EvolDir

July 1, 2016

Month in Review

Foreword

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

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

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

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Conferences

Ankara EcolEvolBiology Aug31-Sep3 2

Dear Colleagues,

The 3nd Ecology and Evolutionary Biology Symposium Turkey 2016 (August 31 - September 3, Ankara) is now accepting abstract submissions at http://bit.ly/eebst_abstract Please find more information at http://bit.ly/eebst2016 We invite talks and poster presentations in all areas of evolutionary biology and ecology. All presentations will be in English and we heartily welcome international participation.

This year's keynote speakers will be Judith Mank (University College London, UK), A. Townsend Peterson (The University of Kansas), John L. Quinn (University College Cork), and Nadia D. Singh (NC State University).

Abstract submission deadline for the Symposium has been extended to 10 June 2016! Early registration closes by June 30.

The organizers of the symposium have arranged with Evolutionary Ecology Research for EER to seriously consider the publication of groups of papers from the symposium as special issues.

We look forward to seeing you in Ankara!

On behalf of the administration board of the Society of Ecology and Evolutionary Biology (Turkey)

İsmail Bekar General Secretary

For contact with organising committee: eebst2016@gmail.com

ismailbekar53@gmail.com

Antwerp NatureConservation Dec15-17

Dear All,

We are very happy to announce the upcoming Zoology 2016 congress and its CRC-satellite symposium, taking place from 15 to 17 December 2016 at Antwerp University and the Antwerp ZOO. This year's edition will be the 23th zoology congress annually organised on behalf of the Royal Belgian and Dutch Zoological Societies. At the Zoology Congress, zoologists studying life in all its aspects (from molecules to ecosystems) will meet and discuss. Young scientists are particularly invited to participate, but all zoologists, at any stage of their careers, are very welcome to submit.

The theme for the keynote presentations is Nature conservation in a changing world. Our planet is in the midst of a wave of man-made extinction. Reversing this dreadful trend will require input from— various fields in biology and beyond. In an attempt to stimulate a multidisciplinary approach to conservation biology, Zoology 2016 has invited four keynote speakers who are studying zoological biodiversity issues from different angles. However, the organizers await submissions from all fields in animal sciences.

Linked to the keynote theme, the Antwerp ZOO Centre for Research and Conservation (CRC) will present the results of its research projects in zoo-science and conservation to a general public during the satellite symposium.

Please, visit the website at www.zoology2016.be for more detailed information, registration and abstract submission.—

We look forward to meeting you at Zoology 2016.

— Prof. Gudrun De Boeck, (Chair Scientific Committee)

Prof. Peter Aerts, (Chair Organising Committee)

— Follow Zoology2016 on—Facebook—and—Twitter

Isabelle Schon <ischoen@naturalsciences.be>

AsilomarCA LocalAdaptation Jul14-17 2

7 weeks until the American Genetic Association Presidents Symposium, Local adaptation: from phenotype to genotype to fitness, at beautiful Asilomar, CA (http://www.visitasilomar.com/).

In the past, many studies dealt only with phenotypes/traits, but today the connection to genotype is becoming feasible for more and more organisms. Our speakers are a blend of established and new investigators, working on a variety of organisms, and who are taking diverse approaches to the question.

The draft program is available at http://www.theaga.org/program.htm Invited speakers: Key Distinguished Lecture by Victoria Sork, UCLA Sally Aitken University of British Columbia Jill Anderson University of Georgia Zac Cheviron University of Montana Emily Dittmar Michigan State University Suzanne Edmands University of Southern California David Field Inst. Science and Tech, Austria Lila Fishman University of Montana Jannice Friedman Syracuse University Steve Keller University of Vermont John Kelly University of Kansas Brian Langerhans North Carolina State University Curtis Lively Indiana University Robert Reed Cornell University Douglas Schemske Michigan State University Rena Schweizer UCLA Kerry Shaw Cornell University Peter Tiffin University of Minnesota

Lynda Delph, AGA President

Anjanette Baker Managing Editor Journal of Heredity agajoh@oregonstate.edu

AGAJOH@oregonstate.edu

Austin AppliedEvol Jun18

Making Evolution Work: Synthesizing research and applied practice

Evolution 2016

Austin

Saturday, June 18 8:30am-11:30am

Explore the intersection of academic and applied evolutionary research around karst watershed conservation. The goal of this Symposium is to bring together researchers from academia, government, and private business to communicate about key challenges and ideas, with an eye toward addressing global issues more effectively.

For more information visit: https://qubeshub.org/groups/sseedsym2016 Apply here to participate: *http://tinyurl.com/jdb6cq6* There is no charge for this symposium, however participation is limited so registration is required. Participants will be notified by June 13. Please share this announcement with others who might be interested.

Questions? Contact Louise Mead (lsmead@msu.edu) or Kristin Jenkins (kristin.jenkins@bioquest.org).

– Kristin P. Jenkins, PhD Director

BioQUEST Curriculum Consortium bioquest.org (608) 622.9394 POBox 126 Boyds, MD 20841-0126

Kristin Jenkins <kristin.jenkins@bioquest.org>

Evolution Austin 2016GradStudentBingo

Calling all graduate students attending Evolution 2016 in Austin next week: Welcome to the first annual Evolution Bingo! Print your Bingo Card at https://nature.berkeley.edu/rosenblum; Complete as many challenges as you can during the meeting; Keep notes about when and how you complete each challenge; Tweet your Bingo accomplishments #Evolutionbingo #lol #evol2016; After the meeting, scan and email your entry to Bree at rosenblum@berkeley.edu by June 23rd, 2016. Prizes include: eternal fame, a membership to SSE, awesome science books, cool t-shirts, and other sur-prizes.

Have fun, make new connections and enjoy the meeting!

Erica Bree Rosenblum, Ph.D. Dept Environmental Science Policy and Management I Associate Professor Museum of Vertebrate Zoology I Affiliated Faculty University of California, Berkeley 94720-3114 PHONE: 510-642-2108 I EMAIL: rosenblum@berkeley.edu WEB: http://nature.berkeley.edu/rosenblum OFFICE: 327 Hilgard Hall LAB: 139 & 146 Hilgard Hall

Erica Bree Rosenblum <rosenblum@berkeley.edu>

Italy ComputLandscapeGenetics Oct12-14

Open computational landscape genetics session

at the

Open Source Geospatial Research & Education Symposium (OGRS) 2016 http://2016.ogrs-community.org *October 12-14*, 2016 Perugia, Italy

- Organizer: OGRS 2016 steering committee (http://2016.ogrs-community.org) led by Dr Ivan Marchesini, National Research Council, IRPI, Italy - Conveners of the session on Open computational landscape genetics: Stéphane Joost, Solange Duruz

Goals of the session: - Gather together people involved in the development of open software applications used in the field of population and landscape genetics or in other subfields of evolutionary biology with a geographic dimension. - Unique opportunity for the scientific community active at the intersection of computer science, evolutionary biology and geographic information science to present recent or previous works, to share knowledge and to discuss the main advantages and drawbacks of developing open source software solutions. - Take stock of the situation as regards different challenges for open computational landscape genetics (e.g. whole genome sequence data, training of biogeoinformaticians, effective use of computational landscape genetic solutions in conservation programmes)

Keynote speakers - Prof. Riccardo Rigon, University of Trento, Italy - Prof. Maria Antonia Brovelli, Politecnico di Milano, Italy

The call for short papers (1000-1500 words) is open until *July 4, 2016*. All publications will be released in collaboration with the PeerJ Open Access publisher. Symposium proceedings will be published within a dedicated PeerJ Collection and the best papers will be seleted for submission to the PeerJ Computer Science journal.

All information and instructions for submission are available here: - http://2016.ogrs-community.org/submission-of-short-papers Initial short paper submitted by the conveners of the session and describing the context of open computational landscape genetics. - https://peerj.com/preprints/1721/ *Important Dates* - Deadline for submission of short papers (1000 to 1500 words): July 4, 2016 - Decision: August 26, 2016 - Program published: September 5, 2016 - Deadline for early registration: September 19, 2016

Registration - http://2016.ogrs-community.org/registration *Additional information*: stephane.joost[at]epfl.ch

On behalf of the OGRS steering committee, Dr Stéphane Joost, EPFL, Switzerland

stephane.joost@epfl.ch

Madison Florida SEPEEG Oct21-23

The 43rd annual Southeastern Population Ecology and Evolutionary Genetics meeting (SEPEEG, pronounced "seepage") will be held on the weekend of October 21-23 at Camp Cherry Lake in Madison, Florida. SEPEEG provides a friendly, informal setting for students, postdocs, and faculty to meet, talk science and relax around the campfire. The meeting will be hosted by the University of Florida Department of Biology. Registration will open on or about September 1, 2016 and will cost $125/person. Some funds will be available for student travel, generously provided by the American Society of Naturalists. A SEPEEG web site will appear in the near future and will be announced on EvolDir. Until then, please contact the organizers, Stuart McDaniel (stuartmcdaniel@ufl.edu) or Charlie Baer (cbaer@ufl.edu) for further information.

-CB and SM

“Baer,Charles” <cbaer@ufl.edu>

Marseilles 20thEvolBiol Sep20-23 AcceptedAbstracts

Dear all,

the list, of the first accepted abstracts of the

20th evolutionary biology meeting at Marseilles , is available see:

sites.univ-provence.fr/evol-cgr/ or aeeb.fr

The deadline for abstract submissions and registrations is June 30.

Best regards

Pierre

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

Roscoff EvolGenomicsSystemsBiol Oct10-14 DeadlineJun22

Dear all,

We have the pleasure to announce a CNRS-Jacques Monod Conference entitled “Evolutionary genomics and systems biology: bringing together theoretical and experimental approaches” that will take place in Roscoff (France) from 10 to 14 October 2016.

Deadline for abstract submission (mandatory for participation to a Jacques Monod Conference): 22 June 2016 (see instructions on CNRS website http://www.cnrs.fr/insb/cjm/2016/Vekemans_e.html) The organizers: Xavier Vekemans (UMR Evo-Eco-Paléo, Lille; xavier.vekemans@univ-lille1.fr) and Christian Landry (Institut Biologie Intégrative et des Systèmes, Laval University, Québec; christian.landry@bio.ulaval.ca)

Presentation of the conference: Genomic tools are becoming essential in biological investigations that relate to agriculture, medicine, biotechnology and biodiversity science. Moreover, evolutionary concepts and an evolutionary genomics perspective are becoming central to interpret any new finding in these fields and develop forward approaches for problem solving. The potential of evolutionary genomics is unparalleled as it provides key insights into our understanding of many fundamental and applied questions such as the evolutionary history of life on earth and the molecular bases of adaptation of species in response to environmental changes in natural populations and crop improvement. However, the maturation of evolutionary thinking in these fields involving genomic approaches is an ongoing process and needs to be supported by initiatives that will update key analytical, conceptual and experimental innovations in evolutionary genomics.

The objective of the proposed conference is to make such synthesis possible by bringing leaders in the field together to discuss their ongoing research and vision of where the field is moving over the coming years. Accordingly, we aim at fostering the link between functional and evolutionary perspectives towards an integrative approach of evolutionary genomics, and propose a conference with: two sessions on evolutionary systems biology and experimental evolution; one session on genome evolution; two sessions on theoretical and empirical population genomics. Because evolutionary genomics largely focuses on processes (how mutations arise and fix in populations) and systems biology on functions (how mutations are translated into phenotypes), we are convinced that this combination will allow to progress towards a better understanding of evolutionary processes and its applications. Besides this focus on an integrative approach, a second aim of the conference is to bring together evolutionary genomic researchers working on a large panel of organisms, from bacteria to humans, including e.g. plants and fungi, in order to foster the cross-exchange of evolutionary concepts, analytical methods and experimental approaches.

Programme and confirmed invited speakers: Session EVOLUTIONARY SYSTEM BIOLOGY AND NETWORK EVOLUTION: Marie-Anne FELIX; Christian LANDRY; Ben LEHNER; Benjamin PRUD’HOMME; Trisha WITTKOPP Session EXPERIMENTAL EVOLUTION: Irene CHEN; Michael DESAI; Duncan

GREIG; Caroline KNIBBE; Olivier TENAILLON Session GENOME EVOLUTION: Doris BACHTROG; Laurent DURET; Tatiana GIRAUD; Henrik KAESSMANN; Maud TENAILLON Session THEORETICAL AND METHODOLOGICAL DEVELOPMENTS IN POPULATION GENOMICS: Mark BEAUMONT; Michael BLUM; Richard DURBIN; Asger HOBOLT; Renaud VITALIS Session ECOLOGICAL AND EVOLUTIONARY GENOMICS: Juliette DE MEAUX; Nicolas GALTIER; Dmitri PETROV; Molly PRZEWORSKI; Christian SCHLOTTERER; Xavier VEKEMANS

Provisional titles of invited communications: BACHTROG Doris (Berkeley, USA) The evolution of chromatin structure BEAUMONT Mark (Bristol, United Kingdom). ABC strategies for inferring demographic history from whole genome data BLUM Michael (La Tronche, France) Detecting genomic signatures of natural selection with principal component analysis CHEN Irene (Santa Barbara, USA) The role of chance in the early evolution of life DE MEAUX Juliette (Köln, Germany) Evolutionary transcriptomics in the Arabidopsis genus DESAI Michael (Cambridge, USA) The statistics of epistasis and pleiotropy in budding yeast DURBIN Richard (Cambridge, United Kingdom) Inferring demography from multiple genome sequences DURET Laurent (Villeurbanne, France) Biased gene conversion: the dark side of recombination FELIX Marie-Anne (Paris, France) Evolutionary systems analysis of Caenorhabditis vulva development GALTIER Nicolas (Montpellier, France) Effective population size, genetic polymorphism and adaptive rate in non-model animals. GIRAUD Tatiana (Orsay, France) Evolutionary genomics of adaptation in fungi as model eukaryotes GREIG Duncan (Plön, Germany) Experimental evolution of pheromonal mate discrimination HOBOLT Asger (Aarhus, Denmark) Accurate approximation to the ancestral recombination graph

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Sweden BiosystEU2017 Aug2017

Dear Colleagues,

The 3d BioSyst.EU meeting will be held at Gothenburg U, Sweden on the 15-18 August 2017. The meeting will feature invited thematic symposia as well as open sessions on systematic and evolutionary biology.

For more information, go to http://www.conferencemanager.se/BiosystEU2017/ We look forward to seeing you in Gothenburg,

The organizing committee

"Catarina.Rydin@su.se" <Catarina.Rydin@su.se>

Tempe Arizona EvolutionSex Nov17-19

Evolutionary Genomics of Sex Conference 2016

When: November 17-19, 2016. Location: Tempe, Arizona #EvSex16

Sponsored by the American Genetic Association and the Center for Evolution and Medicine at Arizona State University

ABSTRACT SUBMISSION NOW OPEN https://easychair.org/conferences/?conf=evsex16 Abstracts due June 30, 2016

TRAINEE TRAVEL AWARDS AVAILABLE

REGISTRATION WILL OPEN AFTER ABSTRACTS ARE ACCEPTED Expected Registration ~$75-$125 Expected Registration Opening: August 1, 2016

Trainee travel awards will be notified before registration opens. To stay up-to-date with announcements about the conference, join the google group: https://groups.google.com/d/forum/evsex16 Public Speakers

Tia-Lynn Ashman, University of Pittsburg: http://www.pitt.edu/ ~ tia1/ Doris Bachtrog, University of California, Berkeley: http://ib.berkeley.edu/labs/bachtrog/ Justin Blumenstiel, University of Kansas: http://www.blumenstiellab.org Amanda Larracuente, University of Rochester: http://blogs.rochester.edu/larracuente/? John Logsdon, University of Iowa: http://biology.uiowa.edu/people/john-logsdon Judith Mank, University College, London: http://www.ucl.ac.uk/mank-group/ Nicole Valenzuela, Iowa State University: http://www.public.iastate.edu/~ nvalenzu/ Melissa A. Wilson Sayres, Arizona State University: http://www.wilsonsayreslab.org Lenora Ott <Lenora.Ott@asu.edu>

UChicago MidWestPopGen Aug26-27

Dear Colleagues,

The field of population genetics has a remarkable tradition of being a tight-knit and nurturing community. In order to better foster that sense of community for popgen groups in the Midwest, *we are organizing the third edition of the Midwest PopGen conference*.

The location this year will be the University of Chicago. The date this year will be: August 26th-27th. The meeting will begin Friday at noon and continue to Saturday evening with a BBQ on Friday evening.

Approximately fifteen 25-minute talks will be selected from submitted abstracts, and there will be a poster session. The meeting will again be trainee-oriented, so students and postdocs are especially encouraged to present their work. There will be a small prize for best poster and best talk by a student and postdoctoral fellow.

If you do plan to attend, please RSVP by adding your name and information to the registration list (http://bit.ly/1Yb3Pkl) and if you would like to given an oral presentation submit your abstracts by July 25th to Candice Lewis <cllewis at uchicago dot edu>. Submitters will be notified if their abstract is chosen for a talk by August 1st. A tentative schedule and accommodation advice are also provided as tabs on the registration Google Sheet (http://bit.ly/1Yb3Pkl).

We hope you can make it and that we can continue this meeting for the population geneticists in our region!

All the best,

John Novembre, UChicago

Don Conrad, WashU

Sebastian Zollner, Michigan

jnovembre@gmail.com

UMontreal RECOMB Oct11-14 DeadlineExt

Following several requests, the deadline to submit papers to the 14th RECOMB Conference on Comparative Genomics, RECOMB-CG 2016, that will be held in Montreal, October 11-14 2016, has been extended until Monday June 13 2016.

Call for papers: http://www.crm.umontreal.ca/2016/Genomics16/appel_e.php Conference website: http://www.crm.umontreal.ca/2016/Genomics16/index_e.php Cedric Chauve, PhD Professor, Department of Mathematics Simon Fraser University http://paleogenomics.irmacs.sfu.ca/ David Sankoff <sankoff2@gmail.com>

Vienna MindTheGap Oct31-Nov1

MIND THE GAP 5 Conference Vienna, Austria October 31 and November 1, 2016

Bridging the gap between theoretical and empirical population genetics

The students of the Vienna Graduate School of Population Genetics are proud to announce the fifth MIND THE GAP conference to be held on October 31 and November 1, 2016 at the campus of Vetmeduni Vienna, Austria.

