology. Expertise in the field of DNA repair and recombination, chromosome structure and dynamics, and/or genomics (NGS approach) is a valuable asset. Additional experience in cell biology techniques like DNA transfection, immuno-localization, fluorescence hybridization and microscopy will be a benefit. Priority will be given to candidates with a proven track record (with several publications as a first author) who will express their motivation in developing their autonomy and their interest for new challenges.

Application://

The position is available to both foreign nationals and Belgian citizens under 'international mobility' status, meaning that they may not have resided in Belgium for more than 12 months over the past 3 years preceding the appointment. The duration is for 2 years (with a possible 1-year renewal) starting on the *1^st of October 2014. *The closing date for applications is *August 31^st 2014.*

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UExeter ModellingMicrobeResistance

Postdoctoral position: Mathematical modelling of drug-resistance in microorganisms and cancers, University of Exeter

We are recruiting a Research Fellow to participate in an exciting interdisciplinary collaboration between a mathematical modelling groups of Dr Ivana Gudelj and Prof Robert Beardmore, University of Exeter, UK and Computational Biology and Oncology Departments at AstraZeneca, Cambridge. This position is available from 1st July 2014 for the period of 2 years. The successful applicant will contribute towards research that uses concepts from ecology and Darwinian evolution applied to micro-organisms, to understand the strength of natural selection in cancer cells.

The successful applicant will be working on the development and analysis of mathematica models in Dr Gudelj and Prof Beardmore's labs at the University of Exeter in close collaborations with colleagues at AstraZeneca, Cambridge. Applicants will posses a PhD in a quantitative discipline (mathematics, physics, engineering or computer science) and be familiar with ordinary differential equations, their use in modelling, analysis (Dynamical Systems techniques) and simulation. The successful candidate should be able to communicate effectively with individuals from a wide range of disciplines.

More information about the project and how to apply can be found at: http://www.jobs.ac.uk/job/AIU198/associate-research-fellow/ "Gudelj, Ivana" <I.Gudelj@exeter.ac.uk>

UFlorida RNAiEvolution

We are currently recruiting a talented postdoctoral researcher to lead a 3-year NSF-funded project examining the functional evolution of RNA interference across animals and plants.

The project will include an exciting mashup of phylogenetic analysis, ancestral sequence reconstruction, structural dynamics modeling, and molecular kinetics, so it should be fun. The overall objective is to characterize how key RNAi genes functionally diversified in animals and plants, with an eye toward understanding structural mechanisms and identifying possible convergence.

Experience in RNAi, phylogenetics, structural modeling and/or molecular biochemistry will be looked upon favorably, as will evidence of creativity and scientific rigor.

If you think you might like to contribute to this project and would like more details, please email a CV and 1-page description of your relevant research interests to me.

Thanks,

Bryan Kolaczkowski

Department of Microbiology and Cell Science University of Florida

bryank@ufl.edu

UGuelph FoodWebEvolution

Post-doc position available immediately

"DNA-based diagnostics for spruce budworm, its parasitoids, and other conifer-feeding species "

A postdoctoral position is immediately available in the Smith lab at the University of Guelph (Ontario) in the application of DNA-based diagnostics in the early detection of species involved in predating upon the spruce budworm (SBW). In particular, experience in the design and implementation of microarrays is necessary.

Applicants should have a Ph.D. and extensive training and experience in one or more of the following areas:

DNA extraction, PCR, qPCR and microarray development. The ideal candidate will also have broad training in evolutionary biology, strong writing skills, and prior management experience.

The successful applicant will play a key role in a recently funded project to develop and apply new methods involving DNA-based diagnostics for the rapid identification natural enemies of the spruce budworm in New Brunswick. The spruce budworm (SBW - Choristoneura fumiferana) is the major coniferous forest pest in eastern North America.

The goal of this project is to design a DNA-based diagnostic for these critical, but difficult to quantify and identify the complement of natural enemies (insect parasitoids and pathogens) that act as natural control agents. To do so, we will adapt, and augment, the existing library of DNA barcodes (small, standardised gene sequences) into a DNA microarray chip enabling us to rapidly identify and quantify the many organisms that interact directly (> 100 species of natural enemies) and indirectly (other conifer-feeding species that serve as alternate/alternative hosts of SBW parasitoids) with the spruce budworm and form the so-called "spruce budworm food web".

Interested applicants should submit a CV, a letter describing their research interests and career goals, and contact information for two references to Dr. Alex Smith (salex@uoguelph.ca). Further information on my research interests and publications can be found at: http://www.uoguelph.ca/˜salex/- and on Google Scholar http://scholar.google.ca/-citations?user=i5jERHcAAAAJ&hl=en . Applications will be considered for an immediate start date.

Alex Smith email: salex@uoguelph.ca web site: https://sites.google.com/site/smithlabfieldwork/ Twitter: @Alex_Smith_Ants

M. Alex Smith PhD Assistant Professor Department of Integrative Biology University of Guelph 50 Stone Road East Guelph, Ontario, Canada N1G 2W1 phone - 519-824-4120 ex 52007 www.uoguelph.ca/-˜salex/ sites.google.com/site/smithlabfieldwork/ @Alex_Smith_Ants

Office - SCIE 2464 Lab - SCIE 2409

"Ignorance more frequently begets confidence than does knowledge" - Charles Darwin

salex@uoguelph.ca

UHawaii Hilo Bioinformatics

Postdoctoral Fellow in Bioinformatics/Evolutionary Genetics to examine short- and long-term organismal response to environmental change

We are looking for a motivated bioinformaticist to join the CREST team at the University of Hawaii Hilo. CREST is a 5-year NSF-funded project (July 2014 - June 2019; see project overview below). Hawaii is world renowned as an ideal setting for evolutionary studies, and Hilo and the Big Island boast exceptional cultural and natural diversity and a high standard of living.

This is an exciting opportunity to work with a diverse team of researchers working collaboratively on the common theme of organismal response to environmental change. The successful candidate will join a team of 9 faculty, 3 technicians, and several graduate students studying the short-term (stress response) and long-term (adaptation) responses of a broad range of terrestrial and marine organisms to environmental change, broadly defined.

The postdoc will provide expertise in the application of bioinformatics analyses and will work alongside project personnel and collaborating bioinformaticists on campus and at outside institutions on the analysis of genomics and transcriptomics data to meet project goals. Responsibilities will include: collaborating in the design of experiments and analysis of data from next-generation sequencing instruments, including RNA-Sequencing, SNP, and full-genome sequencing data; assisting in the management of genomic data and associated phenotypic trait data on various local data storage systems; and preparation of manuscripts, reports and presentations.

CREST Project Overview: The overarching theme of this project is Understanding Biotic Response to Environmental Change in Tropical Ecosystems Through a Place-Based Context. This CREST:TCBES proposal focuses on three synergistic research themes: 1) Organismal Response to Environmental Change (OREC): While local adaptation along environmental gradients and tracking of changing environments involve short-term acclimation and longer term evolution, it is not known if organisms are responding to average environmental conditions or to the extreme conditions experienced in their habitats. The OREC team will examine the short- and long-term responses of key organisms to a range of environmental conditions, both steady and fluctuating, and will incorporate those results into models of landscape-level response to climate change. 2) Behavioral Responses to Environmental Change (BREC): Behaviors central to the survival and reproductive success of animals have evolved through natural and sexual selection in a far different ecological environment than exists today. The BREC team will use emerging genetic and acoustic tools to examine the effect of anthropogenic change on important social behaviors in animals ranging from arthropods to whales. 3) Dynamic Interactions between Symbioses and Environment (DISE): Macro-organisms live in symbiosis with a community of microorganisms; these symbiotic relationships can shift in response to environmental changes. The DISE team will explore adaptations of the mutualism-pathogenesis-parasitism continuum in multiple symbiotic systems. Integration of next-generation DNA sequencing and bioinformatics analysis in each of the research areas

will allow unprecedented insight into the molecular basis of biotic responses to environmental change.

As teaching experience is an important component of the postdoctoral experience, the postdoc will also be encouraged to teach one course or workshop per year at UH Hilo at the graduate** or undergraduate level in his/her area of expertise.

**Tropical Conservation Biology and Environmental Science Graduate Program

http://tcbes.uhh.hawaii.edu/ The position is for one year, renewable.

The successful candidate will be a self-starter and creative problem solver with strong communication and interpersonal skills. Minimum qualifications: PhD involving bioinformatics analysis on an evolutionary problem, experience with genomic techniques and bioinformatics analysis. Desired qualifications: software development and implementation for multidimensional data from genome sequencing, gene expression and SNP genotyping between species, populations and experimental treatments, mathematical modeling of population genetic processes.

For Inquiries: Donald Price 808-932-7178, donaldp@hawaii.edu.

To apply: Please send CV, contact information for 3 references, a cover letter describing how you meet the position's qualifications, and any relevant publications. Please send all materials in a single email to Don Price (donaldp@hawaii.edu) with the subject line Bioinformatics Postdoc.

Anticipated start date: 1 September 2014 (but flexible). Review of applications will begin Monday, 14 July. Individuals from under-represented groups are particularly encouraged to apply.

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UIllinois EvolGenomics

Post-doctoral Position in physiological genomics and high-altitude adaptation

A postdoctoral position is available in the Cheviron Lab at the University of Illinois, Urbana-Champaign (http://bit.ly/1f5N7Zb) as part of an NSF-funded, international collaboration to study the mechanistic underpinnings of hypoxia adaptation and thermogenic performance in high-altitude deer mice [1,2,3,4]. The ideal candidate will have a strong background in evolutionary physiology or evolutionary genetics, experience with bioinformatic and functional genomic analysis, and experience with computational analysis of RNA-seq and/or metabolomic data. Programming proficiency in perl, python or other scripting languages and/or regulatory network analysis will be considered a plus. The position will involve close collaboration with Graham Scott and Grant McClelland at McMaster University, Amina Qutub at Rice University, and Jay Storz at the University of Nebraska. It will also provide opportunities for fieldwork in some beautiful places, like the Front Range of the Rocky Mountains in Colorado and White Mountains of eastern California.

The start date is flexible, but preferably before January 2015, and the position is full-time for two years subject to satisfactory performance in the first year. Further extension may be available subject to funding availability and performance. Salary will be commensurate with experience and skills, and a generous benefits package will be offered. Interested applicants should send a CV, a brief description of research interests and experience, and contact information for three references to Zac Cheviron (cheviron@illinois.edu).

To receive full consideration, please send all application materials before June 30, 2014. I will also be attending the Evolution meeting in Raleigh NC this month, and would happy to meet with potential candidates there.

1. Cheviron et al. (2012) Proc. Natl. Acad. Sci. 109:8635-8640; 2. Cheviron et al. (2013) J Exp. Biol. 216:1160-1166; 3. Cheviron et al. (2014) Evolution. 68:48-62; 4. Storz et al. (2010) J Exp Biol. 213:4125-4136.

cheviron@illinois.edu

ULaReunion EvolutionaryInvasionBiol

Please could you post this post doc offer on EVOLDIR. many thanks

*A Post-Doctoral Fellowship opportunity is available at Réunion University (France): *

We are looking for a highly motivated Post-Doctoral Fellow to work on issues of insular invasion biology, with a focus on the Mascarene archipelago (Mauritius, Réunion and Rodrigues).

Background of the project: The University of Réunion starts a European program on regional cooperation (FEDER POCT) on the Biodiversity of the Western Indian Ocean region, funded by the Regional Council for the period of 2014-2015. In this framework, one task is dedicated to the study and management of invasive species.

Minimum Requirements:

Applicants must have completed their PhD in a relevant subject within the past five years, have strong analytical skills and a good publication record for the stage of their career. Basic knowledge of the French language is a bonus.

Responsibilities of the successful candidate:

- §Initiate, lead and execute the research program, with minimum supervision and within a team - §Develop collaborations with scientists and stakeholders, with other institutions and universities for collecting data on local invasive species - §Build up a regional data base on invasive species for the Mascarene islands, including data on their life cycle, ecology, original distribution area, date of introduction and impacts - §Analyze the invasiveness potential of each species, and the invasive debt for each island - §Employ statistical approaches to analyze and interpret various data sets - §Publish results and present at seminars or conferences.

The fellowship value is 1907 euro per month for the duration of one year, with the possibility of renewal under satisfactory performance. The fellow will have to undertake short trips to each island to validate or collect data, and liaise with research partners. He/She will be based in Réunion, in the lab PVBMT, at CIRAD Pôle de Protection des Plantes, Forest department, 7 Chemin de l'IRAT, 97410 Saint-Pierre.

Information on our lab: http://umr-pvbmt.cirad.fr/ *Closing dates : 16th of June 2014*

Enquiries can be directed to Pr. Dominique Strasberg at dominique.strasberg@univ-reunion.fr

To apply, please send a CV plus a motivation letter to Pr. Strasberg. –

Dr. Claudine Ah-Peng Université de La Réunion, UMR PVBMT Pôle de Protection des Plantes Pôle Forêt 7 Chemin de l'IRAT 97410 Saint-Pierre Ile de La Réunion

T: 00 262 49 92 13

http://moveclim.blogspot.com http://gdrisouthafrica.blogspot.com Claudine Ah-Peng <claudine.ahpeng@gmail.com>

ULiverpool SavannahHerbivoreCommunication

44-month Postdoctoral Research Associate position in Behavioural Ecology

Department of Evolution, Ecology, and Behaviour, University of Liverpool, UK

In collaboration with the University of York, the Mammalian Behaviour & Evolution Group at the University of Liverpool is looking for a behavioural ecologist with relevant experience to work on a NERC-funded project investigating the role of communication networks in structuring ecological communities. You will conduct fieldwork on African savannah herbivores involving playback experiments and ecological monitoring. In addition, you will contribute to data analysis and theoretical modelling of mixed-species group formation.

You should have (or be about to obtain) a PhD in an area relevant to behavioural research. You must be confident in your ability to work effectively on your own in the field in Kenya for a prolonged period (15 months) and experience of fieldwork in Africa is desirable. Skills in design of playback experiments, acoustic analysis, social network analysis, GIS and/or theoretical modelling are also advantageous. The post is available for 44 months in total, and it is envisaged that the appointee will be employed by the University of Liverpool for the initial 26 months (which will be based partly in Kenya and partly at the Leahurst Campus of the University of Liverpool), and by the University of York for the final 18 months (which will be based either in York or at Leahurst, depending on the candidate).

Full details can be found here: http://www.liv.ac.uk/-working/jobvacancies/currentvacancies/research/r-585989/ Closing date: Thursday 24th July 17:00 BST.

Jakob Bro-Jorgensen bro@liv.ac.uk Institute of Integrative Biology, University of Liverpool, Neston CH64 7TE, UK

J.Bro-Jorgensen@liverpool.ac.uk

UMemphis WeevilPhylogeny

Post Doctoral Fellow: 1000 Curculionidae Phylogeny and Evolution Project

A postdoctoral fellowship is available for a highly qualified individual to join the McKenna lab at the University of Memphis to work on a 3-year NSF-funded project examining phylogeny and evolution of the weevil family Curculionidae, a lineage of phytophagous beetles comprising >51,000 described extant species in ~4,600 genera. Research in the McKenna lab is focused on molecular phylogenetics, genomics and evolution of beetles, and the evolutionary-ecology of insect-plant interactions.