MIND THE GAP aims at bringing together theoretical and empirical population geneticists. This conference is the fifth meeting in a series of conferences held in Freiburg (2009), Plön (2010), Cologne (2011), and Vienna (2013).

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

- Evolutionary inference using time series data - Adaptive QTLs and their genomic signatures - Phenotypic plasticity - Introgression: signatures of selected and neutral alleles

Invited speakers: Nick Barton (IST Austria, A) Alan Bergland (Univ. of Virginia, USA) Luis-Miguel Chevin

(CEFE/CNRS, FR) Oscar Gaggiotti (Univ. of St. Andrews, UK) Anna-Sapfo Malaspinas (University of Bern, CH) Fernando Racimo (Univ. of California, Berkeley, USA) Wolfgang Stephan (LMU Munich, GER) Lev Yampolsky (East Tennessee State Univ., USA)

A few remaining speaker slots are still available for which we invite you to apply by July 17th.

Attendance to the conference will be free of charge but space is limited. Details about registration can be found on our website: http://www.popgen-vienna.at/news/-mind-the-gap-5.html – Dr. Julia Hosp Vienna Graduate School of Population Genetics Coordinator www.popgen-vienna.at https://twitter.com/PopGenViennaPhD c/o Institut für Populationsgenetik Vetmeduni Vienna Veterinärplatz 1, 1210 Wien

T +43 1 25077 4338 F +43 1 25077 4390

http://www.vetmeduni.ac.at/en/population-genetics/ https://twitter.com/PopGenVienna julia.hosp@gmail.com

WeizmannInstSci GenomeEvolution Nov1-3

What: Genome evolution conference

When Nov 1-3 2016

Where: Weizmann Institute of Science, Rehovot, Israel

We are happy to announce Genome Evolution 2016, a conference that will be held on campus at the Weizmann Institute of Science on November 1-3 2016. See website: http://www.weizmann.ac.il/conferences/GE2016/ This meeting aims to bring the news in genome evolution by bringing together world leaders and young students and post-docs from around the world. We will cover diverse sub-disciplines ranging from experimental evolution, theoretical and computational evolutionary dynamics, molecular evolution, cancer evolution and more.

Students and postdocs are encouraged to attend, and apply for a poster and oral presentation. Some limited accommodation is available upon early registration.

Tzachi Pilpel, Roy Kishony, Orna Dahan

"pilpel@weizmann.ac.il" <pilpel@weizmann.ac.il>

GradStudentPositions

Auckland InsectOdorantEvolution

Postal Address: Plant & Food Research Private Bag 92169, Auckland Mail Centre, Auckland, 1142, New Zealand Physical Address: Plant & Food Research 120 Mt Albert Road, Sandringham, Auckland, 1025, New Zealand

PhD student position

Plant & Food Research, Auckland, NEW ZEALAND

Professor Richard Newcomb (Richard.Newcomb@plantandfood.co.nz)

Assoc. Professor Thomas Buckley (BuckleyT@landcareresearch.co.nz)

The origin of odorant receptors in insects

A PhD position is available to study the origins of a unique family of receptors for odorants and pheromones that arose early in the evolution of insects. Supported from a grant from the prestigious Marsden Fund, the PhD project will address the timing and role of the first insect odorant receptors. Our hypothesis is that they appeared just before the origin of insect flight and expanded to fill roles in detecting food, predators and/or mates in this new three dimensional environment. The research will involve the isolation of candidate odorant receptors from the transcriptomes and genomes of early insects and their deorphaning in surrogate cell systems.

http://www.royalsociety.org.nz/2015/11/05/was-the-first-smell-of-a-meal-or-a-mate/ The successful candidate will conduct their research within the Auckland laboratories of Plant and Food Research, while being enrolled through the School of Biological Sciences at the University of Auckland. Support includes a $27k p.a. three year stipend with university fees paid. You will work alongside postdoctoral fellows also working on the problem and other members of the Molecular Sensing team within Plant & Food Research, together with collaborators from Landcare Research in New Zealand and the Max Planck Institute for Chemical Ecology in Germany. Candidates should have some background or at least interest in evolutionary genomics, bioinformatics and cell biology.

Richard Newcomb <Richard.Newcomb@plantandfood.co.nz>

Berlin Zurich EvolutionaryEcol

Eawag,the Swiss Federal Institute of Aquatic Science and Technology (Dübendorf, Switzerland), and IGB, the Leibniz-Institute of Freshwater Ecology and Inland Fisheries (Berlin, Germany), are internationally recognized institutes that are committed to the ecological, economical and social management of water. They offer excellent laboratory and field facilities for interdisciplinary research, large-scale experimental facilities, and long-term research programs and data sets. These institutions share common goals towards education, research, and technology transfer at the highest international level.

TheDepartment of Aquatic Ecology (Eawag) and the Department of Ecosystem Research (IGB) seek TwoPhD students in Evolutionary Ecology Projecttitle: Hostâparasite interactions in hybridizing Daphnia, from correlations to experiments

BothPhD students will participate in a collaborative research project with PD Dr Piet Spaak (Eawag) and

Prof. Justyna Wolinska (IGB), financed by the Swiss and German Science Foundations (SNF & DFG).

Eutrophicationis a worldwide environmental problem accelerated by global warming, affecting the stability of aquatic ecosystems and having longâconsequences. We will investigate if and how eutrophication affects two interacting evolutionary processes: disease spread and interspecific hybridization. We will use water fleas (Daphnia), a well-established model in both host-parasite and hybridization research. This project is a combination of field surveys of two eutrophic lakes, a large scale mesocosm experiment (where trophic conditions will be manipulated), the transcriptional profiling of Daphnia exposed to stressful eutrophic conditions, and the development and application of molecular markers to study parasite evolution in eutrophic environments. Overall, through the unique combination of expertise and methods, this project will improve our understanding of disease spread and biodiversity loss under different trophic conditions and, consequently, might provide tools for management of aquatic ecosystems.

Theposition at IGB focuses on host-parasite interactions. The main task will be development of molecular markers (SNPs) for a model parasite species and application of these markers to study parasite evolution. Thus, the student will participate in preparation of samples for de novo sequencing of the whole parasite genome. Developed markers will be applied on field-collected and experimental samples (i.e. amplicon sequencing on Illumina). The bioinformatics component will be performed in collaboration with a postdoctoral researcher, but the student is expected to learn and help with that part. In addition, some microscopy work, field work and/or experimental work might be accommodated, depending on skills and interests.

Theposition at Eawag focuses on interspecific hybridization. Here, the main task will be participation in a large-scale field study and mesocosm experiment, data collection and processing. The student will screen the dynamics of hybridizing Daphnia communities, using already established microsatellite and SNP markers. Also, the student will conduct a large laboratory experiment to assess Daphnia stress responses; here, RNA-Seq methods will be applied. The PhD student will take advantage of the draft D. galeata genome. A postdoctoral researcher will help with analyses of RNA-Seq data.

Althoughthe students will be hosted primarily at their given institution, exchange stays are planned at Eawag and IGB, respectively. Moreover, generous funds are available to cover attendance at national and international conferences. The students will take part in the organized PhD programs (including attending various skills courses) of their respective institution: http://www.eawag.ch/en/teaching/academic-education/ http://www.igb-berlin.de/PhD_Training.html Thepositions will be for a period of three years, and should start as soon as possible (January 2017 or even earlier). The Eawag PhD student will be enrolled at the Swiss Federal Institute of Technology (ETH) in Zürich, the German PhD student at Free University in Berlin.

Theideal candidate should have good molecular skills and a strong background in evolutionary biology, ecology or related fields. In addition, knowledge of statistics, bioinformatics and/or population genetics will be highly advantageous. Excellent communication and writing skills in English, good work ethic, and creative thinking are desired. A Masters Degree (or equivalent) in biology or a related subject is necessary for admission. The working language in the groups is English. In keeping with the IGB's policy regarding gender equality, female applicants are particularly encouraged. Severely disabled applicants with equal qualification and aptitude are given preferential consideration.

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BlackHillsStateU IntegrativeGenomics

Graduate Research Assistantships at Black Hills State University, M.S. Integrative Genomics Program

The Masters in Science in Integrative Genomics program at Black Hills State University (Spearfish, SD) currently has openings for the Fall 2016 semester. This program integrates the field of genomics with a broad array of biology and chemistry fields, such as Ecology, Population Biology, Biochemistry, Pharmacology, Microbiology, and Evolutionary Biology. The curriculum exposes students to modern techniques and instrumentation in the laboratory and field and prepares students for success in academic and other biotechnology-related pursuits.

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

Black Hills State University, located in the heart of the northern Black Hills - Spearfish, South Dakota, offers 75 academic programs at the associate, bachelor, and master degree levels. BHSU, which has over 4,000 students enrolled, has earned a reputation for transforming lives through innovative, high-quality academic programs and a dynamic learning community. Our location within the Black Hills provides a natural laboratory possessing diverse habitats for Integrative Genomics research. Being located near the Sanford Underground Research Facility (the former Homestake Mine in Lead, SD) allows for the study of unique microbial communities in deep underground environments. Research projects of MSIG students have included, but are not limited to: plant and animal phylogeography and population genetics; plant ecophysiology; determination of the mode of action and development of resistance to novel antimicrobial agents; nanoparticle development for the use as biomarkers.

Learn more about the community here:

http://www.visitspearfish.com/ < https://www.youtube.com/watch?v=3D3DBrRRHz2TRDs >

www.youtube.com/watch?v×YjpSw8iqc Information about M.S. Integrative Genomics program requirements and application process can be found here:

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

Raeann.Mettler@bhsu.edu

HemlholtzCentre MetagenomicsResearch

The Department for “Computational Biology of Infection Research” at the Helmholtz Centre for Infection Research offers a Bachelor- /Master-Project on the field of “Metagenomics Research”. We are looking for highly motivated students of bioinformatics, computer science or similar to work on the problems outlined under this link:

URL: https://www.helmholtz-hzi.de/de/karriere/jobportal/master_und_doktorarbeiten/master_and_phd_theses/ansicht/job/details/bachelor_master_project-1/ Best,

Philipp Münch

– Philipp C. Münch

Computational Biology of Infection Research, Helmholtz Centre for Infection Research, Inhoffenstraße 7, 38124 Braunschweig, Germany

AG Stecher, Bacteriology Max von Pettenkofer-Institute, LMU Munich, Pettenkoferstr. 9a, 80336 Munich, Germany

“Philipp C. Münch” <philipp.muench@helmholtz-hzi.de>

ImperialC London EvolutionConservation

Dear All,

Admissions are currently open for the 1-year Masters courses at the Silwood Park < http://www.imperial.ac.uk/visit/campuses/silwood-park/prospective-students/msc-and-mres-courses/ > Campus of the Department of Life Sciences, Imperial College London.

We are an international center for research and training in ecology, evolution, biological conservation and climate-driven ecosystem dynamics. The Department of Life Sciences at Imperial College London is one of the largest life sciences groups worldwide. The Department has an outstanding international reputation for research and excellent facilities for postgraduate research and education.

We offer a range of Masters courses < http://www.imperial.ac.uk/visit/campuses/silwood-park/prospective-students/msc-and-mres-courses/ > in theoretical, empirical and applied ecology, evolution, and conservation at Silwood Park and at the Natural History Museum London. Our courses are taught in partnership with other organisations such as the Royal Botanical Gardens Kew, The Grantham Institute, Zoological Society of London, Durrell Wildlife Conservation Trust, Thomson Ecology, CABI and Surrey Wildlife Trust.

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*

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*

Our graduates have a very high success rate of obtaining PhDs and jobs in Europe, the USA and internationally.

*

Learn a range of skills early in the course from active researchers and practitioners to help shape your project ideas.

*

Research projects range from 3.5 to 9 months depending on the course (MSc versus MRes), and can be based in our department or with external organisations anywhere in the world.

*

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*

Work at, and interact with, world-famous biodiversity and conservation organisations.

*

Our campus is ideally situated in a verdant woodland 30 minutes from London Heathrow and an hour from central London, with easy access to one of the highest concentrations of researchers and conservation organisations in the world.

*

Our network of contacts is global, and you will interact with a steady stream of leading figures who visit for workshops and seminars.

“/A quite extraordinary number of good ideas in ecology have been hatched in the intellectual hotbed of Silwood Park... Its surroundings give it the magic to attract and stimulate academics from around the world to be exceptionally creative.”/ - Stuart Pimm, Doris Duke Professor of Conservation, Duke University.

Contact us:

The Department of Life Sciences, Imperial College London, Silwood Park Campus, Ascot, Berkshire SL5 7PY.

E-mail: amanda.ellis@imperial.ac.uk

Web: https://www.imperial.ac.uk/visit/campuses/silwood-park/ and follow links for prospective students

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INRA Avignon ForestGeneticAdaptation

Dear all,

As part of the GenTree project, we are looking for highly motivated PhD candidates, with a training in functional or evolutionary ecology and modeling to work on innovative strategies for conservation of forest genetic resources under climate change. The project will mostly involve predictive modeling, but some field work will also be required.

The doctoral research will be composed of four main tasks. Tasks 1 and 2 aims to confront two types of predictions of forest genetic resources (FGR) vulnerability: the one across the distribution range of species obtained through bioclimatic niche model with that obtained through a process-based ecophysiological model to shed light on the ecological processes underlying vulnerability. In tasks 3 and 4, an individual-based simulation model integrating ecophysiological, demographic and genetic processes will be used to predict the dynamics of FGR conservation networks under climate change, and to propose innovative management methods of these networks. First, the model will be refined, to better account for regeneration. Then, the model will be used to investigate the role of genetic diversity in the adaptive response of trees populations to climate change, and how management may contribute to this response.

The PhD student will be registered in the doctoral school GAIA (Biodiversité, Agriculture, Alimentation, Environnement, Terre, Eau), of the University Montpellier II (https://gaia.umontpellier.fr/). The PhD will begin no later than November 2016.. Ability to interact in English is required and non-French candidates are welcome. Find out more (link to full PDF)

Thanks

Sylvie ODDOU-MURATORIO

*Directrice de Recherche / Scientist** *Population Biology & Evolution team**

sylvie.muratorio@avignon.inra.fr

*UR629 Ecologie des Forêts Méditerranéennes (URFM) ** *Centre de recherche Provence-Alpes-Côte d'Azur**

Tél. : +33 (0)4 32 72 29 04

Fax : +33 (0)4 32 72 29 02

Domaine Saint Paul, Site Agroparc

CS 40 509 - 84914 Avignon Cedex 9

France

Personalweb page < http://www6.paca.inra.fr/ecologie_des_forets_mediterraneennes/Les-personnes/Personnels-permanents/ODDOU-MURATORIO-Sylvie >

UR629 < http://www6.paca.inra.fr/ecologie_des_forets_mediterraneennes >

*BioPopEvol**Team*

Sylvie Oddou-Muratorio <sylvie.muratorio@avignon.inra.fr>

MasseyU PlantSelectiveSweeps

PhD student position, Massey University New Zealand – selective sweep mapping in forage plant species

A postgraduate studentship is available to pursue PhD research on the identification of selective sweeps associated with artificial or natural selection in forage plant species. This project will be supported from the AgResearch MBIE-funded research programme "Genomics for Production and Security in a Biological Economy". The PhD candidate will be enrolled with Massey University, Palmerston North with the Institute of Fundamental Sciences.

The principal objective is to use genotyping-by-sequencing (GBS) technology to locate genomic selective sweeps resulting from selection for important forage traits. A complementary aspect will be application of a novel transcriptomics approach to identifying candidate genes associated with these traits. These tools will be focused on (1) a nutritive trait selectively bred in white clover; and (2) drought response in white clover and perennial ryegrass populations. The overall goal is to understand genomic responses to selection with a view to extending this knowledge into the development of molecular selection tools for breeding applications.

The first component targets soluble energy levels in white clover leaves. The research will utilise breeding populations selected for differential levels of leaf soluble energy, using GBS data to identify selective sweep signatures associated with this important nutritive trait. A transcriptomics approach, highlighting genes with evidence of plasticity for the trait of interest, will also be used to identify gene loci as candidates for selection and these will be evaluated further in analyses of GBS profiles. The second component will target selective sweeps in white clover and ryegrass associated with plant persistence under drought, utilising pasture populations from environmentally contrasting sites in New Zealand. The contrasting biology of these forage species will provide insight into genetic responses to selective pressure.

The programme will include the participation of Associate Professor Kenneth Olsen (Washington University, USA) incorporating a stay of up to 4 months in the Olsen laboratory, where relevant genetic analysis approaches will be learned.

The successful candidate will have a strong BSc (Hons) or MSc (Hons) degree in genetics, molecular biology or a related discipline.

Expertise in bioinformatics or biostatistics would be desirable.

English language proficiency is essential. The studentship, funded by AgResearch, provides an annual stipend of $30,000 plus payment of domestic tuition fees and research expenses for three years.

For your application to be considered you must apply online, please include the following (i) a cover letter outlining your suitability and interest in the position, (ii) a current curriculum vitae and names of three referees online via https://careers.sciencenewzealand.org/agresearch/agresearch-jobs .

Expressions of interests close when the position is filled.

"Olsen, Kenneth" <kolsen@wustl.edu>

MaxPlanckInst ComparativeGenomics

The Research Group "Computational Biology and Evolutionary Genomics" at the Max Planck Institute in Dresden has an opening for a PhD position.

We are hiring for an evolutionary genomics project that aims at discovering the differences in the genome that underlie phenotypic differences between species. The project will involve applying methods that we have developed in the lab to build high-quality genome alignments, detect functional genomic differences, and associate these genomic to phenotypic differences between species. For promising candidate loci, we will experimentally test whether editing these genomic loci with Crispr/Cas9 in a model organism recapitulates the natural phenotypic differences.