The project involves a large international team of experts in weevil biology and biogeography, taxonomy and systematics, morphology and fossils, genomics, and evolution, as well as experts in phylogenomics and phylogenetic methods. This team will reconstruct the phylogeny of weevils and establish a temporal framework for weevil diversification through analyses of phylogenomic and morphological data from a large sample of exemplar taxa. The resulting data and phylogenies will be used to test long-standing hypotheses about weevil relationships and evolution.

The successful candidate will assist McKenna with molecular lab work and analyses (~25% of time), and is responsible for coding and analysis of morphological data in close collaboration with McKenna and other project senior personnel, developing interactive web-based keys, developing and maintaining databases of specimen and character data, writing papers with collaborators, and assisting McKenna with outreach and education activities (together ~75% of time). The position is based at the University of Memphis, but includes opportunities for travel (national and international) to work with other project senior personnel.

The position offers a competitive salary plus benefits. The initial appointment is for one year, renewable for up to 3 years provided annual reviews show satisfactory progress. The preferred start date is in August 2014, but an earlier date may be possible, and interested individuals are encouraged to apply immediately.

Minimum Position Qualifications A Ph.D. in evolutionary biology, insect systematics or a related field (advanced ABDs may be considered if degree completion is imminent) Experience with morphological systematics of insects (ideally beetles) A strong record of publication in peer-reviewed journals Strong interpersonal, computational and quantitative skills, including a proven ability to work both independently and as part of a team

Desired Qualifications: (Ideal applicant; applicants with a subset of these skills will be considered) Experience working with beetles (especially weevils) Experience working with large morphological data sets using MX or similar Experience with standard molecular techniques and phylogenetic analyses (or a willingness to learn)

To apply, you will need to submit a cover letter stating your research accomplishments and interests, qualifications relevant to the position, a curriculum vitae, two representative publications, and the names and contact information for three references (submit at: https://workforum.memphis.edu/postings/7267). Specific questions relating to the position should be directed to Duane McKenna (dmckenna@memphis.edu).

Review of applications will begin June 25, 2014 and will continue until the position is filled.

The University of Memphis is an equal opportunity/affirmative action employer.

Duane D. McKenna Ph.D. Assistant Professor Department of Biological Sciences Associate, Program in Bioinformatics Associate, W. Harry Feinstone Center for Genomic Research University of Memphis 3774 Walker Avenue Memphis, TN 38152

phone: (901) 678-1386 email: dmckenna@memphis.edu website: https://umdrive.memphis.edu/dmckenna/-public/index.html “Duane McKenna (dmckenna)”

<dmckenna@memphis.edu>

UMiami InsectGenomeCoevolution

The Wilson Group in the Department of Biology at the University of Miami will soon have an opening for a postdoc.

Work in the Wilson Group focuses on symbiosis in sap-feeding insect systems. We ask questions about genome coevolution and host/symbiont metabolic collaboration. Current research is focused on amino acid transport in the context of metabolic and developmental integration of obligate intracellular symbionts and their insect hosts.

Recent publications from our group include:

Price, D. R. G., Feng, H., Baker, J. D., Bavan, S., Luetje, C. W., & Wilson, A. C. C. (2014). Aphid amino acid transporter regulates glutamine supply to intracellular bacterial symbionts. Proceedings of the National Academy of Sciences of the United States of America, 111(1), 320V325.

Duncan, R. P., Husnik, F., McCutcheon, J. P., & Wilson, A. C. C. (2014). Dynamic recruitment of amino acid transporters to the insect/symbiont interface. Molecular Ecology, 23(6), 1608V1623.

Wilson Group PI, Alex Wilson is attending the Evolution 2014 meeting in Raleigh, NC. If you are interested in this opportunity and will be at Evolution 2014 please contact Alex by email at acwilson@bio.miami.edu to arrange a time to meet during the conference.

Alex C. C. Wilson, PhD Associate Professor of Biology University of Miami

1301 Memorial Drive, Coral Gables, FL 33146, USA. Cox Science Building, Room 253

Lab: 305 284 2003 - Fax: 305 284 3039

acwilson@bio.miami.edu http://www.bio.miami.edu/-acwilson Alex Wilson <acwilson@bio.miami.edu>

UMinnesota EvolutionaryGenetics

U of Minnesota.Evolutionary Genetics

A postdoctoral position is available in the laboratory of Peter Morrell (z.umn.edu/morrell) to study barley evolutionary genetics. The primary research involves the examination of genome-level variation in barley, with a particular emphasis on the role of deleterious mutations. The position will provide the opportunity to work with Illumina resequencing data from large panels of wild, landrace, and cultivated barley and to work with experimental populations designed to test genomic prediction models. The position will also provide opportunities to interact with collaborators, including the barley breeding group of Dr. Kevin Smith and with the evolutionary genetics group of Dr. Justin Fay at Washington University in St. Louis.

The appointment is for one year with the possibility of renewal based on satisfactory performance. Salary is competitive and commensurate with experience, and benefits are included.

The University of Minnesota has strong programs in plant and evolutionary biology. Genetics and genomics research at the university has been expanding in part because of number of new faculty who were part of a Genome Variation cluster hire.

Preference is for candidates with a strong background in evolutionary biology, proficiency in UNIX computing, and experience with computational analysis of population genetic data. For more information or to apply, please send a cover letter and a CV with a list of references to pmorrell@umn.edu.

pmorrell@umn.edu

UMontpellier BacteriaPhageCoevolution

Postdoctoral Scientist in Bacteria-Phage Coevolution and Phage Therapy

An 18 month Postdoctoral Scientist position is available on November 1st, 2014 or shortly thereafter at the University of Montpellier II France. The work will be performed in the research group headed by Dr. Michael Hochberg. The project is funded by a grant from the McDonnell Foundation. Context: The proposed project will probe how environments influence the structure of antagonistic coevolutionary interactions. In nature individual organisms are confronted with diverse arrays of abiotic and biotic stresses and mortality factors. This generates higher order complexity because of the multi-scale nature of these interactions, and because both exogenous environments and organisms shift and change in ways which may be difficult to predict. Our goal is to explain patterns in the diversity of interactive traits between host and pathogen, by manipulating this complexity at different scales and teasing apart the contributions of its components to coevolutionary dynamics and population structure. We are interested in both fundamental approaches and their applications to the control of microbial pathogens, in particular the use of bacteriophage in the control of the bacterium *Pseudomonas aeruginosa*. Requirements: (1) PhD and demonstrated experience in microbial evolution, and (2) command of written, scientific English. Candidates with experience in molecular biology and having a solid training in evolutionary biology are particularly encouraged to apply. Interested candidates should apply by July 15th by sending (1) a letter of motivation, (2) a CV with publication list, and (3) the names, institutions and email addresses of three references to Dr. Michael Hochberg at mhochber@univ-montp2.fr

< http://www.eec.univ-montp2.fr/people/ >

Michael Hochberg <mhochber@univ-montp2.fr>

UNebraska Lincoln MolEvol

POST-DOCTORAL POSITION in Molecular Evolution University of Nebraska, Lincoln, NE

A post-doctoral position is available in the Storz lab at the University of Nebraska. This is one of two possible positions associated with an NIH-funded project that is designed to address questions about the roles of mutational pleiotropy and epistasis in shaping trajectories of protein evolution. The project involves the use of a protein-engineering approach to explore the mutational landscape of hemoglobin function in experimentally defined regions of protein sequence space. The work integrates evolutionary analyses of sequence variation with functional analyses of native and recombinant hemoglobins from a diverse range of animal taxa. The post-doc's work would involve ancestral sequence reconstructions, phylogenetic analyses, and comparative genomics, and there is also the opportunity to get involved in experimental aspects of the project involving protein biochemistry.

The ideal candidate would have expertise in molecular evolution, bioinformatics, and genomics and an enthusiasm for integrative evolutionary biology.