Our Institute:

Our group is located at the Max Planck Institute of Molecular Cell Biology and Genetics (MPI-CBG) and we are jointly affiliated with the Max Planck Institute for the Physics of Complex Systems (MPI-PKS), both in Dresden. Both institutes are highly interactive and interdisciplinary workplaces, provide an international atmosphere with English as working language and access to cutting-edge computational and experimental infrastructure and facilities. The MPI-CBG was awarded one of the "Best Places To Work for Postdocs" in 2011.

Requirements:

Applicants should have a background in bioinformatics or computational biology or molecular evolution. Good programming skills (perl, python, shell scripting) in a Linux environment are required. Experience in large-scale genomic data analysis would be an advantage.

Candidates should please email - CV including contact information for at least two references - A summary of previous research experience (max 1 page) to Michael Hiller (hiller@mpi-cbg.de).

Group page: http://www.mpi-cbg.de/research/michael-hiller.html "hiller@mpi-cbg.de" <hiller@mpi-cbg.de>
"hiller@mpi-cbg.de" <hiller@mpi-cbg.de>

MontpellierU DeepSeaGenomics

A PhD position is proposed under the joint supervision of two teams in France: UMR MARBEC Marine Biodiversity, Exploitation and Conservation, Université de Montpellier (Sophie Arnaud-Haond, Sophie.Arnaud@ifremer.fr) et Laboratoire Environnement Profond/Etude des Ecosystèmes Profonds, IFREMER Brest Plouzané (Daniela Zeppili, Daniela.Zeppilli@ifremer.fr), in the context of the project "Pourquoi Pas les Abysses" (Ifremer, France). The candidate will be based in Sète and register at Montpellier University.

The application procedure to be completed before June 30th is available at : http://wwz.ifremer.fr/-Travailler-a-l-Ifremer/Bourses-de-recherche/Bourses-de-theses-2016-2017 * Reevaluating marine biodiversity in deep-sea ecosystems and the drivers of its distribution through metagenomics approaches * **Dead-line for application: 30th of June 2016* * Marine Biodiversity, owing to its difficult access, is still largely unknown. The use of New Generation Sequencing tools (NGS) offers new perspectives to appraise its extent and better understand the biotic and abiotic factors influencing its distribution. The expectations relative to metagenomics and metabarcode tools are of particular importance in remote and hard to access environments such as those characterizing deep sea ecosystems. This PhD proposal is part of a project which ambition is to contribute to the large scale characterization of deep-sea biodiversity through metabarcode, jointly with morphological approaches that will allow appraising strength and weaknesses of those methods in these remote and largely unknown environment. The influence of physico-chemical parameters on the distribution of genomic diversity at intra specific scale and on connectivity among ecosystems and oceans regions will be tackled through the genome scan analysis of some of the main phyla representative of deep sea communities.

Key words: Marine biodiversity, Abyss, metabarcoding, environmental genomics, metagenomics, connectivity, evolution.

Background: Strong background in evolutionary ecology, marine ecology. Basic knowledge on marine meiofauna, as well as strong skills in molecular biology and bioinformatics required. Good relational capacities to work in a collaborative a multidisciplinary context.

Good level in English (spoken, written).

Sophie Arnaud-Haond Ifremer UMR MARBEC (Marine Biodiversity, Exploitation and Conservation) Bd Jean Monnet, BP 171, 34203 Sète Cedex - France Tel: +33 4 99 57 32 61 Adresse secondaire: Station Méditerranéenne de l'Environnement Littoral (SMEL) 2 rue des Chantiers 34200 Sète Tel: +33 4 67 46 33 93

s-arnaud@univ-montp2.fr

NTNU Norway HerbariumEvolutionaryGenomics

The NTNU University Museum, Department of Natural History PhD position in Herbarium Evolutionary Genomics

The NTNU University Museum is seeking a highly qualified, ambitious, and motivated candidate for a PhD position in herbarium-based evolutionary genomics (genomic sequencing, population genetics, evolutionary genetics) in the Martin lab (www.ntnu.edu/employees/-mike.martin) at the Norwegian University of Science and Technology (NTNU, Trondheim, Norway). The position is for 4 years and available from 1 October, 2016.

The position The successful candidate will be a member of the Systematics and Evolution research group (SEG) at the Department of Natural History and will be advised by Associate Professor Michael D. Martin. The successful candidate will conduct his/her research in projects focusing on understanding the history and genomic basis of invasiveness in a plant system (Ambrosia artemisiifolia). The research will primarily involve computational analyses and labwork in an ancient DNA facility, although some fieldwork may also be necessary. The successful applicant will be expected to apply bioinformatic tools and population genetic analyses to genomic data generated from both historical and modern tissues. The ideal candidate will be motivated to perform laboratory work in addition to genomic analyses.

Qualifications Essential qualifications of the successful applicant: - A Master degree in bioinformatics, computational biology, population genetics, evolutionary biology, or closely related fields of biological research - Scripting/programming proficiency in at least one language (e.g. Python, Perl, R, bash)

Favorable qualifications of the successful applicant: - Previous experience in the analysis of Next-Generation Sequencing (NGS) data - Familiarity with UNIX command line - Experience with genomic laboratory work (e.g., NGS library building, in-solution hybridization, RAD/GBS)

Applicants must document excellent results from their education or through later research activity, be highly goal-oriented and able to deliver results on time. The successful applicant must fulfill the requirements of PhD students at NTNU. During the 4-year period, the successful candidate will spend 25% of working hours on duties connected to teaching, collection work, and public outreach for the museum.

As the project leader and collaborators are international, the position requires spoken and written fluency in the English language. Applicants from non-English-speaking countries outside Europe are encouraged to document English skills by an approved test. Approved tests are TOEFL, IELTS and Cambridge Certificate in Advanced English (CAE) or Cambridge Certificate of Proficiency in English (CPE).

Evaluation of candidates will focus on: - The Master thesis (or equivalent) - Scientific publications in peer-reviewed, international journals - Grades from relevant university-level courses - Statement/cover letter about how this position would fit career plan and interest of the applicant - An interview - References

Admission to PhD programs at NTNU require a Master degree (or equivalent) with at least 5 years of studies and an average grade of A or B within a scale of A-E for passing grades (A best) for the two last years of the MSc, as well as an average grade of C or higher of the BSc. Candidates from universities outside Norway are kindly requested to send a Diploma Supplement or a similar document that describes in detail the study and grade system and the rights for further studies associated with the obtained degree: ec.europa.eu/education/tools/diploma-supplement_en.htm.

Information about the working environment The NTNU University Museum, Department of Natural History has at the moment 16 faculty positions, 6 temporary research positions and 12 technical and administrative positions. The research is facilitated through two research groups: the Systematics and Evolution Group and the Conservation Biology Group. The Department cooperates formally with the NTNU Department of Biology and is also responsible for teaching biosystematics (systematics, taxonomy, biogeography, floristics, faunistics) at the university.

The University Museum is located in historic Trondheim, Norway's third most populous municipality. Nestled at the meeting of the Nidelva River and the Trondheim Fjord, the mountainous surrounding area boasts many opportunities for hiking, skiing, fishing, and other outdoor activities. Trondheim itself offers exciting activities for students as well as good connections to major European transport hubs. More information about Trondheim can be found here: en.wikipedia.org/wiki/Trondheim. Information about Norways consistent top placement in global quality-of-life rankings can be found here: oecdbetterlifeindex.org/countries/norway/.

Salary The PhD position follows code 1017, starting grade 50, gross NOK 435 500

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NTNU Norway LifeHistoryAndTelomeres

A PhD position is available at the Department of Biology at the Norwegian University of Science and Technology (NTNU) in Trondheim on the functional relationships between telomere dynamics, individual characteristics and life history traits in a small passerine bird, the House Sparrow (Passer domesticus). The Centre for Biodiversity Dynamics will host the position.

We are seeking a highly qualified candidate with a background in either evolutionary, behavioral or population ecology or eco-physiology. It is an advantage if the candidate has laboratory experience in genetic analyses.

The aim of the PhD project is to investigate central questions related to the functional associations between telomere dynamics, physiological variables, and how these are associated with trade-offs between life history traits such as growth rate, body size, reproduction and lifespan.

Here is the link to the formal announcement: https://www.jobbnorge.no/ledige-stillinger/stilling/127247/phd-position-in-evolutionary-ecology Application deadline is 15. August 2016. For further information contact: thor.h.ringsby@ntnu.no.

Thor Harald Ringsby <thor.h.ringsby@ntnu.no>

NTU Singapore HumanEvolutionGenomics

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

Possible research topics include, but are not limited to: - the contribution of developmental differences in gene expression to uniquely human traits - genetic mechanisms of local evolutionary adaptation in human populations - aetiology of heart disease in humans and the great apes - genetic diversity in great apes (in collaboration with the Singapore Zoo and the Lee Kong Chian Museum of Natural History)

All projects in the lab incorporate aspects of iPSC culture and experimental manipulation, genomics, and bioinformatics. Students will have the opportunity to be involved in both the tissue culture and data analysis aspects, and to contribute intellectually to the development of the project at all stages.

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

Start date: January 2017 or August 2017. Interested applicants will be able to join the lab a few months earlier as research assistants if desired.

Eligibility: The position is open to all applicants that meet NTU admission criteria, but note that the monthly stipend varies according to nationality. Note that GRE scores are not required for students that have an MSc or BSc from institutions in the USA or the UK.

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

International students are encouraged to apply for a SINGA scholarship (http://www.a-star.edu.sg/singa-award/Homepage.aspx), which includes one-time settlement and airfare allowances, and for a Nanyang President's Graduate Scholarship (only available for August 2017 admission) (http://admissions.ntu.edu.sg/graduate/scholarships/Pages/NPGS.aspx), which will significantly increase their monthly stipend.

igr@ntu.edu.sg

OhioStateU SpeciesDelimitation

The Carstens lab is looking for Ph D students to work on one of two projects:

i. Developing and testing methods for species delimitation with gene flow (in partnership with Laura Kubatko). This project could include collection of genomic data from nearly any focal system, along with methods development and evaluation.

ii. Conducting meta-analyses using phylogeographic data from thousands of species. This project would take advantage of a project in development in the Carstens lab to build tools to facility the meta analysis of phylogeographic data.

The Ohio State University has fabulous resources for graduate students, including college and university fellowships, a program for biologists that allows you to earn a minor in statistics, and extraordinary computational resources.

If you're potentially interested in these projects, please visit our website < http://carstenslab.org.ohio-state.edu/ > and send Bryan an email. Alternatively, track him or his students down at the Evolution 2016 Meeting in Austin.

Bryan C. Carstens Department of Evolution, Ecology, & Organismal Biology The Ohio State University 318 W. 12th Avenue Columbus, OH 43210-1293 web: http://carstenslab.org.ohio-state.edu blog: http://u.osu.edu/carstens.12/ Google Scholar twitter: @bryanccarstens skype: bryan_carstens office: 614.292.6587 cell: 734.474.8527 fax: 614.292.2030

Bryan Carstens <bryan.c.carstens@gmail.com>

Queensland FruitFlyEvolution

PhD scholarships - Macquarie University and CSIRO (Australia)

Closing Date: Expressions of interest close at midnight on 30 June, 2016

Three PhD opportunities are available on projects investigating pre-'and post-'copulatory sexual performance of Queensland fruit fly (Bactrocera tryoni, aka Qfly). Each of these projects is part of a significant collaboration between Macquarie Universitys Department of Biological Sciences and Australias Commonwealth Scientific and Industrial Research Organisation (CSIRO). Projects include:

(1) Polyandry and paternity patterns, (2) Mediation of mating-'induced sexual inhibition, (3) Genetics and genomics of reproductive fitness.

(1) Polyandry and paternity patterns

Molecular techniques will be used to assess multiple paternity and patterns of sperm use in natural and laboratory populations, and to identify male traits (e.g., size, age, rearing environment, experience, nutritional state) associated with paternity advantages under controlled environmental conditions. The host research groups have been working on Q-'fly mating behaviour, physiology, and reproduction for many years, and have access to a vast array of facilities and techniques in house and through collaboration. Existing knowledge and access to ample facilities provides an excellent platform for a motivated and imaginative student to advance this field through the adoption of diverse approaches and methods.

This project would be carried out under supervision of Prof Phil Taylor and Prof Michael Gillings of Macquarie University and Drs John Oakeshott, Ronald Lee and

Owain Edwards of CSIRO. The successful applicant would be based principally at Macquarie University in Sydney.

(2) Mediation of mating-induced sexual inhibition

Virgin female Qflies show high levels of sexual receptivity, but once mated they reject courtship attempts of subsequent males. Previous research has highlighted reproductive accessory gland fluids produced by males and passed with the ejaculate as key. This project will use a combination of genetics/genomics, biochemistry, and metabolomics approaches to identify the factors mediating mating-'induced sexual inhibition of female Qflies, to understand their production, and to determine their modes of action. Oakeshotts group at CSIRO has considerable experience investigating the biochemistry and genetics/genomics underpinning mating induced sexual inhibition and related behavioural changes in insects. This group has deep skills in metabolomics and proteomics, and have the in-'house state-'of-'the-'art facilities required for successful metabolomics and proteomics. Taylors group at Macquarie has carried out all of the research on mating induced sexual inhibition in this species to date, and comprises a large research community working on diverse aspects of Qfly behaviour and physiology.

This project would be carried out under the supervision of Dr John Oakeshott of CSIRO (with additional support from Drs Matt Taylor, Gunjan Pandey and Peter Campbell) and Prof Phil Taylor of Macquarie University. The successful applicant would be based principally at CSIRO in Canberra.

(3) Genetics and genomics of reproductive fitness

The purpose of this research is to identify the genetic basis of reproductive characteristics that drive mating performance of male Queensland fruit fly (e.g., pheromone composition, calling behaviour, reproductive effort, sperm transfer, ability to induce sexual inhibition in mates). The strategy for this research is to first identify the genes underlying these traits of interest, or genetic markers linked to these genes, using quantitative or association genetics methods. Once identified, this information can be used to understand the population genetic processes key to the implementation of the Sterile Insect Technique now in development for the control of Queensland fruit fly. A PhD project would be developed around traits that the project team has identified as being important in driving mating success, and would aim to quantify the level of variation in the trait, identify the genetic basis for this variation, and develop and test strategies to retain variation during domestication for subsequent selection experiments.

This project would be carried out under the supervision of Drs Ronald Lee, John Oakeshott and Owain Edwards of CSIRO and Prof Phil Taylor at Macquarie University. The successful applicant would be based principally at CSIRO in Canberra.

Ronald Lee <ronald.lee@mq.edu.au>

RKI Berlin dsDNAVirusEvolution

We are offering a PhD position (public sector wage scale TVoD grade E 13). The contract is limited to three years. The position will be available immediately.

Tasks and responsibilities: The applicant will be in charge of a research project consisting in the high-throughput genomic characterization of double stranded DNA viruses (herpesviruses, papillomaviruses and polyomaviruses) infecting wild bonobos, chimpanzees and gorillas. The applicant will use the data generated at the bench to reconstruct in silico the evolutionary history of many viral lineages in the hominine lineage and thereby extract local patterns of dsDNA virus evolution, e.g. investigate the co-divergence/cross-species transmission balance.

Profile: - Master degree in biology, medicine or veterinary medicine - Familiarity with basic molecular biology methods (nucleic acids extraction, PCR, Sanger sequencing, etc.) - Experience with next generation sequencing will be appreciated - Willingness to develop skills in bioinformatics and statistics; applicants having already developed such skills are especially looked for - Strong interest for ecology and evolution - Required language skills (CEFR-level): advanced knowledge of English (at least C1). Although no German skills are required, applicants will be encouraged to develop such skills to maximize their integration in our institute.

The applicant should have good planning capacities, appreciate independent work and be ready to adapt quickly to new situations. We expect applicants to have excellent communication skills and be motivated to integrate an international research group comprising people with very varied interests.

Applications should be submitted via the public service job portal Interamt at www.interamt.de by 26 June 2016. Please note the position identification number: 335774 (62/16).

For more information, please contact: Dr. Sébastien Calvignac-Spencer Robert Koch Institut Seestrasse 10, 13353 Berlin Telefon: ++49 30 18754 2502 E-Mail: CalvignacS@rki.de

"CalvignacS@rki.de" <CalvignacS@rki.de>

Spain 3 ForestAdaptiveEvolution

Within the frame of the Spanish MINECO grant 'FUTURPIN' (2016-2018, Adaptive framework for future management of genetic resources in Mediterranean pines), co-participated by three leading research institutions in their respective fields of expertise, we are searching for 3 prospective highly-motivated PhD candidates with interest in forest genetics and ecophysiology, plant-biotic interactions, evolutionary biology and climate change effects on terrestrial vegetation. We offer 3 four-year pre-doctoral grants associated to already ongoing projects carried out under the umbrella of FUTURPIN. Successful candidates will be based in one of the three research institutions: CSIC-MBG (Pontevedra), UdL (Lleida) and INIA-CIFOR (Madrid, coordinating institution).

The three projects aims together at bridging the gap between (i) the existing lack of knowledge on the genetic architecture of life history traits and how the environment explains the integration of phenotypic traits (ii) the design of strategies for the management of forest genetic resources pursuing the persistence of Mediterranean pine populations and the maintenance of intraspecific genetic diversity in the near future. The projects will study intraspecific variation in life history traits across populations in several Iberian pine species, aiming to progress in the understanding of different adaptive syndromes.

This is a preliminary call to contact interested candidates and facilitate interaction prior to the launch of the official call by the Spanish Science and Technology Agency (formerly known as FPI grants). We expect the call will be launched in summer 2016. The UdL grant will be covered by the hosting institution with conditions equivalent to a FPI grant.

Strong motivation, well founded analytical thinking and good oral and written communication skills in English are essential. Previous international experience is beneficial. Prospective candidates should send a short CV and motivation letter (max. one page) outlining their previous experience, why they are interested in this particular topic and by which project they are most attracted.

If interested please send CV and letter to José Climent (climent@inia.es), Rafael Zas (rzas@mbg.csic.es) and Jordi Voltas (jvoltas@pvcf.udl.es) as soon as possible, preferably before 15th July.

Details of the FPI funding scheme can be found in http://www.idi.mineco.gob.es/portal/site/MICINN/-?lang_choosen=en

Details about each project are as follows:

INIA-CIFOR: Project 1 deals with the evolutionary compromises between life-history traits and the real-time genetic change between generations deriving from differential fitness of the integrated phenotype. The PhD student will be co-supervised by Dr. José Climent (INIA-CIFOR) and by Dra. Rosario Sierra (ETSIA, Univ. Valladolid), in close collaboration with Dr. Ricardo Alía (INIA-CIFOR).

MBG-CSIC: Project 2 focuses on resistance and tolerance to biotic stress (herbivory) and on the reproductive temporal dynamics (masting) in Iberian pines, analysing their intraspecific genetic variation and the phenotypic and genetic relationships with the other life history traits addressed by the other subprojects. The PhD student will be supervised by Dr. Luis Sampedro and Dr. Rafael Zas at the MBG-CSIC (Pontevedra, Spain).

UdL: The PhD student will analyse the variability of intraspecific responses to the environment (driven by water scarcity) for several Iberian pines. He/she will collaborate to develop applications of emerging phenotyping technologies potentially useful in forest genetics. The PhD student will be supervised by Dr. Jordi Voltas in collaboration with Dr. Juan Pedro Ferrio (Universidad de Concepción, Chile).

Ample interaction among teams integrating FUTURPIN will be essential for the success of all PhD projects, and further collaborations with top scientists in forest genetics, ecophysiology and evolution worldwide will be strongly encouraged and facilitated.

An extended description of the groups' research activities can be found in:

wwwsp.inia.es/en-us/Investigacion/centros/CIFOR (Forest Ecology and Genetics Group, CIFOR-INIA)

www.genecolpines.weebly.com (Genetics and Forest Ecology Group, Misión Biológica de Galicia, MBG-CSIC)

www.medforlab.com (Research Group on Mediterranean Forests: Products, Ecophysiology and Adaptation, University of Lleida)

http://sostenible.palencia.uva.es/ Sustainable Forest Management Research Institute (University of

Valladolid-INIA)

José M Climent

Dpt. Forest Ecology and Genetics

INIA-Forest Research Centre

Ctra. A Coruña Km 7.5

Madrid 28040

Tel +34 91 347 6862

Jose M Climent <climent@inia.es>

TrinityC Dublin PlantGenomics

PhD Studentship in plant breeding/genetics (Ireland)

Walsh Fellowship Reference 2016014

Using next generation sequencing to track changes in the genomic composition of perennial ryegrass swards over time

We seek a highly motivated graduate who wants to gain a PhD in the area of genomics, working in collaboration with scientists at Ireland's leading agricultural research agency (Teagasc) and Ireland's leading university (Trinity College Dublin; TCD). This position is funded through the Teagasc Walsh Fellowship Scheme and will attract an annual tax-free allowance of euro22,000 to cover university fees and stipend.

What it's about: Perennial ryegrass is Ireland's most important plant species. It is used as forage, and underpins the livestock and dairy sectors. Perennial ryegrass swards are highly heterogeneous and can change over time in response to environmental variation and management practice. In order to gain a better insight into this phenomenon, we will monitor changes in the genetic composition of PRG swards over time. We will test whether these changes are random, or whether they can be related to management practices causing some plants to be preferentially selected over others. This will lead to a greater understanding of âpersistence'.

Where it's based: This studentship is based in the Forage Genomics Group in the Crop Science Department, at the Teagasc campus in Oak Park, Carlow; a vibrant market town about 50 mins south of Dublin. Oak Park is the national centre for tillage and bioenergy crops research, and the site incorporates a 239ha research farm with state of the art laboratory facilities for molecular biology (http://www.agresearch.teagasc.ie/oakpark/). This is an exciting opportunity to work in a professional multi-disciplinary environment where you will gain experience in genomics, computational biology and grasslands management from experienced scientists in the Forage Genomics group (Susanne Barth, Dan Milbourne) and Grasslands Science Department (Michael O'Donovan and Deirdre Hennessy) in Teagasc, and the Department of Botany at TCD (Trevor Hodkinson).

The ideal candidate: The studentship would suit someone with a primary (minimum BSc Hons, 2.1 or equivalent) or Masters level degree in life sciences, statistical genetics, and computational biology.

The PhD will involve lab-work, field-work and, importantly, it will have a strong computational biology/bioinformatics component. A full driving licence is a pre-requisite for the position, since it will require frequent visits to field trials located at Teagasc's Grasslands and Dairy Production Research Centre in Co. Cork.

Applications are invited immediately, with a view to starting in September 2016 or March 2017. The closing date for applications is 31 July 2016. Please apply by sending a CV and covering letter outlining your background and why you are interested in the post to either Dr Dan Milbourne (dan.milbourne@teagasc.ie) or Prof. Trevor Hodkinson (Trevor.Hodkinson@tcd.ie). Please put the reference number listed above in the subject line of your email to identify your email as being associated with an application for this post.

Trevor Hodkinson Associate Professor Botany / School of Natural Sciences Trinity College Dublin, the University of Dublin Dublin 2, Ireland +353 1 896 1128 Trevor.Hodkinson@tcd.ie https://www.tcd.ie/Botany/staff/ http://-people.tcd.ie/hodkinst https://scholar.google.com/-citations?user=3DOphAvBgAAAAJ&hl=3Den https:/-/twitter.com/TrevorHodkinson Trevor Hodkinson <HODKINST@tcd.ie>

UAntwerpen BirdParasiteEvolution

Our research group is looking for a PhD candidate for a project on evolutionary ecology of poultry mites Dermanyssus gallinae and related species. The project will combine an evolutionary ecological background with an applied focus on the role of D. gallinae as a poultry pest. The project will study the comparative ecology of mites in poultry farms and in wild bird nests; genetic and phenotypic variation in mites on poultry and various wild hosts; and ecological interactions between different Dermanyssus species in the wild. The research will be a combination of field experiments, lab experiments and molecular work (neutral genetic markers).

The candidate must be willing to submit a written application to the FWO/SB call for “strategisch basisonderzoek”. This call is open for basic research which should in the longer term lead to applications with economic added values. Application involves a 15-page project proposal submitted by 15 September, and a presentation for a jury. We will provide ample support for the candidate in both the writing and preparation of the presentation. If awarded the candidate receives a 4-year full scholarship of approximately 2.000€/month plus a bench fee, and will be enrolled in the Antwerp Doctoral School which provides free supplementary doctoral training. Our research group is a dynamic environments with multiple postdocs and PhD students studying ecology and evolution of vertebrates and their parasites (www.uantwerpen.be/eveco).

If you are interested please contact Erik Matthysen at erik.matthysen@uantwerpen.be as soon as possible, but at the latest before the 1st of August 2016.

Prof. Dr. Erik Matthysen Evolutionary Ecology Group University of Antwerp +322653464

New street address since 10 June 2016: Campus Drie Eiken room D1.32 Universiteitsplein 1, 2610 Wilrijk

Matthysen Erik <erik.matthysen@uantwerpen.be>

UBritishColumbia ConservGenetics

I am looking for a MSc student to join my research team at The University of British Columbia (Okanagan Campus) to take part in a conservation genetic study of western rattlesnakes, a species at-risk in Canada. This opportunity recently emerged and I am hoping to find a highly motivated graduate student to join the project in January 2017. The project offers opportunities for both laboratory and field-based research, and direct collaboration with researchers and managers from government and participating universities. Individuals with a population genetics background and strong analytical skills are especially encouraged to apply. Prior experience with molecular laboratory techniques and working in a field setting are desirable.

Visit the Ecological and Conservation Genomics laboratory website (http://people.ok.ubc.ca/mirussel/) for more information on our current research directions. Additional information about our Biology graduate program at UBC can be found at the following website: http://biol.ok.ubc.ca/graduate.html . To apply, send me via e-mail (michael.russello@ubc.ca) a CV, unofficial transcript, and contact information for at least two references.

Dr. Michael Russello, Associate Professor Department of Biology The University of British Columbia Okanagan Campus 3247 University Way, FIP346 Kelowna, BC Canada V1V 1V7 michael.russello@ubc.ca

michael.russello@ubc.ca

UCalgary GenomicsHostParasiteInteractions

*Genomics of a host-manipulating parasite

We are looking for an enthusiastic student with combined interests in genomics, parasitism, and ecology to research the molecular and ecological mechanisms that determine how larvae of an iconic manipulator (the brainworm Dicrocoelium dendriticum) modifies the behaviour of its ant intermediate host. The project is a collaboration between Dr. James Wasmuth (Univ. Calgary) and Dr. Cameron Goater (Univ. Lethbridge) based in Alberta, Canada.

The student will take a major role in sequencing and annotating the genomes of both infected ants and parasite larvae collected at different phases of host manipulation. The main aim is to utilize this model system to test the chemical-mediation hypothesis for the manipulation of host behaviour by parasites. The student will gain expertise in DNA sequencing, from the molecular biology of DNA sequencing, through to the bioinformatics tools that are used in modern genome analyses. The student will also have an opportunity to contribute to ongoing field-studies involving infected and uninfected ants at sites in southern Alberta.

The Wasmuth and Goater labs are members of the Host-Parasite Interactions (HPI) training program, which is a $1.6m investment by the Canadian Natural Sciences and Environmental Research Council (NSERC). The HPI program is made up eleven labs from three Canadian universities (www.ucalgary.ca/hpi). In addition to promoting close and integrative research links, the program offers students a wide range of opportunities, including career-oriented workshops, an annual training bootcamp in the Rocky Mountains, science engagement with the public, and travel scholarships.

The student should have completed a B.Sc. (or equivalent) in the life sciences with a strong academic record (e.g. GPA 3.6 in Canadian standards or 2i in UK). Experience in either a molecular biology or bioinformatics lab is a considerable advantage.

If you are interested, please send your CV, copy of your transcripts (unofficial is fine), and a brief letter explaining your motivation to undertake PhD-level inquiry. If you have any questions, please email James at: jwasmuth@ucalgary.ca.

"jwasmuth@ucalgary.ca" <jwasmuth@ucalgary.ca>

UCLouvain Belgium PlantHybridFitness

Fora good candidate with a MSc degree in evolutionary biology I have funding available for the first 15 months of a PhD position, starting in October 2016, to work in my group on the subject of fitness of natural hybrids between two Rhinanthus species (see Natalis & Wesselingh Oecologia 2012, Am J Bot 2012, Evolution 2013).

Theaim of the project is to study fitness in hybrids of known and unknown descent and link their performance to the composition of their genome. The work will involve field observations (plant size, pollinator behaviour, seed production), greenhouse work (hand-crossing plants) and genetic analyses using NGS techniques. UCLouvain is located in Louvain-la-Neuve, a small campus town in the French-speaking part of Belgium, at only 30 km from Brussels, Namur and Leuven.

Itwill be necessary to apply for another type of grant to get funding for the full 4-year PhD period, for which the first opportunity will present itself in September 2016 (and there will be two more opportunities after that before the first funding runs out). The net monthly salary is €1831 in the first year.

Agood candidate has: - a university degree in Biology, obtained within the last 7 years, that gives access to a PhD programme (so a 2-year MSc degree in Europe) - excellent study results - a passion for evolutionary ecology - good communication skills in English or French: the grant application process involves giving an oral presentation and answering questions on the project in front of a selection committee

Someknowledge of bio-informatics, especially on how to work with NGS data, would be very useful, but is not mandatory.

Ifyou are interested, please send me your CV (including a detailed listing of your study results and a short description of the subject of your MSc thesis) and motivation by email before 16 July 2016. I will select the best candidate by the end of July. Ideally, you are available at least part-time to assist in preparing the grant application during the month of August (the deadline for submission is around the 1st of September 2016), but this can be done at a distance as well, you do not have to come to Belgium for that.

Formore information, contact me by email at renate.wesselingh@uclouvain.be

Prof.Renate A. Wesselingh BiodiversityResearch Centre Earth& Life Institute UCLouvain Croixdu Sud 4-5, box L7.07.04 B-1348Louvain-la-Neuve Belgium

renate.wesselingh@uclouvain.be

UGdansk OrchidEvolution

Two PhD positions are open in 2016 to 2019 at the University of Gdansk, within an international network focusing on evolution of orchid symbiosis and metabolism, Orchidomics (funded by the Polish National Science Centre; Maestro7-NZ to M.-A. Selosse; 2016 to 2020).

Fields of interest and research objective: Prof. M.-A. Selosse's team is based in Brazil (Viçosa), France (National Museum of Natural History, MNHN-Paris) and Poland (Gdansk) and studies the ecology and evolution of mycorrhizal symbiosis, i.e. the association of plant roots with soil fungi, in tropical and temperate regions. The current project focuses on our special interest in mycorrhizae of temperate orchids and their role in plant physiology. In most cases, fungi provide soil minerals to the plant, in exchange for photosynthetic sugar. Yet, during orchid germination, the fungi provide carbon to germinating seedlings that have no reserve. Moreover, in some orchid species, adult plants also recover carbon from their fungi: some are achlorophyllous and non-photosynthetic (mycoheterotrophic species) while others are green and mix photosynthesis with exploitation of fungal carbon (mixotrophic species). We aim to study these various nutritional strategies (germination, adult autotrophy, mycoheterotrophy and mixotrophy) within several evolutionary and ecological frameworks, using metabolomic and transcriptomic approaches in situ. These original approaches open the way to a new integrated vision of plant biology and its evolution.

Research environment: The core team is at the Department of Plant Taxonomy and Nature Conservation, University of Gdansk (UG, Poland). Here, the Orchidomics team encompasses 5 full researchers, including one postdoctoral researcher working on bioinformatics. The PhD candidates, based at UG, will be part of the international network of renowned European scientific institutions involved in Orchidomics. This includes Adam Mickiewicz University in Poznan̄ (Prof. I. MakaÂ^{3}owska), the Faculty of Biotechnology of UG and the Medical University of Gdan̄sk (Prof. E. ojkowska), MNHN in Paris (Prof. M.-A. Selosse) and its Molecular Facilities (Dr. R. Debruyne), and the University of Fribourg (P.-E. Courty). After developing their respective skills, the PhD candidates may contribute as co-authors to other projects within this network and in Brazil. The PhDs include scientific training (internship) at MNHN or other universities of the network, and a cotutelle (joint PhD programme) will be considered upon request.

Position description: Orchidomics explores nutritional traits of orchids along ecological gradients and evolutionary diversification of terrestrial orchids, based on field sampling and using cutting-edge omics methods. The positions open will involve the candidate in field sampling and field data collection (as part of the team), generating transcriptomic or metabolomic data (on their respective samples), interacting with colleagues for bioinformatics analyses and paper writing.

PhD #1 will investigate how nutrition and physiology respond to abiotic conditions in situ throughout the orchid's lifespan. The candidate must have an interest in and basic knowledge of plant ecology and ecophysiology. The candidate will especially learn and develop metabolomic analyses, but will receive training in all omics.

PhD #2 will investigate the evolution of metabolism in taxa where mycoheterotrophy emerged. The candidate must have an interest in and basic knowledge of evolution and/or symbiotic interactions. The candidate will especially learn and develop transcriptomic analyses, but will receive training in all omics.

The PhD candidates will work together and with the team on a basis allowing first authorships for each of them. Candidates must have earned a Master's Degree in the life sciences. We value a background in molecular biology and an interest in team working. We require a good level of spoken and written English.

Duration: 3 years, from 01.10.2016 to 30.9.2019.

Salary: Competitive scholarship on the basis of local standards.

How to apply: Prepare a cover letter in English explaining your interest. Indicate which PhD (ecological or evolutionary focus, i.e. #1 or #2) you are applying for and why. Give the names and email addresses of two people with first-hand knowledge of your skills and past research experience. Add a curriculum-vitae (2 pages maximum). Send your completed application in a single pdf file to the principal investigator (ma.selosse@wanadoo.fr).

Call for applications open until the positions are filled. For full consideration, apply by July 10th, 2016.

Marc-André SELOSSE

Professeur du Muséum national d'Histoire naturelle, Paris Professeur invité aux universités de Gdansk (Pologne) & Viçosa (Brésil) Institut de Systématique, Evolution, Biodiversité (UMR 7205) CP 50, 45 rue Buffon, 75005 Paris, France

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UGeneva Switzerland ParasiteDiversity

*Graduate student position, University of Geneva, Switzerland, Master proposal: *

We are looking for a motivated student who is interested in carrying out a master project in Switzerland on parasites of European bullhead (*Cottus gobio*) and brown trout (*Salmo trutta*).

The aim of the project is to characterise parasite communities and unravel the genetic make-up of selected parasite species infecting European bullhead and brown trout. You will compare parasite diversity, infection levels and genetic structure of parasite populations infecting pairs of stream and lake fish populations. The study will be conducted in collaboration with researchers from the Natural History Museum of Geneva and the EAWAG research centre in Kastanienbaum.

If you are interested send us an email with a short letter of interest and a brief CV here <isabel.blasco-costa@ville-ge.ch>.

Isabel Blasco Costa Chargée de recherche T. +41 22 418 6387 F. +41 22 418 6301 isabel.blasco-costa@ville-ge.ch *isa.blasco.costa@gmail.com <isa.blasco.costa@gmail.com>*

Muséum d'histoire naturelle (MHN) Département de la culture et du sport route de Malagnou 1 1208 Genève (Switzerland) www.ville-geneve.ch Isa Blasco <isa.blasco.costa@gmail.com>

ULausanne EvolutionaryAdaptation

The Department of Ecology and Evolution, University of Lausanne, is currently inviting applications for 1 PhD position in Ecological and evolutionary responses to climate change in the group of Prof. Jake Alexander, starting 1^st September 2016 or soon thereafter. The position is funded through the ERC project "Novel interactions and species' responses to climate change" (NICH) for 3 years (1 year contract renewable for 2 additional years, at 100 %).

A great ecological challenge is understanding and predicting the responses of species, communities and ecosystems to global climate change. Progress will hinge on our ability to predict how responses are shaped by evolution and species interactions, and especially by entirely novel interactions among species whose ranges don't yet overlap. Within this project, we aim to test the ecological consequences of novel competitors for the persistence of alpine plant populations, and the potential for longer-term evolutionary responses to changing competitive environments. Furthermore, we will test the ability of functional traits to predict the outcome of novel competitive interactions, which will feed into process-based models of climate change range dynamics. The project will combine a range of experimental and modelling approaches, including whole community transplant experiments and competition experiments along an elevation gradient in our field sites in the western Swiss Alps.