For more information about research in the lab, see: http://storzlab.unl.edu/ If interested, please send a CV and contact information for a few references. The position could start as early as summer 2014, but the start-date is flexible. Funding is potentially available for 3+ years. Salary will be determined by the NIH pay scale and will include full benefits. Please feel free to contact me (jstorz2@unl.edu) with any questions.

Lincoln is a great midwestern college town with high quality of life and miles of bike trails. The School of Biological Sciences at the University of Nebraska has a great core group of evolutionary biologists.

I will be attending the SMBE meeting in Puerto Rico (8-12 June) and the Society for Experimental Biology meeting in Manchester, UK (1-5 July), and I would be happy to meet with prospective candidates in person.

Jay Storz

Jay F. Storz Susan J. Rosowski Associate Professor of Biology School of Biological Sciences University of Nebraska Lincoln, NE 68588 Phone: 402/472-1114 E-mail: jstorz2@unl.edu

http://storzlab.unl.edu Jay Storz <jstorz2@unl.edu>

UNorthCarolina Greensboro EvolutionaryGenomics

NIH-funded Postdoctoral Opportunity in Genomics A highly motivated Research Associate is sought for multiple genomic research projects in honey bees. The primary responsibility will lie in the analysis of RNA-Seq and Methyl-Seq data sets. In addition, the candidate may take the lead on a comparative genomic project within the genus Apis and realize related research ideas. Therefore, programming and related bioinformatic skills, analytical thinking, team work, and communication skills are essential. An interest in social insect biology and evolution is preferred. Salary will be commensurate with experience. PhD desirable, but not required. The position will be in the Department of Biology at the University of North Carolina in Greensboro and is initially funded for one year. Review of applications will begin immediately until position is filled.

To apply for this position, please visit UNCG's JobSearch website https://jobsearch.uncg.edu to complete the application process for position #999620 " Research

Associate. A CV and a personal statement, including contact information for two professional references, are required. Please contact Dr. Olav Rueppell (http://biology.uncg.edu/faculty/olav_rueppell/) for additional details.

EEO/AA

o_ruppel@uncg.edu

UNorthCarolina Greensboro HoneybeeGenomics

NIH-funded Postdoctoral Opportunity in Genomics A highly motivated Research Associate is sought for multiple genomic research projects in honey bees. The primary responsibility will lie in the analysis of RNA-Seq and Methyl-Seq data sets. In addition, the candidate may take the lead on a comparative genomic project within the genus Apis and realize related research ideas. Therefore, programming and related bioinformatic skills, analytical thinking, team work, and communication skills are essential. An interest in social insect biology and evolution is preferred. Salary will be commensurate with experience. PhD desirable, but not required. The position will be in the Department of Biology at the University of North Carolina in Greensboro and is initially funded for one year. Review of applications will begin immediately until position is filled.

To apply for this position, please visit UNCG's JobSearch website https://jobsearch.uncg.edu to complete the application process for position #999620 " Research Associate. A CV and a personal statement, including contact information for two professional references, are required. Please contact Dr. Olav Rueppell for additional details.

EEO/AA

– Dr. Olav Rueppell Professor of Biology Univ. North Carolina at Greensboro 206B Eberhart Bldg. Greensboro, NC 27403, USA Tel.: (1) 336-256-2591 Fax: (1) 336-334-5839 http://www.uncg.edu/bio/faculty/olav_rueppell/lab/index.html orueppell@gmail.com

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Uppsala 2 ModelingMetapopulationDynamics

Dear all, I would appreciate help to spread this announcement of two postdoc positions at the Swedish Species Information Centre, Uppsala, Sweden.

http://www.slu.se/sv/om-slu/fristaende-sidor/aktuellt/lediga-tjanster/las-mer/?eng=1&Pid=1521 Best regards, Tord

Two postdocs: Metapopulation dynamics in hierarchical, dynamic landscapes The Swedish Species Information Centre is a national centre for knowledge on biodiversity. Our work includes compiling and storing biodiversity data and assessing the viability of species in Sweden. We are currently recruiting two postdocs who will work on the spatial dynamics of sessile species living in hierarchically structured, dynamic landscapes.

We are seeking two postdocs who will work within three subject areas: metapopulation dynamics of species with different life-history traits; development of models for metapopulation dynamics of sessile species using solely distribution pattern data; dispersal range estimation combining modelling of data on metapopulation dynamics and spatial genetic structuring. We have data on metapopulation dynamics and local abundance growth from repeated surveys of epiphytes and their host trees starting around 2000. We also have samples from the entire metapopulation of one model species (Lobaria pulmonaria) to be used for the population genetic studies. One aim of these studies based on systematically collected data from repeated surveys is to evaluate our ongoing metapopulation modelling based on Citizen Science Data that has been reported to www.artportalen.se. The model system is epiphytic bryophytes and lichens living in hierarchically structured, dynamic forest landscapes. The work is funded by the Swedish Research Council.

Tord Snäll Docent/Associate Professor

Sveriges lantbruksuniversitet Swedish University of Agricultural Sciences

ArtDatabanken/Swedish Species Information Centre Box 7007, SE-750 07 Uppsala Besöksadress: Bäcklösavägen 10 Telefon: +46(0)18-67 26 12, Mobil: +46(0)76-766 26 12 www.slu.se/artdatabanken www.slu.se/artdatabanken/tordsnall Tord.Snall@slu.se

USheffield GenomicsOfSpeciation

A two-year postdoc is available for a creative and motivated person to work on the genomics of adaptation and speciation in Timema stick insects. The postdoc will work with Patrik Nosil in the Department of Animal and Plant Sciences at the University of Sheffield (also in close collaboration with Zach Gompert at Utah State University).

The position is funded by an European Research Council grant focused on testing hypotheses about how genomes evolve as species formation unfolds from beginning to end. One major goal is to directly isolate the role of the process of natural selection in generating observed patterns of genomic divergence between host-associated populations and species of stick insects. The approach is to combine âstandard' observational whole genome sequencing with field transplants experimentally measuring selection at the genomic level. The results will provide insight into the temporal and genomic dynamics of speciation. For an example of the types of questions and data to be handled see Soria-Corrasco et al. 2014 in Science.

What we require: The postdoctoral fellow will be responsible for leading hypothesis-driven analyses of large DNA sequence data sets (i.e., genome-scale data from 100's of individuals). A Ph.D. is required. The successful applicant must have demonstrated expertise in population genetics, phylogenetics, genomics, or computational statistics. In addition, preference will be given to candidates with: (i) experience with UNIX, high performance computing, and programming in C or C++ (preferred) or in R and Perl or Python, (ii) the ability to develop and apply statistical or computational methods to solve problems, (iii) a history of independent and creative thinking in the design or execution of big data analysis, and (iv) specific expertise in research on speciation, theoretical models of evolution, or phenotypic plasticity.

What we offer: A two-year contract hosted in a vibrant department and lab group. The position will come with flexibility for pursuing independent research ideas surrounding the general theme of genome evolution during speciation.

The position will remain open until a suitable candidate is found.

To apply, contact Patrik Nosil by email (p.nosil@sheffield.ac.uk) and include a CV and brief (1-page) statement of research interests.

For more information on the lab: http://nosil-lab.group.shef.ac.uk/ p.nosil@sheffield.ac.uk

USheffield PopulationGenomics

A postdoc position is available to work with Dr Kai Zeng and Prof Jon Slate at the University of Sheffield. The position is funded by the Natural Environment Research Council (NERC) to carry out population genomic studies in great tits (/Parus major/). Questions of interest include examining how demography and natural selection shape patterns of diversity across the genome, by using existing methods and developing new methods. The project involves whole-genome sequencing of multiple great tit individuals using high-throughput sequencing instruments, and the subsequent bioinformatic/population genetic analysis of the data. Therefore, expertise in population/evolutionary genetics, computer programming and statistical analysis of large-scale datasets is essential. Experience in preparing DNA samples for high-throughput sequencing instruments is an advantage, but non-essential.