We are seeking a highly motivated PhD student holding a Masters degree or equivalent in ecology, evolutionary biology or another relevant discipline, with a strong interest and expertise in evolutionary and ecological concepts, (experimental) field ecology and statistics. Excellent scientific writing skills in English, as well as a driving license, are also required.

The Department of Ecology and Evolution offers a diverse and stimulating working environment, and Lausanne a city with a high quality of living and ready access to cultural and recreational activities.

For further information please contact Prof. Jake Alexander by e-mail: jake.alexander@unil.ch

To apply, please submit a cover letter describing your research background and interests. Your application further includes a curriculum vitae and the contact information of two referees, all submitted as a single PDF file. Application review will begin on 1^st July 2016, and continue until the position is filled. Please send your application to: jake.alexander@unil.ch

Jake Alexander <jake.alexander@unil.ch>

UMaine EvolutionDiseases

PhD Position: Ecology and Evolution of Diseases (University of Maine)

Job Description:

A Ph.D. research assistantship is available through the Ecology & Environmental Sciences Program (http://umaine.edu/ees-graduate/) in the College of Natural Sciences, Forestry and Agriculture, School of Food and Agriculture at the University of Maine, Orono. The student will develop and conduct research on the ecology and evolution of infectious diseases in wildlife and domestic animals using genetic approaches. Research topics may include the investigation of: (1) eco-evolutionary drivers of transmission and spillover, (2) host-pathogen adaptation, (3) the genetic basis for heterogeneity in host susceptibility, and (4) disease transmission pathways using genetic data. This position will involve interdisciplinary research with strong field, laboratory and analytical components. Data collection may require international fieldwork (depending on the choice of research topic).

The student will have the unique opportunity to be part of the new interdisciplinary Center for One Health & the Environment (https://sbe.umaine.edu/school/center-for-one-health-the-environment/) and have the potential to collaborate with the UMaine Animal Health Laboratory (https://extension.umaine.edu/veterinarylab/).

Salary: $19,467 annual stipend, tuition waiver (up to 9 credit hours/semester, 1 credit hour in summer), 50% health insurance

Qualifications: Bachelor's degree in biology, ecology, evolution, microbiology, immunology, epidemiology, genetics, bioinformatics, or a related field. Preferred candidates will have a Master's degree or equivalent experience and be accomplished in writing, statistics, molecular methods, population/ phylogenetic analyses, and field skills.

How to Apply: Interested qualified applicants are encouraged to email a cover letter, CV/resume, unofficial transcripts, writing sample, and the names and contact information for three references to Pauline Kamath (paulinekamath@gmail.com).

Expected Start Date: January 17, 2017

Last Date to Apply: September 1, 2016

Pauline Kamath, Ph.D.

College of Natural Sciences, Forestry and Agriculture

School of Food and Agriculture

University of Maine, Orono

Email: paulinekamath@gmail.com

Pauline Kamath <paulinekamath@gmail.com>

UManchester EvolMolInnovation

The evolution of molecular innovation: how proteins gain and lose functions and interactions

Simon Lovell, David Robertson, Sarel Fleishman, Dan Tawfik https://www.findaphd.com/search/-ProjectDetails.aspx?PJID=75491&LID=1020 Detailed knowledge of the evolution of these interactions is important for understanding the evolution of function, if we are to engineer interactions for biotechnological and synthetic biology applications, and to understand how pathogens, particularly viruses, manipulate the host. In this project we propose a multidisciplinary approach to understanding the evolution or protein-protein interactions, combining tools from atomistic protein design, phylogenetic analysis, and in vitro selection.

Of key importance is the evolution of binding specificity, since change in specificity can lead to “rewiring” of interaction networks. The interfaces through which proteins interact, however, are complex, typically containing many amino-acid residues that collectively must contribute to binding specificity as well as binding affinity, structural integrity of the interface and solubility in the unbound state. The result is a complicated set of constraints on the evolution of protein structure and on the interactions made. Innovation therefore requires a set of evolutionary changes that maintain all of these characteristics for the entire chain of intermediates.

Funding is available for one studentship (fees and stipend), commencing September 2016. This studentship is supported by the University of Manchester and the Weizmann Institute of Science (Israel). The successful student would be required to spend 2 years in Manchester and 2 years in Israel. Only UK and EU applicants are permitted to apply; we expect candidates to hold (or be about to obtain) a minimum 2:1 Bachelors degree in a relevant subject.

Applications should be submitted online no later than 5pm Tuesday 14 June 2016: http://www.ls.manchester.ac.uk/-phdprogrammes/howtoapply/ David L Robertson, PhD www.manchester.ac.uk/ceb david.robertson@manchester.ac.uk

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UMassey Auckland YeastEvolutionGenomics

We are seeking an enthusiastic PhD student to join the Institute of Natural and Mathematical Sciences at Massey University, Auckland, New Zealand. The successful candidate will have the chance to work in a fast-growing interdisciplinary field on the interface of biology and computer science. You will make use of wet-lab as well as bioinformatics techniques to work on a joined project of the Schmeier and Pfeiffer labs on exploring the genotype-phenotype relationships in evolving yeasts from experimental evolution studies. You will learn about the newest computational and statistical means to analyse data from next-gen sequencing and other genomics technologies, and how to interpret these data from an evolutionary perspective.

The ideal candidate for this scholarship has experience in molecular biology techniques such as DNA/RNA extraction, sterile bench work, and biochemical assays; and experience in the analysis of next generation sequencing data, e.g. genome assemblies, SNP calling, RNA-seq data processing, comparative genomics, and statistics. Prior experience in working with yeasts and a strong background in evolutionary biology are of advantage, but not strictly necessary.

The studentship covers all university fees and includes an annual tax-exempt stipend of NZ$25,000 for three years.

Applicants must have a BSc(Hons) or MSc degree in a relevant discipline and the willingness to learn and apply new techniques and work in a team. Both local and international students are encouraged to apply. Non-native English speakers must satisfy the English Language Requirements of Massey University in order to be considered.

Massey University Auckland is located on the North Shore of Auckland, New Zealand, a city regularly ranked one of the most liveable in the world. This is your chance to experience the amazing Auckland lifestyle and the excitement of joining a vibrant young science team.

To apply for the position, please send a cover letter stating your interest in the position and why you think you would be a good candidate, a Curriculum Vitae, a copy of your academic transcript, and the names of two referees. Applications will be accepted until the position is filled.

Enquiries and applications to either Dr. Sebastian Schmeier (s.schmeier@massey.ac.nz) or Prof. Dr. Thomas Pfeiffer (T.Pfeiffer@massey.ac.nz). More information at: http://sschmeier.com and http://www.thomaspfeiffer.com pfeiffer.massey@gmail.com

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UMuenster 2 ProteinEvolution

Within the European Union Innovative Training Network (ITN) - Directed Protein Evolution for Synthetic Biology and Biocatalysis (ES-Cat) - the Bornberg lab at the University of Münster in Germany currently has available:

2 PhD-Positions in Molecular Protein Evolution (Biochemist/Molecular Biologist)

Project 1: Directed evolution starting from de novo proteins

The candidate will work on the de novo emergence and evolution of new proteins using candidate genes from comparative genomic data and their reconstructed presumed ancestors, with an emphasis on experimental characterization of biophysical properties and enzymatic functions of expressed proteins. This project shall lead to a completely new strategy for designing proteins with desired functions “from scratch” by using directed neutral drifts without the need for extensive screening of sequence space.

Candidates should have (or are about to obtain) a MSc or equivalent in Molecular Life Sciences, Biochemistry, Biology or Biotechnology (or relevant related discipline), and should have research experience in some of the following fields: molecular cloning, protein overexpression, protein characterization (in particular enzyme kinetic analysis), structural biology (protein crystallography or NMR).

Project 2: Evolutionary design of novel proteins/enzymes

The candidate will work on the evolutionary design of new enzymes derived from comparative genomic data and their reconstructed presumed ancestors. For the latter particular focus will be on those ancestors from which multiple enzymatic functions have evolved. This will lead to the characterization of a multi-trait fitness landscape and a new paradigm for the design of proteins and enzymes with hitherto inaccessible functional capacities.

Candidates should have (or are about to obtain) a MSc or equivalent in Molecular Life Sciences, Biochemistry, Biology or Biotechnology (or relevant related discipline), and should have research experience in some of the following fields: basic knowledge of bioinformatics (sequence analysis, phylogenies), molecular cloning, protein overexpression, protein characterization (in particular enzyme kinetic analysis), structural biology (protein crystallography or NMR).

General particulars for both positions

Both positions are part of an international, EU-wide consortium (ITN ES-Cat, http://www.bioc.cam.ac.uk/hollfelder/Research/es-cat, in the framework of Horizon 2020), including partners from Industry and Academia Elsewhere in Germany and in the United Kingdom, Belgium, Netherlands, Czech Republic and Israel (http://www.bioc.cam.ac.uk/hollfelder/Research/es-cat/partners). Participation entails extensive interactions with project partners and a comprehensive training program covering technical, scientific, interdisciplinary and communication skills.

At the time of recruitment by the University of Münster, the prospective candidates must not have resided or carried out their main activity (work, studies, etc.) in Germany for more than 12 months in the 3 years immediately prior to the reference date. Candidates that have more than 4 years of relevant work experience after their MSc are not eligible to apply.

The University of Münster is an equal opportunity employer and is committed to increasing the proportion of women academics. Consequently, we actively encourage applications by women. Female candidates with equivalent qualifications and academic achievements will be preferentially considered within the framework of the legal possibilities. We also welcome applications from candidates with severe disabilities. Disabled candidates with equivalent qualifications will be preferentially considered.

The salary will include social security and be composed of living and mobility allowances and a family allowance where appropriate, as outlined in the Marie-Curie Grant Agreement and Horizon 2020 - Marie SkÂ^{3}odowska Curie Actions Work-Program http://ec.europa.eu/research/participants/data/ref/-h2020/wp/2016_2017/main/h2020-wp1617-msca_en.pdf . For more information regarding the Bornberg lab visit www.bornberglab.org How to apply

Qualified candidates are invited to send an e-mail to Dr. Bert van Loo (b.vanloo@uni-muenster.de) or Prof. Erich Bornberg-Bauer (ebb.admin@uni-muenster.de) to which a 2-page pdf should be attached that includes in the following order and sorted starting by latest events: their personal data, scientific career, education, special relevant skills, list of publications, names of prospective referees and a short specific statement of research interests.

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UOldenburg SalpsandKrillBiodiversity

The working group Biodiversity and Biological Processes of polar Seas at the ICBM (Institute for Chemistry and Biology of the Marine Environment), Carl von Ossietzky University Oldenburg in Oldenburg, offers two positions:

3-year Scientist-position in Molecular biology (TVL-E13, 100%) (#1)

3-years PhD-position (TVL-E13/50%) in Molecular biology (#2)

within the project PEKRIS (The PErformance of KRIll vs. Salps to withstand in a warming Southern Ocean), funded by the BMBF (Federal Ministry of Education and Research) from July 1st 2016 to June 30th 2019.

The scientist candidate should perform the work on the tunicate Salpa thompsoni, whereas the PhD candidate should perform the work on Antarctic krill, Euphausia superba.

For detailed project information contact Prof. Dr. Bettina Meyer b.meyer@uni-oldenburg.de

Project aim: The overall goal of the Subproject 1 of the PEKRIS project (“Physiological and genetic traits of krill vs. salps supporting potential adaptation to a warming Southern Ocean”), are to understand the general principles of thermal adaptation of krill and salps defined by their genetic make-up. It is aspired to characterize the thermal window of krill and salps in the Southern Ocean in respect to important physiological life cycle functions (lipid accumulation and utilization, reproduction, growth metabolic activity). The goal of the transcriptomic approach is to identify differentially expressed genes which contribute to these important life cycle functions and new candidate genes of both species, which contribute to their plasticity and adaptation to temperature stress. We aim to identify gene clusters and networks, which define sensitivity and adaptability of both species from which almost no (salps) or only few (krill) essential functional transcriptomic information are available.

Profile of the Candidates: The successful candidates are expected to have an academic university degree (Master or Diploma) and hold a doctoral degree (Scientist position #1) or academic university degree (PhD position #2) in molecular biology, genetics, biology or marine biology. The Scientist candidate must be very well familiar with basic and advanced techniques to investigate cDNA-gene-expression-profiles in invertebrates, for example Real-Time-PCR (SYBR Green und TaqMan Chemie), TaqMan Low Density Arrays, next generation sequencing as well as bioinformatics, analysis and interpretation of next generation sequencing data, multi-variate statistic etc. The PhD candidate must be familiar with basic techniques in molecular biology (RNA isolation, qPCR, bioinformatics) on invertebrates. Both candidates should have skills in experimentation and maintenance of invertebrates. The international nature of the project requires fluency in spoken and written English and good presentation and publication skills. The successful candidates are embedded in the working group of Biodiversity and biological processes in Polar Seas, headed by Prof. Dr. Bettina Meyer. It is expected that both candidates work in close cooperation self reliably on this project. The position requires the ability to manage months-long research expeditions as well as expedition to our cooperative scientific partners at the AAD in Kingston, Tasmania.

The Carl von Ossietzky University Oldenburg is dedicated to increase the percentage of female employees in the field of science. Therefore, female candidates are strongly encouraged to apply. In accordance to Â§21 Section 3 NHG, female candidates with equal qualifications will be preferentially considered. People with disabilities will be given preference if equally qualified.

Please send your application for the specific position (Scientist position #1 or PhD position #2) including a cover letter with motivation, copies of your certificates, a list of your most relevant publications, a CV, and the names and addresses of two referees as a single pdf-file not exceeding 10 MByte via e-mail to Prof. Dr. Bettina Meyer (b.meyer@uni-oldenburg.de) or by mail to the ICBM office c/o Elke Hoxha (Elke.Hoxha@uni-oldenburg.de), Postfach 2503, D-26111 Oldenburg, Carl-von-Ossietzky-Str. 9-11. All applications must be submitted by July 30th 2016. Our ideal starting date would be October 1st 2016.

– Prof. Dr. Bettina Meyer Ecophysiology of pelagic key species Helmholtz Virtual Institute PolarTime

Section Polar Biological Oceanography Alfred Wegener Institute Helmholtz Centre for Polar and Marine Research bettina.meyer@awi.de Am Handelshafen 12 D-27570 Bremerhaven Building E, room 2340 phone: +49 (0)471 4831 1378 fax +49 (0)471 4831 1149

Professor, Biodiversity and Biological Processes in Polar Seas Institute for Chemistry and Biology of the Marine Environment (ICBM)

Carl-von-Ossietzky University b.meyer@uni-oldenburg.de Carl-von-Ossietzky-Straße 9-11 D-26111 Oldenburg Building W3, room 0-025 phone: +49 (0)441-798-3567 fax: +49 (0)441-798-3404

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UPadova Italy PenguinAdaptationGenomics

>>> REMINDER: Application deadline on June 17 2016, 1pm <<<

PhD position in population genomics and adaptation in penguins

We are looking for a highly motivated student interested in investigating the evolution of cold-adapted traits in the Emperor penguin using genomic, ecological and physiological data. The PhD position is provided by the Molecular Ecology group at the University of Padova (Unipd), Italy, but in close collaboration with the University of Ferrara (Unife), Italy, the Centre National de la Recherche Scientifique/University of Strasbourg (CNRS-UniStra), Strasbourg, France and the Centre Scientifique de Monaco (CSM), Monaco.

The PhD student will be part of a stimulating, international and interdisciplinary network, acquiring expertise on population and adaptation genomics at Unife/Unipd and on ecology and physiology, including proteomics, at CNRS/CSM. The candidate must of course be willing to spend a substantial amount of her/his working time at these different institutions. The PhD student will also have the opportunity for direct sampling experiences in Antarctic and sub-Antarctic territories.

The supervision of the student will be shared by Celine Le Bohec at CNRS/CSM, Emiliano Trucchi and Giorgio Bertorelle at Unife, and Leonardo Congiu and Lorenzo Zane at Unipd. Please contact us for further details on the different aspects of the project.

The position is for three years. The net monthly salary offered by the Italian PhD programme is ca. 1,000 Euros. Salary is increased by 50% during the time spent at non-Italian partners.

Please, submit online your application before June, 17, 2016 (1 pm local time) at the web address: https://pica.cineca.it/unipd/dottorati32/ ("Dottorati di ricerca XXXII ciclo - a.a. 2016/17 / Call for admission to the PhD Courses 2016/17"). Follow the instructions and, in the online application form, select the PhD Course in "Biosciences" and the curriculum in "Evolution Ecology and Conservation". Select the option with a scholarship but do not select any of the four available "temi vincolanti/research topics" at this stage. When preparing the cv to be uploaded in the system, start with a statement of interest where you specify the project you wish to apply to, that is "Genomics of extreme adaptations to life in the Antarctic". For more details, please check at http://dottorato.biologia.unipd.it/ < http://dottorato.biologia > under the list of potential research projects and supervisors for 2016, clicking on " Evolution, Ecology and Conservation " For further information on the application submission, please contact lorenzo.zane@unipd.it

Emiliano Trucchi <emi.trucchi@gmail.com>

UPorto ULisbon 12 Biodiversity

TWELVE SCHOLARSHIPS ARE AVAILABLE FOR THE BIODIV PhD PROGRAMME Call 2016-17 http://biodiv.pt/call-2016-17 The Doctoral Programme in Biodiversity, Genetics and Evolution (BIODIV), invites applications for 12 scholarships for the 2016-17 academic year.

Funded by FCT - Portuguese Foundation for Science and Technology, BIODIV is organized by the two largest Portuguese universities - University of Porto and the University of Lisbon - in partnership with CIBIO-InBIO (Research Center in Biodiversity and Genetic Resources/ Associate Laboratory) and cE3c (Centre for Ecology, Evolution and Environmental Changes).

The PhD Programme offers a variety of specialization options and the opportunity to work with leading scientists in an interdisciplinary research environment.

The call for applications is open between the 25 of May and the 25 of June, 2016.

Information about the programme and on 'How to apply' is available at BIODIV's website (http://biodiv.pt/call-2016-17).

Maria Sant'Ana

W: http://biodiv.pt/call-2016-17 E: applications@biodiv.pt T: + 351 252 660 411 F: + 351 252 661 780

duartenvg@gmail.com

USaskatchewan MammalLifeHistoryEvolution

Funded Ph.D. position on the energetics of mammalian life history variation.

I am currently advertising one Ph.D. student opening in my lab (www.lanelab.ca) in the Department of Biology at the University of Saskatchewan. Ideally the student will begin September, 2016, but a January or April, 2017 start date may also be feasible. A full stipend ($20k CAD/yr for 4 years) is guaranteed, but the successful student will be expected to apply for any funding for which they may be eligible (e.g., NSERC post-graduate scholarships for Canadian citizens, University of Saskatchewan scholarships for international applicants).

The Project: Energetics of life history variation in a wild hibernating mammal. Energetic tradeoffs (e.g., among growth, maintenance and reproduction) form the basis of life history evolution theory. Until relatively recently, however, it has been difficult to measure relevant energetic traits in the wild. As a result, empirical tests of life history tradeoffs are relatively rare. For the proposed project, we are looking for a Ph.D. student interested in taking advantage of recent approaches/technology (e.g., field respirometry, doubly-labeled water, body composition analysis) to test and advance life history theory. The study system is a fully-censused, long-monitored, population of Columbian ground squirrels. Individuals of this species hibernate for 8-9 months of the year, meaning that all energy acquisition and allocation to reproduction occurs in a short 3-4 month active season. We have been collecting detailed life history data from all individuals in a population in the Rocky Mountains of Alberta since 2003. We have also collected pilot data on resting and field metabolic rates, body condition and body temperature profiles during hibernation. These datasets will provide the foundation, upon which the student will be able to build with new data collection, to address their research questions. We have also been collecting data from additional populations, across varying elevations in the Rockies, providing an ideal opportunity to investigate energetics across an ecologically important environmental gradient.

Relevant literature:

- Dobson, F.S., J.E. Lane, M. Low and J.O. Murie. In Press. Fitness implications of seasonal climate variation in Columbian ground squirrels. Ecology and Evolution. PDF available upon request. - Fletcher, Q.E., J.R. Speakman, S. Boutin, J.E. Lane, A.G. McAdam, J.C. Gorrell, D.W. Coltman and M.M. Humphries. 2014. Daily energy expenditure during lactation is strongly selected in a free-living mammal. Functional Ecology 29: 195-208. - Lane, J.E., L.E.B. Kruuk, A. Charmantier, J.O. Murie and F.S. Dobson. 2012. Delayed phenology and reduced fitness associated with climate change in a wild hibernator. Nature 489: 554-557.

The successful applicant will have a GPA >80% (converted to the UofS 1-100 scale) over the past two years of schooling and a degree in a relevant discipline (i.e., Ecology, Evolutionary Biology, Physiology, Environmental Biology). All fieldwork will occur in Alberta?s Rocky Mountains and accommodation will be provided in the

Biogeoscience Institute (University of Calgary; http://wcm.ucalgary.ca/bgs/). A passion for fieldwork is a must, as are strong scientific communication skills (both written and oral) and statistical proficiency (or a willingness to gain it). Evidence of scientific productivity (manuscripts published or in preparation, conference attendance and presentation) is also expected. This position is open to both Canadian and international students.

If you are interested in applying, please submit a cv (including names and contact details of references), a short (1 pg) description of research interests and an unofficial copy of your transcripts to jeffrey.lane@usask.ca. Applications will be evaluated as they?re received. To ensure full consideration of your application, therefore, please submit asap. Any questions can be directed to Jeff Lane.

Thank you in advance for your interest in this position, however, only those selected for an interview will be contacted.

jeffrey.lane@usask.ca

"Lane, Jeffrey" <jeffrey.lane@usask.ca>

UToulouse HumanPaleogenomes

We invite applications for a PhD position funded by the Federal University of Toulouse (IDEX APR 2016) for 36 months at the University of Toulouse (France).

PhD studentship on Archaeology of social structures and family relationship by paleogenomic

Applications are invited for a three-year PhD fellowship in the field of Ancient DNA and Paleogenomics. The research program will be developed within the framework of a joint PhD program between the Molecular Anthropology and Image Synthesis lab of the University of Toulouse, France, led by Pr. Eric Crubezy, Nicolas Valdeyron, Traces laboratory, UMR 5608, University Jean Jaures, Toulouse, France. This collaboration will build on 1 / laboratory on ancient DNA of the UMR 5288, and on his CNRS researchers (http://amis.cnrs.fr/equipes/article/equipe-1) and L. Orlando (Copenhagen) IDEX funding in palaeogenomics for 4 years, we will benefit from his expertise. 2/ on the team of UMR 5608 Traces for everything culture, social modeling proposal, contextualization.

* Background*

Eurasian populations of the past 12,000 years lend themselves more easily to the new palaeogenomics techniques. So far the results have turned to the history of settlement, the paleogeniticians implying that these samples are representative of the people who lived at some point. This results in a lack of understanding of archaeologists and prehistorians who dig sites and who have demonstrated since 1980 on demographic data that funeral deposits are generally not representative of the natural mortality of the population.

Objectives

So we chose to study the relationship from genomic data in the two oldest collective burials known in Europe (3500 BC. J-C.), outstanding deposits by their conservation. Currently a thesis on paleogenetic study of these two burials and it appears that the diversity of paternal lines is very small and we favor the hypothesis burial clan patrilineal. We intend to go further in the study and our goals are: (i) clarify the genetic relationship; (Ii) quantifying the levels of consanguinity between individuals; (Iii) to decrypt the 'social' dimension of the Neolithic funerary. To answer these questions, we must go to the study, not a limited number of genetic markers, but that of the genome. The relationship will be assessed through about a million SNPs nuclear and analysis 'runs of homozygosity' (Identity By Descent) will allow us to quantify the level of consanguinity present in individuals analyzed. Individuals showing excellent preservation of DNA, and a small fraction of microbial DNA, will qualify as candidates for sequencing the entire genome at an average coverage of at-least 8X, to genotype all sites polymorphs present in the genome and to study the ancestry and the admixture of these subjects.

We are seeking a highly motivated, hard worker and productive student who is interested and capable of interacting and contributing to a research team consisting of archaeologists, molecular biologists, bioinformaticians, and evolutionary biologists. The ideal candidate will show great abilities to work in an international environment and strong expertise in computational biology, statistics, high-throughput sequencing, population genomics, and will be familiar with the most common tools used in molecular genetics.

Lacan M, Keyser C, Ricaut FX, Brucato N, Duranthon F, Guilaine J, Crubezy E, Ludes B. Ancient DNA reveals male diffusion through the Neolithic Mediterranean route.Proc Natl Acad Sci U S A. 2011 Jun 14;108(24):9788-91.

Lacan M, Keyser C, Ricaut FX, Brucato N, Tarrus J, Bosch A, Guilaine J, Crubezy E, Ludes B. Ancient DNA suggests the leading role played by men in the

Neolithic dissemination.Proc Natl Acad Sci U S A. 2011 Nov 8;108(45):18255-9.

Candidate Profile

S/he should have strong background in computational science for processing NGS data, performing mapping and identifying polymorphisms; in order to use software to analyze population genetics and relationships.

S/he should also be familiar with basic tools and concepts in molecular biology, particularly in molecular methods for generating large-scale sequence/SNP datasets. First-hand experience in the analysis of ancient DNA and/or High-Throughput-Generation Sequencing data will be considered positively.

Job description

The PhD student will be expected to: Manage and carry through his/her research project; Take PhD courses (equivalent to 30 ECTS); Write scientific articles as well as the PhD thesis; Participate in scientific meetings; Teach and disseminate research; Key criteria for the assessment of candidates; A master's degree related to the subject area of the project, at the time of the employment; The grade point average achieved; Professional qualifications relevant to the PhD program; Relevant work experience.

Language skills (the applicant must be fluent in English; as a

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UWageningen LivebearingFishEvolution

UWageningen_Netherlands.LivebearingFishEvolution

PhD position Wageningen University (The Netherlands): Life history evolution in livebearing fish

A PhD position is available in Bart Pollux's research group in the Experimental Zoology group, Department of Animal Sciences at Wageningen University, the Netherlands. The aim of this project is to study life history evolution in natural populations of ecologically divergent live-bearing fishes in Costa Rican rivers. The project will quantify the relationships between local environmental conditions and reproductive strategy (placentation, superfetation, polyandry). This will then be linked to the fish's physiological performance and fitness during gestation. This project will use an integrated approach to life history evolution in natural populations that focuses on ecological field studies and common garden studies to quantify heritability of LH traits. Depending on the student's interest the project can be extended to include e.g. geometric morphometrics, physiological performance studies (metabolic rate, fast-start escape, sustained swimming ability) and muscle structure/function (immunohistochemistry, qPCR). The PhD candidate will join a team of four other PhD students led by Dr. Pollux that studies the evolution of reproductive adaptations in livebearing fish. The current project will take place in close collaboration with Dr. Andrew Furness (University of California Irvine, USA).

Requirements

For this interdisciplinary project we look for an enthusiastic, result-driven person with an excellent MSc degree in biology (evolutionary ecology, population ecology, life history evolution), experience with fieldwork (preferably in the tropics) and a proven interest in evolutionary questions. The candidate should have excellent research and communication skills, be creative and independent (yet at the same time a team player) and be proficient in English (both oral and written). Experience with Matlab (modeling) and SAS or R (statistics) and the ability to speak Spanish are considered an additional advantage. OVERSEAS APPLICATIONS ARE ENCOURAGED.

Conditions of employment and additional information

We offer a fully funded 4-year PhD position (1.0 FTE) to undertake research on life history evolution in livebearing fish within the Experimental Zoology group at the Animal Science Department of Wageningen University, the Netherlands. Initially, we offer a temporary position for a period of 1.5 year, with an extension of 2.5 years after successful performance. Gross salary per month is very competitive, increasing from euro 2.174,- in the first year up to euro 2.779,- in the fourth year, for a fulltime appointment. This position is financed by a Vidi grant from the Netherlands Organisation for Scientific Research (NWO) awarded to Dr. Pollux. For further information, please contact Bart Pollux (bart.pollux@wur.nl; http://www.bartpollux.nl). The application deadline is Wednesday 6 July 2016. The preferred starting date is 1 September 2016 (negotiable). Applications should include a letter of motivation, CV and names of three references. Please send application materials directly to bart.pollux@wur.nl.

Bart Pollux <b.pollux@gmail.com>

UZurich BiologicalInvasions

PhD Studentship in Evolution/Evolutionary ecology

Project title: Understanding invasions - from the genetic basis to the ecological dynamics of spreading populations

The position is located in the Altermatt lab and the Wagner lab at the Department of Evolutionary Biology and Environmental Studies (IEE) of UZH and the Department of Aquatic Ecology of Eawag.

The University of Zurich (UZH) is one of the leading research universities in Europe and offers the widest range of study courses in Switzerland.

Eawag, the Swiss Federal Institute of Aquatic Science and Technology, is an internationally networked aquatic research institute within the ETH Domain (Swiss Federal Institutes of Technology).

Biological invasions are among the biggest threats to natural ecosystems. Unfortunately, the causes of invasions remain elusive, due to the large spatiotemporal scales involved and the poor integration of macroecology and evolutionary biology. Additionally, we lack an integration of ecological and evolutionary theory with experimental data. In this project the doctoral researcher will conduct laboratory invasion experiments, using the model organism Tetrahymena thermophila in miniaturized landscapes suitable to study macroecological and evolutionary dynamics (Giometto et al. 2014 PNAS, Altermatt et al. 2015 Methods Ecol. Evol., Fronhofer & Altermatt 2015 Nature Comm.), in order to track and understand the resulting eco-evolutionary dynamics from genes to populations. During these invasions, Tetrahymena undergoes evolutionary adaptations that alter its ability to invade which affects the ecological invasion dynamics. Whole genome sequencing and computational analyses of sequence data will reveal the genomic basis of observable phenotypic changes of invading organisms. The experimental findings will be integrated into a consistent theoretical eco-evolutionary framework using mathematical models and agent-based simulations. This interdisciplinary and synthetic project will promote our causal understanding of invasions and range dynamics.

Competitive applicants will have previous experience in evolutionary ecology, molecular ecology or evolutionary biology. They will have substantial programming skills and optimally experience in analyzing high-throughput sequence data. Excellent experimental skills are a must. A background in modeling is a plus. Candidates will be highly motivated, enthusiastic and independent persons with a passion for science. Excellent communication and writing skills in English, good work ethics, and creative thinking are desired. A Masters level degree (or equivalent) is necessary for admission. The working language is English.

The project will be co-supervised by Prof. Dr. Florian Altermatt, Prof. Dr. Andreas Wagner and Dr. Emanuel Fronhofer. The project will be based at University of Zurich and at Eawag. Zurich offers a stimulating and international research environment, excellent research facilities and a lively and social working place. The position will be for a period of four years, and should start in January 2017 or soon thereafter. The PhD student will be enrolled at University of Zurich and be part of the PhD Program in Evolution.

The project is financed by the University of Zurich Research Priority Program "Evolution in Action" (http://www.evolution.uzh.ch/en.html).

For further information, consult

Altermatt lab: http://homepages.eawag.ch/~altermfl/Home.html Wagner lab: http://www.ieu.uzh.ch/wagner/ or directly contact

Prof. Dr. Florian Altermatt, E-mail: florian.altermatt@eawag.ch or

Prof. Dr. Andreas Wagner, E-mail: andreas.wagner@ieu.uzh.ch

University of Zurich and Eawag offer a unique research and working environment and are committed to promoting equal opportunities for women and men. Applications from women are especially welcome. Applications must be submitted by 15 August 2016.

We look forward to receiving your application. Please submit your application including a motivation letter with a description of pertinent experience, a complete CV (incl. publication list), the names (with e-mail addresses) of three academic references, and copies of certificates of academic qualifications via the Eawag Jobs & Career webpage, any other way of applying will not be considered. This link https://apply.refline.ch/673277/0445/pub/1/index.html will take you directly to the application form.

Prof. Dr. Florian Altermatt Department of Evolutionary Biology and Environmental Studies, University of Zurich, Winterthurerstr. 190, CH-8057 Zurich, Switzerland. Alternative Address: Eawag: Swiss Federal Institute of Aquatic Science and Technology, Department of

Aquatic Ecology, ÃÅ“berlandstrasse 133, CH-8600

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UZurich EvolutionHIV

PhD position: Evolutionary epidemiology and immunology of HIV (University of Zurich)

We are looking for a highly motivated PhD-Student on a project at the interface of evolutionary biology, immunology, and infectious-disease epidemiology. The project combines computational modeling with the analysis of complex clinical and immunological data in order understand HIV transmission and its adaption to the immune system. Accordingly, the candidate should have in addition to a strong computational background, skills to deal with complex and diverse data, and a strong interest in infectious-diseases and evolution. The PhD student will carry out his project in the context of the University of Zurich's Research Priority Program "Evolution in Action: From Genomes Ecosystems" (http://www.evolution.uzh.ch/en.html) and the Swiss HIV Cohort Study (www.SHCS.ch). These collaborations represent the ideal setting for this project since they provide the necessary evolutionary and clinical background. The student will work on a range of specified research projects, but will also be highly encouraged and expected to develop and investigate his/her own research questions.

The applicant should hold a Masters degree in a discipline relevant to the project (e.g. Evolutionary Biology, Epidemiology, Statistics, Mathematics, Biomedical Sciences, Physics, Computer Science). The PhD will take place within the PhD-Program Evolutionary Biology of the Life Science Zurich Graduate School (run jointly by the University of Zurich and the ETH Zurich). Research will be conducted at the Division of Infectious Diseases at the University Hospital of Zurich; University of Zurich (supervision: Roger Kouyos). The Division of Infectious Diseases provides a highly interdisciplinary and translational research environment with links both to clinical practice and basic science. Moreover, we are strongly interconnected with a variety of other research institutes in Zurich and beyond. In particular, we maintain strong collaborations with the Institute of Medical Virology at the University of Zurich, and the Institutes of Theoretical Biology and Computational Biology at the ETH Zurich.

Applicants should send a cover letter, a detailed CV, and contact information for two or three academic references to: roger.kouyos@uzh.ch.

Roger Kouyos <roger.kouyos@gmail.com>

UZurich Multiple EvolutionaryGenomics

Several PhD position at the University of Zurich

URPP Evolution in Action: From Genomes to Ecosystems http://www.evolution.uzh.ch/en.html offers about 10 new PhD position starting around 1 January 2017.

The deadline is 1 July, so please apply quickly through PhD program of Evolutionary Biology of Life Science Graduate School Zurich. http://www.evobio.uzh.ch/en.html The program offers interdisciplinary researches integrating evolution, next generation sequencing and medicine.

Prof. Dr. Kentaro K. Shimizu, Chair of Evolutionary and Ecological Genomics Department of Evolutionary Biology and Environmental Studies University of Zurich Winterthurerstrasse 190, CH-8057 Zurich, Switzerland E-mail: kentaro.shimizu@ieu.uzh.ch Direct phone +41 44 63 56740 Secretary phone +41 44 63 54970 (Ms. Nicole Zweifel, Mon, Wed, Fri, nicole.zweifel@ieu.uzh.ch) FAX +41 44 63 56821 http://www.ieu.uzh.ch/en/staff/professors/shimizu.html Video by Science Channel of JST (Caption in English, spoken in Japanese) http://sciencechannel.jst.go.jp/Q150001/detail/Q150001001.html Interview by National Geographic (in Japanese): http://natgeo.nikkeibp.co.jp/nng/article/20150304/437906/ Kentaro SHIMIZU <kentaro.shimizu@ieu.uzh.ch>

UZurich OrchidEvolution

PhD Position Genomics of early-evolving reproductive barriers in orchids

A PhD position is open for a highly motivated student with a keen interest in plant evolutionary genomics, population genetics and bioinformatics/statistics. The project seeks to understand the genomic and molecular basis of pollinator-mediated reproductive isolation and ecological speciation between sexually deceptive orchids of the genus Ophrys. In particular, the successful candidate will analyse the extent of linkage, clustering and phyical interaction among candidate loci under pollinator-mediated selection. To do so, s/he will produce high-quality genome assembly and annotation data for the study organism using state-of the-art tools and technology to enable the population genomic study of the architecture of traits controlling pollination. This will involve the integration of genomic with various phenotypic and Omics data sources. Potential field/research stays in the Mediterranean can be accommodated in the project. For background information on the study system, please see e.g. Schlüter & Schiestl (2008, Trends Plant Sci.) and Sedeek & al. (2013, PLoS One; and 2014, Mol. Ecol.).