The post is available for up to 3 years, and is available from September 2014 or as soon as possible afterwards. The starting salary is £28,972- £35,597 perannum, depending on experience and qualification. Note that the information regarding pay and starting date is only provisional at this stage, and will be announced when it is finalised. Informal enquiries are highly welcomed and should be sent to k.zeng@sheffield.ac.uk.

k.zeng@sheffield.ac.uk

VillanovaU EvolutionTeachingResearch

Postdoctoral position Evolutionary Biology and Ecology

Evolutionary Biology and Ecology - The position is 50% research and 50% teaching, including specialized course(s) in an area of expertise (specifics below). The successful candidate will collaborate with an established faculty member in Biology. Applicants are invited to contact potential faculty mentors (see below for list). For more information about the department in general, visithttp://www.villanova.edu/artsci/biology/ . Postdoctoral positions in the Department of Biology have several advantages, and are an excellent way to prepare for a tenure-track position at many universities and colleges. As a Postdoctoral Fellow, you will:

- Develop and maintain a productive research collaboration with an established faculty member in the department.

- Teach in two undergraduate courses (lecture and lab, one in evolution and a second course in ecology). In addition, opportunities exist to develop a course in your area of expertise.

- Participate in the academic life of the department by serving as an undergraduate research mentor, serving on a departmental committee, and attending faculty meetings.

- Enhance your background in curriculum development by promoting the personal and professional development of undergraduate and graduate students and fostering critical thinking and problem solving, all within a context of a liberal arts education, helping students become future leaders that contribute to their field and society.

Applicants should have a Ph.D. To apply, go online at https://jobs.villanova.edu, and submit a complete curriculum vitae, plan of proposed research with a faculty mentor, teaching statement, undergraduate and graduate transcripts, and three letters of recommendation. Review of applications will begin on July 5 and continue until filled, with the desired starting date for this appointment August 22, 2014.

If questions, contact Dr. Russell Gardner, Chair (russell.gardner@villanova.edu; 610-519-4830). Also refer to the FAQ page associated with job searches: http://www1.villanova.edu/villanova/artsci/biology/jobs/jobs_faqs.html Faculty with research interests in Evolution and Ecology: Aaron Bauer Systematics, evolutionary morphology, and historical biogeography of amphibians and reptiles http://www1.villanova.edu/villanova/artsci/biology/facstaff/biodetail.html?mail=aaron.bauer@villanova.edu&xsl=bio_long Samantha Chapman Ecosystem ecology http://www1.villanova.edu/villanova/artsci/biology/facstaff/biodetail.html?mail=samantha.chapman@villanova.edu&xsl=bio_long Robert Curry Evolutionary and behavioral ecology http://www1.villanova.edu/villanova/artsci/biology/facstaff/biodetail.html?mail=robert.curry@villanova.edu&xsl=bio_long Vikram Iyengar Behavioral ecology; entomology; chemical ecology http://www1.villanova.edu/villanova/artsci/biology/facstaff/biodetail.html?mail=todd.jackman@villanova.edu&xsl=bio_long Todd Jackman Molecular systematics, phylogeography, herpetology http://todd.jackman.villanova.edu J. Adam Langley Global change ecology http://www1.villanova.edu/villanova/artsci/biology/facstaff/biodetail.html?mail=jonathan.langley@villanova.edu&xsl=bio_long Michael Russell Evolutionary and reproductive ecology of marine invertebrates; paleobiology http://www1.villanova.edu/villanova/artsci/biology/facstaff/biodetail.html?mail=michael.russell@villanova.edu&xsl=bio_long Villanova is a Catholic university sponsored by the Augustinian order. An AA/EEO employer, Villanova seeks a diverse faculty committed to scholarship, service, and especially teaching, who understand, respect, and can contribute to the University's mission and values.

Todd Jackman, Professor Department of Biology Villanova University Mendel Hall Villanova, PA 19085

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VirginiaTech VirulenceEvolution

Virulence Evolution and Disease Ecology * Postdoctoral Position *

An NIH-funded postdoctoral position is available in the lab of Dr. Dana Hawley in the Department of Biological Sciences at Virginia Tech. The candidate will work with a cross-disciplinary, multi-institutional team of researchers investigating the evolution of virulence in the naturally-occurring songbird pathogen *Mycoplasma gallisepticum*. The incumbent will largely be responsible for the generation and parameterization of within- and between-host models for this system in order to test novel hypotheses about virulence evolution. The incumbent will also participate in and help guide empirical studies on this system. Occasional travel to Princeton University will be required in order to interact with the modeling co-PI, Dr. Andy Dobson. Position includes a competitive salary and fringe benefits. Funding is available for up to two years, renewable annually based on performance.

Minimum qualifications include a Ph.D. in biology, ecology and evolutionary biology, applied math, or a related field; strong oral and written communication skills; the ability to work independently and as part of a research group; and a demonstrated ability to efficiently produce strong peer reviewed publications. Candidates with a background in infectious disease modeling or applied mathematics will be given preference. Empiricists with strong quantitative skills are also encouraged to apply.

Interested candidates should submit a curriculum vitae and statement of interest upon applying online at www.jobs.vt.edu (posting # SR0140097). Two letters of recommendation should be sent via email directly to Dr. Dana Hawley at hawleyd@vt.edu. If have any questions regarding this position, please contact the search chair, Dr. Dana Hawley at hawleyd@vt.edu <itemoore@vt.edu> or 540/231-8946.

Review of applications will begin *July 15th, 2014 *and the proposed start date is negotiable. Virginia Tech is an Equal Opportunity/ Affirmative Action Institution. Individuals with disabilities desiring accommodations in the application process should notify the search chair by the review begin date.

Dana M. Hawley Associate Professor Department of Biological Sciences Virginia Tech Derring Hall Room 4036 1405 Perry Street Blacksburg, VA 24061 (540) 231-8946 HawleyD@vt.edu <HawleyD@vt.edu>

WorkshopsCourses

Arolla Switzerland SocialEvolution Jul13-15

WORKSHOP

SOCIAL EVOLUTION: MERITS AND LIMITATIONS OF INCLUSIVE FITNESS THEORY

WHEN: 13-15 July 2014 WHERE: Arolla (Swiss Alps)

DESCRIPTION: Inclusive fitness theory is generally assumed to sufficiently explain the evolution of social behaviour. However, empirical evidence is accumulating that other evolutionary concepts need to be involved to explain cooperation and social structure in a wide range of taxa. This includes the archetypical examples of altruism, like the reproductive division of labour in eusocial hymenoptera and the cooperative breeding groups observed in many vertebrates. Recent evidence from insects and vertebrates reveals that high levels of relatedness can even reduce rather than further cooperation and altruism.

The aim of this workshop is to combine pertinent evolutionary theoreticians and empiricists to discuss complementary evolutionary mechanisms to inclusive fitness theory. This is a topic of great interest to students and biologists in general, because there is a growing awareness that explanations based on inclusive fitness, which have dominated the theoretical and empirical literature for the past half century, cannot account for many examples of apparently altruistic behaviour observed in nature.