The ideal candidate should be highly motivated and able to articulate her/his motivation for this project clearly. S/he should be well organised, with a thorough understanding of evolutionary biology, population genomics and molecular biology, and would ideally have an interest in orchid pollination. The candidate is expected to be proficient in statistical data analysis, with a good working knowledge of R and proven experience in bioinformatics, ideally with an ecological genomics background. Programming/scripting skills in other languages are an advantage. Since the student will have to prepare libraries for Illumina sequencing, laboratory skills are necessary; previous field experience is a plus. Proficiency in English and good communication skills are essential, as is a completed MSc degree (or equivalent) in biology or a related discipline, and the proven ability to carry out research independently. The candidate will be enrolled in the Life Science Zurich Graduate School (LSZGS) programme in Evolutionary Biology (www.evobio.uzh.ch/en.html) and therefore must be eligible to undertake a PhD at the University of Zurich (UZH). In particular, a recognised Masters certificate (or equivalent) must be produced prior to the start of the project.

We offer a 4-year PhD position at the University of Zurich, Switzerland, at a competetive salary (>45 kCHF/year before tax) funded by the Universitys Research Priority Programme Evolution in Action. The student will be a member of two collaborating labs at the Botanical Institutes (www.systbot.uzh.ch and www.botinst.uzh.ch), located in the beautiful Botanic Gardens and within walking distance of Lake Zurich. The successful candidate will work in a young, active, interdisciplinary and stimulating environment and will have access to state-of-the-art tools and techniques.

Your application should consist of a letter of motivation (1-2 pages), your CV and (if applicable) publication list, and the names and e-mail adresses of three academic referees. The letter of motivation should detail why you are personally interested in the project, why you find it relevant and why you think you are well-suited to undertake it. Please send your application (or any requests for further information) electronically to Dr Philipp Schlüter (philipp.schlueter at systbot.uzh.ch) as a single PDF file. Screening of applications will begin immediately and continue until the position is filled. The start date is 1st of January 2017.

Philipp Schlueter <philipp.schlueter@systbot.uzh.ch>

WesternSydneyU MetabolismEvolMammals

Opportunity for postgraduate students in animal physiological and evolutionary ecology at the Hawkesbury Institute for the Environment, Western Sydney University

Header: WesternSydneyU. MetabolismEvoEcology-Mammals

Project: How does resting metabolic rate interact with environmental conditions to affect the energetic performance, survival and reproductive success of small mammals?

Research Leader: Dr Christopher Turbill, Hawkesbury Institute for the Environment, Western Sydney University

Project Description: We seek outstanding research students to join our group and lead projects that make use our unique modal study system, well-equipped laboratory and outdoor experimental facilities to determine the ecological function and evolutionary drivers of variation in the resting metabolic rate of small mammals. We have developed an innovative approach that combines artificial selection on resting metabolic rate with ecological experiments in field enclosures. Our selective breeding experiment has established replicated populations of mice with contrasting metabolic phenotypes. An exciting opportunity is now available to lead projects that use these selected mice populations to test predictions about i) the genetic and physiological causes underpinning these different metabolic strategies, and ii) the ecological consequences of these different phenotypes under manipulated conditions using semi-outdoor and large wild foraging enclosures. These projects would allow students to conduct unique field experiments to address questions at forefront of research in physiological and evolutionary ecology.

To Apply: Interested applicants should send a CV, academic transcript and a brief summary of their research interests to c.turbill@westernsydney.edu.au

Applications will be assessed as they are received. Students (domestic or international) with a high level of relevant qualifications, research experience and enthusiasm will be invited to apply for a Higher Degree Scholarship from Western Sydney University. To rank highly, students will need to have completed a Masters by Research (or international equivalent), first class Honours (domestic students) and at least one publication or extensive research experience.

Expressions of Interest for Higher Degree Scholarships at Western Sydney University < http://www.uws.edu.au/graduate_research_school/grs/scholarships/main_round_scholarships > close - 9th October 2016.

Benefits: Students that secure a scholarship (with the potential of fee waiver for high-quality international students) can apply for top-up funding to support living expenses, research costs, and conference attendance. Students will also enjoy the logistical, academic and social benefits of working in a very active, research-focused and internationally diverse institute within Western Sydney University. The Hawkesbury Campus (Richmond, NSW) is located at the foot of the Blue Mountains on the western outskirts of Sydney, Australia.

Dr Christopher Turbill Hawkesbury Institute for the Environment Western Sydney University Contact: +61 (0)2 4570 1456

C.Turbill@westernsydney.edu.au

Jobs

ArizonaStateU BioinformaticsSoftwareEngineer

URL: http://cartwrig.ht/jobs/2016/05/31/Software-Engineer/ The Cartwright Lab at Arizona State University is looking for a Software Engineer to be part of a team developing software related to bioinformatics and phylogenomics. To apply visit http://links.asu.edu/job-23154BR . (Job ID is 23154BR.) The closing date is June 10th at 3PM Arizona Time.

A full ad follows.

Requisition ID: 23154BR Job Title: Associate Scientific Software Engineer Salary Range: $51,100 - $60,000 per year; DOE Close Date: 10-June-2016

The Biodesign Center for Personalized Diagnostics is seeking an Associate Scientific Software Engineer to perform professional work in the research, design, development, implementation and maintenance of scientific software applications.

Essential Duties

- Designs, develops, implements, tests, documents and maintains scientific and engineering software applications. - Analyzes and writes software functionality requirements, designs specifications, manuals, and user guides. - Interacts, trains, and works with users on how to use software and solve problems. - Distributes developed software to the scientific community as necessary. - Analyzes project specifications and creates project sub-tasks and implementation schedules. - Reviews, modifies, and rewrites existing software to optimize it or adapt it to fit new requirements. - Coordinates the activities of subordinates; trains and instructs other personnel; leads, directs, checks, and integrates the work of others. - Researches, evaluates, and implements third-party products and vendor applications.

Minimum Qualifications

Bachelor's degree in Computer Science or related field 3-years prior experience developing software in a research environment; OR any equivalent combination of experience and/or education from which comparable knowledge, skills and abilities have been achieved.

Desired Qualifications

- Demonstrated knowledge of relevant software engineering practices and design methodologies - Demonstrated knowledge of principles, practices, developments, and techniques used in systems analysis and applications programming - Experience in designing and implementing software applications - Experience in analyzing pre-existing software to identify and resolve complex problems - Evidence of effective communication skills (orally and writing) with the ability to convey technical issues

Working Environment

- Activities are performed in an environmentally controlled office setting subject to extended periods of sitting, keyboarding, and manipulating a computer mouse - Frequently required to stand for varying lengths of time and walk moderate distances to perform work - Occasional bending, reaching, lifting, pushing and pulling up to 25 pounds - Regular activities require ability to quickly change priorities which may include and/or are subject to resolution of conflicts - Communicate to perform essential functions - Use equipment such as calculator, telephone, computer (monitor, keyboard and mouse), printer, fax, and copier

Department Statement

The Biodesign Institute addresses today's critical global challenges in healthcare, sustainability, and security by developing solutions inspired from natural systems and translating those solutions into commercially viable products and clinical practices.

The Center for Personalized Diagnostics is a research center within the Biodesign Institute that focuses on personalized medicine. Promising advances in the area of personalized medicine have shown us that life-threatening diseases are as distinct in character as the individuals they afflict. The Virginia G. Piper Center for Personalized Diagnostics has been established with an eye toward overcoming the health care challenges posed by disease variance. Our Center is developing new diagnostic tools to pinpoint the molecular manifestations of disease based on individual patient profiles. The strategy promises not only to improve therapeutic care, but also to greatly reduce treatment costs by allowing for early disease detection.

ASU Statement

Arizona State University is a new model for American higher education, an unprecedented combination of academic excellence, energy and broad access. This New American University is a single, unified institution comprising four differentiated campuses positively impacting the economic, social, cultural and environmental health of the communities it serves. Its research is inspired by real world application blurring the boundaries that traditionally separate academic disciplines. ASU serves more than 90,000 students in metropolitan Phoenix, Arizona, the nation's fifth largest city. ASU champions intellectual and cultural diversity, and welcomes students from all fifty states and more than one hundred nations across the globe.

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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

Australian NatlU ResOfficer ReptileDiversity

A research officer position is available in the Moritz lab at the Australian National University. The appointee will join a team employing a mix of phylogenomics, spatial modelling and phenotypic analyses to document and understand reptile diversity in the Australian tropics. Applicants should have strong skills in quantitative analyses using R and a background and relevant graduate degree in evolutionary biology. Field experience would be an advantage. Applications close June 12, 2016 and should be submitted via the ANU (jobs.anu.edu.au). Enquiries are welcome and should be sent to Craig Moritz (craig.moritz@anu.edu.au). For further details please see: *http://jobs.anu.edu.au/cw/en/job/508870/research-officer Craig Moritz Research School of Biology & Cntr for Biodiversity Analysis Australian National University +61 2 6125 5651 (CM office) +61 2 6125 9492 (via Claire, M-W am only)

gekkojessie@gmail.com

CarnegieInst PlantEvolutionaryBiol

Re: New Staff Associate Position Available at Carnegie Institution for Science, Department of Plant Biology, Stanford, CA

Dear colleagues,

We are seeking an exceptional, early-career scientist (recent PhD/early postdoctoral) in the field of computational biology for the position of staff associate. The candidate should have the creativity, tenacity and discipline to explore original and innovative ideas. We are seeking a colleague who has, through unconventional research, a potential to create new fields and/or revolutionary technologies. We expect the new member to interact synergistically with department faculty while developing an independent research program. Candidates should have a Ph.D. in the natural or physical sciences, computational biology or engineering, and research interests relevant to plant biology. We will provide a supportive environment for five years, with the expectation that following this period the staff associate will be recruited as a mid-career investigator in academia, government or industry. Scientists with an interest in evolutionary problems or multi-scale modeling are especially encouraged to apply. Candidates should submit a CV, a list of 3 referees, and a 3-page research statement that includes a description of their major contributions to science and future research plans, no later than September 2, 2016. Submission must be done online (https://jobs.carnegiescience.edu/jobs/staff-associate-position/).

Carnegie Institution for Science is a private, nonprofit organization for scientific discovery, founded by Andrew Carnegie in 1902 and intended to be home to exceptional individuals at the cutting edge of their fields. Today, the Carnegie Institution hosts six departments in strategically located settings, which cover a broad spectrum of natural and physical sciences ranging from astronomy, developmental biology, genetics, plant science, global ecology, astrophysics and geochemistry. Carnegie's Department of Plant Biology is located on the Stanford University campus and we interact closely with members of Biology, Chemistry, Engineering and Medical School departments. Our faculty focus on a wide range of questions at the core of plant biology (https://dpb.carnegiescience.edu/). Carnegie is an equal opportunity employer.

Seung Yon (Sue) Rhee Carnegie Institution for Science, Plant Biology Department Website: https://dpb.carnegiescience.edu/labs/rhee-lab Lab twitter: @SueRhee2 Department website: https://dpb.carnegiescience.edu/ Department twitter: @CarnegiePlants Department facebook: https://www.facebook.com/carnegieplantbio/ "Rhee, Sue" <srhee@carnegiescience.edu>

CIRAD Reunion PlantDiversity

Cirad - PVBMT lab - Réunion - Researcher in Plant Community Ecology

Cirad, the French agricultural research and international cooperation organization working for the sustainable development of tropical and Mediterranean regions, invites applicants for a permanent position as researcher in plant community ecology. The successful applicant is expected to join the 'Plant Communities and Bio-Invaders in Tropical Environments' lab (PVBMT) in Réunion. PVBMT lab participates in several international programs in island biology and invasion ecology aiming at understanding how the diversity of plant communities and biotic interactions vary along elevation gradients through permanent monitoring systems.

The successful applicant will sustain active research with teams involved in the measurement and monitoring of species diversity and community structure. He/She will develop innovative approaches to analyse the ecological and evolutionary mechanisms that explain the structure of plant communities, from existing field surveys at a regional and transoceanic scale. He/She will conduct experimental studies of plant functional and life history traits both in the field and in controlled conditions (in situ and ex situ). This approach, based on comparative biology will be used to interpret the responses of plant communities to the introduction, naturalisation or invasion of non-native species. He/She is also expected to collaborate with public and private stakeholders in conservation programs such as habitat restoration, invasive alien species management and native species propagation.

Place: France (Montpellier), and then Réunion. Note that Cirad researchers are generally expected to develop their career in several places including developing countries.

Pre-requisites: PhD in population biology, evolution and/or ecology; an excellent academic level in terms of publications and international scientific exchanges in the field of ecology; prior post-doctoral experience, preferably in an overseas tropical environment would be appreciated. Solid conceptual knowledge of population ecology and evolutionary biology, methodological expertise in experimental ecology and related statistical analysis, and experience in the treatment of wide-ranging data sets concerning diversity and the distribution of plant populations. Expected qualities include expert knowledge of, and an interest in, biological conservation, together with the ability to work in a team and in partnership with stakeholders working in the field. Important parts of the job require French speaking, reading and writing.

Contact: samuel.nibouche@cirad.fr, olivier.flores@cirad.fr

Applications online at http://www.cirad.fr/en/jobs/-vacancies/researchers/plant-community-ecologist up to July 27th, 2016.

Reference to mention: 2474

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Virginie Ravigné Chercheuse CIRAD - Département BIOS - UMR PVBMT Pôle de Protection des Plantes Station Ligne Paradis 7 chemin de l'Irat 97410 Saint Pierre +262 262 49 92 24 +262 692 33 18 89

Virginie RAVIGNE <virginie.ravigne@cirad.fr>

CornellU LabTech environmentalDNA

Title: Lab manager/tech for freshwater & coastal ecology/evolution David Lodge's new laboratory in the Department of Ecology and Evolutionary Biology at Cornell University seeks a lab manager who will also contribute significantly to the technical work of the lab. The Lodge Lab will conduct research in the ecology of global freshwater and coastal marine ecosystems, with a current focus on applying environmental DNA (eDNA) analysis to the characterization of communities and populations of species of conservation relevance.

The Lodge Lab manager should have strong interest in ecology, evolution, and/or environmental science. The person in this position will manage operations in the Lodge Lab, including budgeting, purchasing, and supervision of any additional technical staff working in the lab or field; manage the work flow and project management; and implement laboratory protocols and maintain lab equipment as needed.

The lab manager will also have a major role in the data collection and management–especially genetic data, organization and storage of data, analysis and interpretation of data, and drafting reports and manuscripts. Communication with both internal and external colleagues, partners and collaborators, including other individuals in the lab, on campus, and with federal, state, and NGO partners will be an important part of the job. Initially the lab manager may make 1-2 trips to the University of Notre Dame to assist in moving the existing laboratory to Cornell University, and will also be responsible for setting up the new laboratory at Cornell.

Qualifications include a Master's degree in a science field or equivalent experience, and at least 3 years of experience conducting research and running a laboratory. The winning candidate will be personable and able to develop strong working relationships with a variety of people; must be flexible, able to multi-task, possess excellent organizational and communication skills; take pride in providing exceptional service while working in a team-oriented environment; and must have excellent judgement and professionalism.

Prior experience with purchasing and budget creation, drafting reports, manuscripts, and grant proposals will be essential. This is a full-time, 12-month appointment which is renewable depending on the availability of funding and successful performance. The job was first posted in mid-June 2016, and is available immediately. Other details and instructions for applying can be found: https://cornell.wd1.myworkdayjobs.com/-CornellCareerPage/job/Ithaca-Main-Campus/Research-Support-Specialist-III_WDR-00007943-2?shared_id=-20e627cb-6ed4-4bf2-a048-4173fe939ded Kristy Deiner <alpinedna@gmail.com>

CSIC Spain EvolutionColourVision

Dear colleagues,

I have a postdoctoral position to study the evolution of colour vision, using Bombus terrestris as model organism, at the genetic level.

Candidates should have a strong publication record and experience with molecular techniques, as the project will involve producing genetically modified bumblebees.

Please contact me for further details.

Yours,

Miguel A. Rodriguez-Girones

Estación Experimental de Zonas Ãridas (CSIC)

Carretera de Sacramento s/n

La Cañada de San Urbano

04120 Almería

rgirones@eeza.csic.es

http://www.eeza.csic.es/Pollination_ecology/
rgirones@eeza.csic.es

MonashU DengueEvolution

Research Fellow - Eliminate Dengue Program

Job No. 549061 Faculty / Portfolio: Faculty of Science School of Biological Sciences Location: Clayton campus Employment Type: Full-time Duration: 12 month fixed-term appointment Remuneration: $92,114 - $98,880 pa Level A PhD (includes 17% employer superannuation)

The Opportunity

An exciting opportunity has opened for a Research Fellow to join the dynamic team of researchers within the Eliminate Dengue Program. If you have past experience in using next generation sequencing that has resulted in publication(s) we strongly we encourage you to apply.

The Eliminate Dengue research program is an international scientific collaboration that is developing an innovative biological control approach to reduce the ability of mosquitoes to pass dengue between people. As the Research Fellow you will contribute to the research effort of the University and develop your research expertise through the pursuit of defined projects.

As the successful candidate you will apply theoretical knowledge and techniques to investigate the evolution of Wolbachia after introduction into Aedes aegypti. Excellent interpersonal and communication skills are crucial as you will collaborate with laboratory and field biologists across disciplines, and write and present manuscripts and results at scientific meetings.