INFO & REGISTARTION: http://biologie.cuso.ch/index.php?id=1128&clear_cache=1&tx_displaycontroller[table]=members&tx_displaycontroller[showUid]=1898

SPEAKERS: Prof. Rufus Johnstone, University of Cambridge (UK) Prof. Laurent Lehmann, University of Lausanne (CH) Dr Christina Riehl, Harvard University (US) Prof. Hanna Kokko, Australian National University (AU) Dr Erol Akcay, University of Pennsylvania (US) Dr Elli Leadbeater, University of London (UK)

Caroline Betto-Colliard Department of Ecology and Evolution Biophore Building University of Lausanne CH-1015 Lausanne Switzerland

tel: + 41 21 692 4218 fax: + 41 21 692 4265 Office: 3206

http://www.unil.ch/dee/page55421.html caroline.betto-colliard@unil.ch

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Barcelona GMM and phylogeny Sep8-12 LastCall

Dear colleagues,

This is the last call for the course “GEOMETRIC MORPHOMETRICS AND PHYLOGENY- 5th edition”.

INSTRUCTOR: Professor. Chris Klingenberg (University of Manchester, UK).

DATES: SEPTEMBER 8-12, 2014; 38 teaching hours.

PLACE: Facilities of the Centre of Restauració i Interpretació Paleontologica, Els Hostalets de Pierola, Barcelona (Spain).

Organized by: Transmitting Science, the Institut Catalá de Paleontologia Miquel Crusafont and the Council of Hostalets de Pierola.

More information: http://www.transmittingscience.org/courses/gm/gm-and-phylogeny/ or writing to courses@transmittingscience.org

This course provides an overview of the interface between geometric morphometrics and phylogenetics. It aims to give an overview of the different approaches and methods that link the two fields and to enable participants to apply them to their own research problems. Lectures that introduce concepts and methods are integrated with demonstrations of software that put them into practice right away. The main emphasis is on mapping shape data on existing phylogenies to reconstruct the evolutionary history of shape diversification, as well as comparative methods that take phylogeny into account. To enhance the practical approach of the course, participants are encouraged to bring their own data to conduct analyses and discuss results.

Please feel free to distribute this information between your colleagues if you consider it appropriate.

With best regards

Soledad De Esteban Trivigno, PhD. Course Director Transmitting Science < http://www.transmittingscience.org/ >

Soledad De Esteban Trivigno <soledad.esteban@transmittingscience.org>

Copenhagen SpeciesDistModelling 25-29Aug

LAST WEEK TO REGISTER!

The Center for Macroecology, Evolution and Climate is now accepting applications for our annual PHD course entitled “Modelling species distributions under climate change”, to be held at the University of Copenhagen August 25-29.

Read more about it here, including information on how to apply:

http://macroecology.ku.dk/teaching/int_phd_course/ Please note that this course is available to PhD students ONLY, and applications received outside of the application period will not be considered; this year’s deadline is June 6.

Applications and other inquiries should be directed to David Nogués-Bravo: dnogues@snm.ku.dk.

Katharine Ann Marske, PhD

Assistant Professor

Center for Macroecology, Evolution and Climate Natural History Museum of Denmark University of Copenhagen Universitetsparken 15 DK-2100 Copenhagen Ø Denmark

kamarske@snm.ku.dk

CostaRica TropicalEvolBiol

Hello everyone, I apologize for the cross-posting. However I wanted to share the following information:

OTS is offering several graduate level courses for 2015. All are accredited courses, meaning students that participate will receive academic credit. OTS is a consortium of over 50 universities worldwide so credits from our courses are recognized by all the member institutions (http://bit.ly/1078fLg). The course catalog can be found here http://bit.ly/1nl5E8k Courses offered for 2015:

An Introduction to Tropical Ecology:

-Coordinator: Jane Zelikova

-Course duration: 4 weeks (December 29, 2014 - January 24. 2015)

-Deadline: September 30, 2014

-Credits: 4.0

Tropical Ferns and Lycophytes:

-Coordinator: Robbin Moran & Eddie Watkins

-Course duration: 2 weeks (January 7 -22, 2015)

-Deadline: October 1, 2014

Ecología Tropical y Conservación:

-Coordinator: Federico Chinchilla

-Course duration: 7 weeks (January 12 - February 21, 2015)

-Deadline: OPEN ENROLLMENT

Biodiversity Conservation through the Lens of Indigenous Communities

-Coordinator: Claudine Sierra & Mariana Altrichter

-Course duration: 2 weeks (May 24 - June 9, 2015)

-Deadline: February 3, 2015.

Systematics, Ecology, Evolution and Uses of Palms

-Coordinator: Andrew Henderson, Henrik Balselv, Chuck Peters, Scott Zona

-Course duration: 2 weeks (May 25 - June 7, 2015)

-Deadline: February 3, 2015.

Tropical Biology: An Ecological Approach

-Coordinator: TBD

-Course duration: 6 weeks (June 8 - July 19, 2015)

-Credits: 6 credits awarded by the University of Costa Rica

-Deadline: February 3, 2015

Sistemática de Plantas Tropicales

-Coordinator: TBD

-Course duration: 5 weeks (June 30 - Agosto 3, 2015)

-Credits: 6 credits awarded by the University of Costa Rica

-Deadline: February 3, 2015

Payment for Ecosystem Services: Putting Theory into Practice in Costa Rica (http://bit.ly/1a13abb)

-Coordinator: Erin Sills < http://cnr.ncsu.edu/fer/directory/sills.php > -Course duration: 2 weeks (May 25 - June 8, 2015) -Credits: 2 semester credits awarded by the University of Costa Rica

-Deadline: February 3, 2015

Ecology and Evolution of Coleoptera (Beetles)

-Coordinator: Christopher Carlton, Richard Leschen, Nathan Lord, & Victoria Bayless

-Course duration: 3 weeks (June 5 - 24, 2015)

-Deadline: February 3, 2015

Inquiry in Rainforests: an in-service program for teachers (http://bit.ly/1aJyauv)

- Coordinator: Barbara Bentley and Joe Levine

- Course duration: 2 weeks (July 8 - 21, 2015)

- Application deadline: March 1, 2015.

Monitoring Tropical Forest Dynamics In A Changing Climate

- Coordinator: Johanna Hurtado (http://www.teamnetwork.org/) and Susan Letcher (Bio < http://openscholar.purchase.edu/susanletcher/ >) - Course duration: 2 weeks (July 21 to August 3, 2015)

-Course Credits: 2.0 -Application Deadline: February 3, 2015.

Monitoring Terrestrial Vertebrates Using Camera Traps: Field and Analytical Techniques

-Coordinator: Johanna Hurtado (http://www.teamnetwork.org/)

-Course duration: 2 weeks (August 3-13, 2015)

-Course credits: 2.0

-Application deadline: February 3, 2014, followed by rolling admission until full.

Best,

Andrés Santana Graduate Education Department Organization for Tropical Studies San Pedro, Costa Rica. 676-2050 (506) 2524-0607 ext. 1511 Skype: andres.santana_otscro www.ots.ac.cr twitter: @ots_tropicaledu < https://twitter.com/-ots_tropicaledu >

andres.santana@ots.cr

Ecuador TropicalForestConservation Sep8-27

Course “Ecology and Conservation of Tropical Forest” 8 al 27 September 2014 Components:

Entomology Ancestral Knowledge Botany Herpetology Culture and Identity Ornithology Mammals / Primates

The cost per person is 590 euro or 740 usd, including: Accommodation: 19 days at home-stay (Forest Oglán Alto). Food: 19 days (3 meals: breakfast, lunch, snack) at the Research Station. Transportation: Quito - Oglán - Quito Course materials Certificate of participation Payment of income to the protective forest Oglán Alto (community resources).

Places are limited. Registration deadline until August 10, 2014. The reservation entail an initial deposit of 200 euro or 300 usd.

More information: cursoamazonas@eccoinstitute.org

Instituto de Ecologia, Cooperación y Comunicación. ECCO INSTITUTEUNIVERSIDADCENTRALDELECUADOR, ESTACIÃNCIENTÃFICAAMAZÃNICA JURI JURI KAWSAY, El Oglán Alto, Bosque y Vegetación Protector. Acuerdo No. 136 del Ministerio del Ambiente, enero 2005. Arajuno - Pastaza - Ecuador

Curso “Ecología y Conservación del Bosque Tropical”

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al 27 de septiembre 2014 Componentes: Entomología Saberes Ancestrales Botánica Herpetología Cultura e Identidad Ornitología Mamíferos / Primates

El coste por persona es de 590 euro o 740 usd, que incluye:

Alojamiento: 19 días en la casa-estancia (bosque del Oglán Alto). Alimentación: 19 días (3 comidas diarias: desayuno, almuerzo, merienda) en la Estación Científica. Curso académico Transporte: Quito - Oglán - Quito Materiales del curso Certificado de participaciónPago del ingreso al bosque protector del Oglán Alto (recursos para la comunidad).

Plazas limitadas. Plazo de inscripción hasta el 10 de Agosto del 2014. La reserva de plaza conllevará un deposito inicial de 200 euro o 300 usd. Más información: cursoamazonas@eccoinstitute.org

Instituto de Ecologia, Cooperación y Comunicación. ECCO INSTITUTEUNIVERSIDADCENTRALDELECUADOR, ESTACIÃNCIENTÃFICAAMAZÃNICA JURI JURI KAWSAY, El Oglán Alto, Bosque y Vegetación Protector. Acuerdo No. 136 del Ministerio del Ambiente, enero 2005. Arajuno - Pastaza - Ecuador

M del Mar Soler Hurtado <mdelmar17@hotmail.com>

LakeheadU PaleoDNA LabPractical

Practical DNA Training Program:

A two-week (9 business days) intensive laboratory-based training program designed to teach participants the fundamentals of molecular techniques including DNA extraction, amplification (using PCR), sequencing and interpretation.

This training program is offered at various times throughout the year and we will work with you to find a suitable time for training.

The next two scheduled courses for the Practical DNA Training Program are July 28 - August 8, 2014 and August 18 - 28, 2014.

For more information please contact us at 807-343-8877 or paleodna@lakeheadu.ca or visit our website www.ancientdna.com and click on ’Training Programs’.

Thank you.

Karen.

Karen Maa <kmaa@lakeheadu.ca>

Lausanne Switzerland StatisticalGenetics Sep1-12

COURSES

SWISS INSTITUTE IN STATISTICAL GENETICS 2014

4 MODULES - Population Genetics Data Analysis - Elements of R for Genetics and Bioinformatics - Quantitative Genetics - Mixed Models in Quantitative Genetics

POPULATION GENETICS DATA ANALYSIS - Module 2

Teachers: Prof. Jérôme Goudet & Prof. Bruce Weir

WHEN? 1 - 3 September 2014 WHERE? University of Lausanne

INFO AND REGISTRATION: http://www.cuso.ch/-activity/?p28&id83 Description: This module serves as a foundation for many of the later modules.

Estimates and sample variances of allele frequencies, Hardy-Weinberg and linkage disequilibrium, characterization of population structure with F-statistics. Relationship estimation. Statistical genetic aspects of forensic science and association mapping. Concepts illustrated with R exercises.

ELEMENTS OF R FOR GENETICS AND BIOINFORMATICS - Module 3

Teachers: Prof. William Muir & Prof. Bruce Walsh

WHEN? 3 - 5 September 2014 WHERE? University of Lausanne

INFO AND REGISTRATION: http://www.cuso.ch/-activity/?p28&id81 Description: This module introduces programming skills required for analysis of genetic data, in the R statistical environment.

The module assumes prior knowledge of R. We will briefly review how R scripts are built up from interactive commands, and then discuss how to turn these into R programs based on user-defined functions.

We will cover R's debugging system, its tools for enhancing efficiency of code, and its methods for handling errors and warnings. In many genomic applications, R packages already exist to perform specialized statistical and bioinformatic analyses, and we will introduce packages for handling large datasets, and the Bioconductor repository of genomic packages.

QUANTITATIVE GENETICS - Module 4

Teachers: Prof. William Muir & Prof. Bruce Walsh

WHEN? 8 - 10 September 2014 WHERE? University of Lausanne

INFO AND REGISTRATION: http://www.cuso.ch/-activity/?p28&id84 Description: Quantitative Genetics is the analysis of complex characters where both genetic and environment factors contribute to trait variation. Since this includes most traits of interest, such as disease susceptibility, crop yield, and all microarray data, a working knowledge of quantitative genetics is critical in diverse fields from plant and animal breeding, human genetics, genomics, to ecology and evolutionary biology.

The course will cover the basics of quantitative genetics including: Fishers variance decomposition, covariance between relatives, heritability, inbreeding and crossbreeding, and response to selection. Also an introduction to advanced topics such as: Mixed Models, BLUP, QTL mapping; correlated characters; and the multivariate response to selection.

MIXED MODELS IN QUANTITATIVE GENETICS - Module 5

Teachers: Prof. William Muir & Prof. Bruce Walsh

WHEN? 10 - 12 September 2014 WHERE? University of Lausanne

INFO AND REGISTRATION: http://www.cuso.ch/-activity/?p28&id82 Description: The analysis of linear models containing both fixed and random effects. Topics to be discussed include a basic matrix algebra review, the general linear model, derivation of the mixed model, BLUP and REML estimation, estimation and design issues, Bayesian formulations.

Applications to be discussed include estimation of breeding values and genetic variances in general pedigrees, association mapping, genomic selection, direct and associative effects models of general group and kin selection, genotype by environment interaction models.

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Caroline Betto-Colliard Department of Ecology and Evolution Biophore Building University of Lausanne CH-1015 Lausanne Switzerland

tel: + 41 21 692 4218 fax: + 41 21 692 4265 Office: 3206

http://www.unil.ch/dee/page55421.html
caroline.betto-colliard@unil.ch

Madrid UCM Master EvolutionaryBiol

Dear EvolDir members:

The Master in Evolutionary Biology at Complutense University of Madrid (Spain) is about to open its application period for the new course, starting in autumn 2014.

The Master is an official postgraduate program directed to students seeking a comprehensive introduction to the major questions in evolutionary biology. To complete the program, students have to complete 60 ECTS credits. All students take four compulsory courses (The genetic basis of evolution, Natural selection and adaptation, Phylogenetic systematics, Patterns and processes in macroevolution, each 6 ECTS) and produce a Master's Thesis (12 ECTS). The program is completed with four more 6-credit courses, to be chosen among the following: Molecular phylogenies, Phylogeography and its applications, Animal phylogeny, Evolution and phylogeny of plants, Life-history evolution, Mechanisms of speciation in plants, Principles of experimental design, Data analysis in ecology and evolution, and Methods in evolutionary biology.

Information about the Master: www.ucm.es/biologia-evolutiva Prospective students will have three different deadlines to submit applications:

- Early application: 20 March - 10 April 2014. This early application is designed for students who need an admission letter in order to apply for travel grants or studentships, or for those who need to apply for permits to study at Complutense University. Foreign students have to apply for this permit to secure admission in the program.

- Ordinary application: 10 to 27 June 2014.

- Late application: 4-11 September 2014. This will be opened only if there are vacancies.

Further information about the documents required to complete applications is available at the University website: www.ucm.es/biologia-evolutiva Best regards,

Javier Pérez-Tris Master coordinator

jperez@ucm.es

MDIBL Maine EnvironmentalGenomics Aug2-9

Next-Generation Summer Course in Environmental Genomics at the Mount Desert Island Biological Lab

A technical course to guide research into how environmental conditions affect gene responses and the fitness of organisms

Date: August 2 to August 9, 2014. Number of participants: Restricted to 25.

HURRY: ONLY FOUR SPACES REMAIN TO BE FILLED

http://www.mdibl.org/courses/-Environmental_Genomics/399/ The faculty at MDIBL is pleased to again offer a training course in Environmental Genomics, aiming to better understand technologies and approaches used to discover how gene function is influenced by environmental conditions while accounting for variation that exists within and among natural populations. This course is built on the paradigm that the research field will most effectively grow by properly designing large-scale experiments enabled by drastically increased sample-throughput and lower sequencing costs. Most importantly, the bioinformatics challenges of manipulating and analysing population-level genomics data must be addressed.ââ

This course is designed to train the next-generation of environmental scientists, which have included in past years: university professors, postdoctoral researchers, doctoral students and government scientists, representing institutions from North America and Europe. Most responded in the departure survey that the course curriculum, choice of technologies, and effectiveness provided sufficient training to either begin or enlarge an environmental genomics project in their own laboratories. All reported that they would recommend this course to a colleague.

This course trains researchers to design studies, and to collect and analyse RNA-Seq gene expression data. Daphnia is used for training because of its growing use as a model system for environmental genomics and for improving environmental health protection, yet the skills learned during the course will be applicable to all study systems with maturing genomics resources. Much time is devoted to guiding the current and future projects of attendees.

Ultimately, participants will be better positioned to incorporate these technologies into their own research laboratories, while better understanding how functional genomics and automation can be applied to ecology, evolution and environmental toxicology.â

Course Faculty include: * John Colbourne (University of Birmingham & MDIBL) * Joseph Shaw (Indiana University & MDIBL) * Benjamin King (MDIBL) * Andrew Whitehead (University of California Davis) * Gary Churchill (Jackson Laboratory) * Trudy Mackay (North Carolina State University) * Thomas Hampton (Dartmouth College) * John Novembre (University of Chicago) * Michael Herman (Kansas State University) * Wes Werren (The Genome Institute at Washington University)

plus many more.

Mount Desert Island Biological Laboratory Old Bar Harbor Rd., Salisbury Cove, ME 04672 MDIBL - http://www.mdibl.org j.k.colbourne@bham.ac.uk

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Sweden BioinformaticDataAnalysis Nov3-7

Dear all,

Please find below the schedule and general aims of the course, “An introduction to bioinformatic tools for metagenetic and population genomic data analysis”, offered November 3-7 2014 at the Sven Lovén Centre for Marine Sciences on the island of Tjärnö outside of Strömstad on the Swedish West Coast.

There is no course fee. Accommodation and meals are covered by the Faculty of Science, University of Gothenburg. Students will need to provide their own means of transportation to and from the course, however.

The course will be open to a maximum of 20 students, as large parts of the course will consist of hands-on exercises. The aim is a broad mix of students both from the University of Gothenburg and from the outside, mainly PhD students but postdocs are also welcome to apply.

For registration, please fill out the form at https://docs.google.com/forms/d/-1f6NPwYreiYnAIdmJG24mgG3ysOg4o_dCMB7sx-VbPyA/viewform . Deadline for registration is September 15th 2014.

Please note that ALL students must bring their own computers - either Mac with Xcode Developer tools installed or a PC with any form of Linux installed.

Best wishes,

Pierre De Wit Sarah Bourlat

An introduction to bioinformatic tools for metagenetic and population genomic data analysis,

2.0 higher education credits Course description This course aims at detailed understanding and hands-on experience of using state of the art bioinformatics pipelines for one's own biological research questions. An important aspect of the course is to show how genomic data can be applied to address and answer research questions in the fields of genetics, ecology, population biology, biodiversity monitoring and conservation. The students will be trained in the latest bioinformatic methods to analyze high throughput sequencing data, which is present in many research projects. The course will cover basic computing tools required to run command line applications, processing high throughput sequencing data of the CO1 gene from environmental samples to reveal biodiversity and analysis of sequencing data from whole genome scans for population genomic studies.

The first part of the course introduces general computing tools for beginners such as the UNIX command line environment, bash commands, data formatting using regular expressions and basic scripting in the unix shell with a series of examples and exercises. The course introduces bioinformatics software for analysis of sequence data from metagenetics (The high-throughput sequencing of a molecular marker from an ecosystem or a community of organisms, used for large-scale analyses of biodiversity), through a series of live demonstrations (AmpliconNoise, TaxAssign, QIIME). The course also introduces basic and advanced concepts of population genomics data analysis such as genome/transcriptome assembly, annotation (BLAST), alignment/mapping, differential Gene expression, functional enrichment tests, SNP genotyping, PCA, outlier tests. The course corresponds to 1 week of full time studies and and is composed of lectures, demonstrations and computer labs.

Preliminary course schedule - Day 1: Introduction to general computing tools Format: 3 hours lecture and demo sessions, 3 hours computer labs, assigned exercises

Day 1 of the course will be an introduction to general computing tools, such as the unix command line environment. We will go through bash commands (less, nano, ls, ll, wc, |, tail, head, mkdir, cat, grep, for loop), regular expressions, basic scripting, and running python scripts from the unix shell with a series of examples. Exercises and assignments will be based on Haddock and Dunn âPractical Computing for biologists' and can be carried out independently. There will also be a presentation of useful bioinformatics software.

This portion of the course is to refresh the students' knowledge of the command line environment and the shell, a tool for interacting with the computer through typed instructions at the command line. Exercise sessions will be carried out in pairs to encourage collaborative problem solving. All lectures will be made dynamic through live demonstrations of the command line. Detailed course material including commands and scripts will be available through the course web page.

This part of the course corresponds to learning outcome 2a: âAbility to use basic commands in the Unix command line environment' (reformatting data with regular expressions, basic scripting, running python scripts from the unix shell)

Days 2 and 3: Metagenetic data analysis pipelines Format: Lectures and live demonstrations of software

Days 2 and 3 will focus on analysis of a high-throughput sequencing dataset from an environmental sample. This approach allows us to gather novel data on species composition of a sample for biodiversity

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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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UFribourg GenomicsSpeciationContinuum Sep4-5

Workshop 'GENOMICS OF THE SPECIATION CONTINUUM', Fribourg, Switzerland, 4-5 September 2014

Dear colleagues,

This is just to remind you of the 1 July abstract submission deadline for contributed talks and posters for our workshop. Registration without abstract submission will close 1 August, or earlier when the maximum number of participants has been reached.

Updated workshop information:

Invited Speakers: NICOLAS BIERNE, CNRS Montpellier (FR) ALEX BUERKLE, University of Wyoming (USA) TANJA PYHÄJÄRVI, University of Oulu (FI) MIKKEL SCHIERUP, Aarhus University (DK) OLE SEEHAUSEN, EAWAG (CH) JOHN WIENS, University of Arizona (USA)

Organizers: CHRISTIAN LEXER, University of Fribourg (CH) DANIEL WEGMANN, University of Fribourg (CH) HEINZ MUELLER-SCHAERER, University of Fribourg (CH) ALEX WIDMER, Swiss Federal Institute of Technology (ETH), Zurich (CH)

Our yearly Fribourg Ecology & Evolution workshops gather lively small crowds of PhD students and researchers around our invited speakers. Previous editions of this workshop series have triggered stimulating discussions on topics of mutual interest in an informal setting, and we look forward to continuing this tradition with this year's event. For more information about the workshop and venue, please visit:

http://www.unifr.ch/biol/ecology/CUSO/EEday2014/index.html Abstract submission is now open and closes 1 July. Registration is now open and closes 1 August.

Christian Lexer Professor of Evolutionary Biology University of Fribourg, Department of Biology Unit of Ecology & Evolution Chemin du Musée 10, CH-1700 Fribourg, Switzerland Tel (office) +41 (0)26 300 8868 Tel (lab): +41 (0)26 300 8895 Fax: +41 (0)26 300 9698 Mobile: +41 (0)77 472 0789 Email: christian.lexer@unifr.ch Web: http://www.unifr.ch/biol/ecology/lexer/index.html christian.lexer@unifr.ch

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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.