Our ideal candidate will hold a PhD in evolutionary genomics, population genomics, or a related discipline, with strong skills in bioinformatics analysis of whole genome sequence data using next generation sequencing. Experience sequencing and analysing bacterial genomes is highly desirable.

If you believe you fit this profile we welcome your application.

This role is a full-time position; however, flexible working arrangements may be negotiated.

Your application must address the selection criteria. Please refer to "How to apply for Monash Jobs".

Enquiries

Ms Marietta Chiodo, Research Partnership Manager, 03 9905 0051

Applications

To view a detailed Position Description and to submit an application please visit: http://www.jobs-monash.jxt.net.au/ Enter '549061' in the keyword search and click enter.

Closing Date

Thursday 16 June 2016, 2016, 11:55pm AEST Thanking you, Sabrina

RECRUITMENT ADVERTISING TEAM Sabrina Hinton 9902 9480 Judith Harvey 9902 9524 Jennifer McKenzie 9902 9569

HR Operations Centre | Monash HR Monash HR | Monash University Level 1, 211 Wellington Road | Mulgrave VIC 3170

JOB Adverts <adverts@monash.edu>

Monsanto CornBreeding

To apply, please click here: https://jobs.monsanto.com/-job/st-louis/regional-white-corn-line-development-breeder/769/2140690 Monsanto's white corn breeding program is seeking a Regional Line Development Breeder to work as part of a collaborative breeding team to develop and implement a new model for conducting plant breeding in a global environment. The successful candidate will have responsibility for developing, evaluating, and advancing new corn inbred lines and hybrids with high commercial impact across the SSA and Mexico regions. The incumbent will work closely with the Regional and Global breeding teams, Corn Breeding global support and enabling teams, and key internal customers and stakeholders including Technology Development, Pre-Foundation and Product Management to coordinate activities to implement and execute a highly successful corn breeding program with global impact.

Key Business Responsibilities (key goals and deliverables including business, organizational and people). Develop a strategy, implement plans and test the feasibility and success of novel models for multi-regional plant breeding.

Develop high impact commercial inbred lines for SSA and Mexico

* Interact with local Breeding, TD and Commercial teams to become familiar with germplasm pools, market needs and selection criteria in the target geographies of SSA and Mexico * Responsible for germplasm evaluation, selection and advancement decisions for the population development and screening stages of the breeding program * Work closely with breeding and testing teams, Commercial Breeders and Pipeline Managers across the target geographies to coordinate breeding activities and effectively advance lines to pre- commercial testing Develop and implement latest enabling technologies in the Regional Breeding Program

* Collaborate with Technology Deployment Leads and support functions to enable tools such as predictive analytics and genome-wide selection in the program * Utilize data analytics and visualization tools to generate novel approaches to Line Development Breeding * Drive development of analysis approaches and decision tools by interacting with data managers and analytics teams * Utilize latest native trait and pathology tools in line development and evaluation * Coordinate breeding program operations with global enabling locations (i.e. Mexico DH)

Required Skills/Experience:

* PhD (or completion within 6 months) in Plant Breeding, Plant Sciences, or Data Science with experience in plant breeding * Demonstrated experience in project management * Proficiency working with database applications, spreadsheet, and visualization software * High capacity to collaborate and work with cross-functional teams, build broad networks, and gain advocacy with others * Self-motivated and creative with strategic supervision * Excellent written and oral communication skills * Valid driver's license Desired Skills/Experience:

* Strong background in data management, genomics, or analytics * Strong record of process improvement * Ability to forecast and manage resource budgets * Ability to travel up to 35% of the time

Thank you,

Anne C. Moise Account Executive 2990 Ponce de Leon Blvd, Suite 400 Coral Gables, FL 33134 p) 305-704 4795 http://www.tmp.com/ anne.moise@tmp.com anne.moise@tmp.com

OregonStateU FishConservation

The Coastal Oregon Marine Experiment Station at Oregon State University (OSU) is recruiting for a full-time, 9-month, tenure-track Assistant/Associate Professor who will serve as the State Fisheries Geneticist. Major duties include (a) performing applied research and providing technical advice on the use of genetic tools for freshwater and marine fish conservation and fisheries management; and (b) working in partnership with the Oregon Department of Fish and Wildlife (ODFW) to define genetic information needs and build programmatic capacity to collect, store, retrieve, analyze and use genetic information for fisheries science and management applications. This position is jointly funded and supervised by OSU and ODFW and will be based in Newport, Oregon at the Hatfield Marine Science Center. Required qualifications include a Doctorate in Genetics, Fisheries or a related field. Preferred qualifications include a record of successful collaborative research with partners outside of academia and a demonstrable commitment to promoting and enhancing diversity. To review the posting and apply, go to http://oregonstate.edu/jobs. Apply to posting #P00377UF. For full consideration apply by 07/31/2016. OSU is an AA/EOE/Vets/Disabled.

"Sampson, David" <david.sampson@oregonstate.edu>

RBG Kew Bioinformatician PlantFungalTreeofLife

Senior Bioinformatician The Plant and Fungal Trees of Life project (PAFTOL) Royal Botanic Gardens, Kew https://careers.kew.org/vacancy/senior-bioinformatician-paftol-254750.html Closing date: 20th July 2016

Kew is a global resource for plant and fungal knowledge. We are in the process of building a team of talented, creative individuals with outstanding track records to help us build the Plant and Fungal Trees of Life, a major piece of global science infrastructure that is central to RBG Kew's Science Strategy 2015-2020. If you are a motivated and enthusiastic scientist with a strong background in bioinformatics then this is a unique opportunity for you to play a pivotal role in a team addressing a critical grand challenge in the life sciences. As the senior bioinformatician to the project, you will play a leading role within our dynamic and interdisciplinary team.

The project: There are few grander challenges in science than the tree of life - uncovering the complete evolutionary history linking all life on Earth. As part of RBG Kew's Science Strategy 2015-2020, we are initiating a five-year multimillion-pound project, the Plant and Fungal Trees of Life (or PAFTOL, for short), to complete the tree of life for all genera of plants and fungi, drawing on our outstanding collections, our broad collaborative networks and the latest high-throughput sequencing technologies.

This ambitious project will create a unifying framework for comparative plant and fungal research and takes us a step closer to building the tree of life for all known species. We will generate high impact findings publishable in top science journals, but we want the results to reach beyond the science community. To achieve this we will build innovative big-data and visualization tools accessible to a scientist or a school child. PAFTOL has recently secured generous funding from the Calleva and Sackler Foundations, and we are now ready to get the work underway. This is a truly exciting time to join Kew and become an integral part of a high-profile, cutting edge global endeavour.

The role: Developments in bioinformatics analyses have not kept pace with the unprecedented technological revolution driving relentless improvements in DNA sequencing and computational infrastructure. We need someone to apply high-throughput computational muscle to proven bioinformatics workflows. You will act as expert adviser and workpackage leader responsible for all aspects of bioinformatics development in PAFTOL. As the project grows you will take on leadership and mentoring roles for additional DevOps and bioinformatics experts.

The team: You will join a truly multidisciplinary team comprising experts from across a range of fields including systematics, evolution, genomics, bioinformatics, spatial analysis, data architecture and software development. You'll work alongside a highly supportive team of Kew staff who have actively developed the PAFTOL concept.

You: This is not a mission for the fainthearted. You could be an academic/postdoc who wants to play a leading role in building a vital piece of science infrastructure, or a bioinformatician tired of working for multiple masters and keen to sink their teeth into a single challenging project. This position offers the opportunity to do real science and deliver a step change in plant and fungal knowledge. Whatever your background, you'll have an agile mind, positive approach to problem-solving, and an enthusiasm for science and the pursuit of knowledge.

How to apply: Please complete an application via the Kew jobs portal https://careers.kew.org/vacancy/senior-bioinformatician-paftol-254750.html .In addition, please upload 1) a covering letter describing your motivations and qualifications for the role, 2) your CV, which should include a full list of your professional achievements (e.g. publications, grants, software).

Salary: £32,429 - £42,550 per annum, depending on skills and experience. For informal enquiries, contact Dr. Abigail Barker a.barker@kew.org Closing date: 20th July 2016 Interview date: 28th July 2016

The Royal Botanic Gardens, Kew is a non-departmental public body with exempt charitable status, whose principal place of business is at Royal Botanic Gardens, Kew, Richmond, Surrey TW9 3AB, United Kingdom.

William Baker <W.Baker@kew.org>

RBG Kew ComparativeFungalBiol

Senior Research Leader/Section Head - Comparative Fungal Biology Royal Botanic Gardens, Kew

An opportunity has arisen for a Senior Mycologist at the Royal Botanic Gardens Kew within the Department of Comparative Plant and Fungal Biology. We are seeking a highly motivated and enthusiastic individual to build a strong research group and manage a small team of mycology researchers, with the aim of delivering high-quality science in an area of fungal biology that is relevant to Kew's mission as outlined in the recent Science Strategy available on Kew's website.

The role will suit a scientist who already has a strong background in publishing high-impact papers and experience in managing their own grant-funded research programme. Research foci in the Comparative Fungal Biology team range from fungal phylogenetics through to mycorrhizal interactions and ant-fungal mutualisms. Mycologists in other Kew Science departments focus on areas such as fungal taxonomy, conservation and plant health. With an estimated 1.25 million well-curated specimens of dried fungi in the Fungarium, Kew houses one of the world's oldest, largest, and most important mycological reference collections located among excellent laboratory resources, making it an excellent base for international research in mycology.

Applicants should have a PhD in some aspect of fungal biology, significant postdoctoral experience, a strong publication record and excellent communication skills.

It is vital that you can demonstrate an ability to build, lead, motivate, manage and mentor a team of researchers including research leaders, research fellows, postdocs and PhD students. You will have a strong track record in raising research funding through grant applications and in managing research budgets. You will also need to have an established international reputation in your scientific field and an extensive publication record, with broad and deep knowledge of the existing literature and research in the field.

A standard RBG Kew application form should be completed along with a list of publications and a list of successful funding applications (if you are not the lead applicant, please state your contribution to the proposal).

Salary will be up to £54,479 per annum, depending on skills and experience. Benefits include competitive annual leave allowance, excellent pension, a flexible benefits scheme, as well as a great working environment.

For full details on this role please visit our website link https://careers.kew.org/vacancy/senior-research-leader-section-head-comparative-fungal-biology-263921.html from our website.

Closing date: 10 July 2016

The Royal Botanic Gardens, Kew is a non-departmental public body with exempt charitable status, whose principal place of business is at Royal Botanic Gardens, Kew, Richmond, Surrey TW9 3AB, United Kingdom.

William Baker <W.Baker@kew.org>

ReedCollege EvolBiology

We would consider anyone who studied adaption, speciation, conservation, evolutionary response to environmental change etc. while we would also consider ecologists, I think evolutionary biology related to the environment would very much complement our current department.

Suzy Renn

Reed College Tenure-Track Position in Environmental Biology The Biology Department at Reed College invites applications for a tenure-track faculty position in Environmental Biology that will support both the Biology Program (http://www.reed.edu/biology/) and the interdisciplinary Environmental Studies Program (http://www.reed.edu/es/).

We seek candidates, preferably at the rank of assistant professor, with demonstrated excellence in biological research related to the environment that is complementary to areas and approaches currently represented in the Biology Department and Environmental Studies Program. Qualifications include a PhD and postdoctoral or professional experience.

Reed is a distinguished liberal arts college with approximately 1400 students that offers a demanding academic program to bright and dedicated undergraduates. Candidates should articulate their 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 upper level, lecture/laboratory course in the candidate's area of expertise. Additional teaching opportunities include involvement in a team-taught interdisciplinary course in environmental studies and a team-taught introductory biology course, as well as offering an advanced seminar course. Formal teaching experience at the college level will be viewed favorably but is not required.

The Reed community believes that cultural diversity is essential to the excellence of our academic program. All applicants 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 include a cover letter, curriculum vitae, research plan (two page maximum length), 3 representative publications, and names for three references. The cover letter should address how the applicant's research program and teaching plans are suited to Reed College and complementary to the Biology Department and Environmental Studies Program.

All materials should be submitted at https://apply.interfolio.com/35398 by 14 October 2016 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.

Suzy Renn <renns@reed.edu>

StEdwardsU VisitingAssistProf

Visiting Assistant Professor Department of Biological Sciences School of Natural Sciences St. Edward's University Austin, TX

Link to job posting here: https://stedwards.applicantpro.com/jobs/417800.html Apply by July 5, 2016 for full consideration

St. Edward's University invites applications for a one-year Visiting Assistant Professor to begin in August, 2016.

Responsibilities

The teaching load is 12 hours per semester of undergraduate biology courses. Fall courses include first year courses for majors (Cells, Genetics and Organ Systems; Organisms and Populations) and/or non-majors (Contemporary Biology; Biology Principles). Specific courses will be determined by the time of appointment. Spring courses will be similar but may vary depending upon the background and interest of the candidate as well as the needs of the Department. There are no formal academic advising or university service responsibilities associated with this one-year position, but opportunities to become involved in the Department, the School of Natural Sciences, and the University will be available.

Qualifications

A Ph.D. in a biological discipline is required. A strong commitment to, and potential for excellence in, undergraduate teaching is required. Successful completion of an employment and/or criminal history background check is required.

About St. Edward's University

Founded in 1885 by the Congregation of Holy Cross, St. Edward's University is a private, Catholic liberal arts institution of more than 5,300 students located in Austin, Texas. It is an exciting time to be part of the St. Edward's community as the university increases its global engagement to educate students for the opportunities and challenges of a 21st century world. SEU is a diverse community that appreciates faculty and students from all backgrounds. The Department of Biological Sciences offers B.A. and B.S. degrees in biology, and B.S. degrees in Bioinformatics and Medical Laboratory Science and is part of the School of Natural Sciences.

Application Process

Applications will be accepted and reviewed until the position is filled, with full consideration given to those received by July 5, 2016. Applicants should submit application and all requested documentation online through http://stedwards.applicantpro.com/jobs/ . A complete application packet (single pdf preferred) will include:

1) Cover letter, addressing why the applicant is a good fit for the position, indicating a commitment to the university's mission (http://www.stedwards.edu/about/-mission) and to serve a diverse student body and prepare them for a global community 2) Curriculum Vita 3) Teaching Statement 4) Undergraduate and Graduate transcripts (unofficial at this stage) 5) The names and contact information for three references (or names of references if applying discreetly).

St. Edward's University is an equal opportunity employer and hires only U.S. citizens and documented workers.

Contact Bill Quinn with application questions at billq(at)stedwards.edu

Amanda Kenney <akenney@stedwards.edu>

SucculentKarooResStation ResearchManager

1 position as research manager at the striped mouse project in South Africa,

starting between August and October 2016 for 1-3 years

We are looking for an extremely motivated and independent biology student with a master's degree to join the striped mouse project for a minimum of 1 and a maximum of 3 years as research manager. Somebody who would like to gain experience in field work and scientific management. Managers get free accommodation at the station and R4500/month to cover their daily costs. Travel costs can be refunded by up to an additional R 12 000 / year. As such, the position compensates for all arising costs but does not represent a real employment.

The research manager will work closely together with the station manager and both managers will share responsibilities. However, each will have specific main duties, but should also be able to deal with all other duties (for example when the other manager is on leave, or when a new manager has to be trained).

We already have an acting station manager while our present research manager will leave the project end of the year to search for a PhD position. The new research manager will be instructed by the present research manager and both will overlap for 1-3 months.

Great opportunity: This is a great opportunity to spend 1-3 years in Africa, acquiring important skills in field biology and project management, while improving your CV. These skills will become valuable whether you later continue with a PhD or other jobs. It will be very hard and demanding, but also a once in a life time experience!

You must be hard-working, highly motivated, able to work independently, good in communicating with people, able to supervise others, and not afraid of snakes. You should love to live at a remote place in nature, without regular internet and cell-phone reception. Most importantly, you are fascinated by nature and science!

Job description: Five working days a week (Mo, Tue, Thu, Fr, Sat), with Wednesday being used for a shopping trip to town (not counted as working day) and Sundays being free. Included are four weeks of holiday for 12 months, which has to be taken outside the main breeding season (August to November) during periods when other students are present at the research station.

Shared duties

Striped mice:

. Trapping

. Observing

. Radio-tracking, putting radio-collars on

. Blood sampling

. Collect data for specific research projects (to be determined. Examples would be collecting urine samples, data on basking, cognitive testing .)

Primary duties research manager / secondary duties station manager

. Data:

o Weekly data entry

o Weekly data check

o Monthly data backup

o Monthly data report

o Training and supervision of field assistants

o Training of students and postdocs

o Support for students and postdocs

o Management of transmitters

o Management of field and laboratory supplies

Primary duties station manager / secondary duties research manager

. Technical support research station:

o Water system incl. sewage system

o Solar system

o Gas bottles replacement

o House and furniture

o Running of the respirometry laboratory

o Management of the captive colony

o Management of the research station car

o Management of bank account and cash box

o Management of research station supplies

Compensation:

. Free accommodation.

* A monthly compensation of R 4 500, which is sufficient to pay all costs of living (approx. 3500/month). * For travel costs, R12 000 per year can be refunded, but proof (receipts) must be presented for this. This refund is only payable after 12 months. * You will become a honorary researcher at the University of the Witwatersrand in the group of Prof. N. Pillay. * Scientific co-authorship or even becoming a first author will be possible if the manager contributes to the success of projects by not only collecting the majority of data, but also by data analysis and writing of the manuscript.

Responsibilities:

. The manager has to cover the costs to get to the station, including travel costs and visa fees. For this, a refund can be paid (see above).

* The manager needs to arrange for a health insurance covering him / her during the stay. A copy must be sent to C. Schradin before travelling to the stations.

Place and project: Succulent Karoo Research Station in the Goegap Nature Reserve near Springbok in the Northern Cape of South Africa. The research projects are on the socio-ecology of small mammals, studying ecological and physiological reasons of social behaviour, behavioural flexibility, and physiological adaptation.

How to apply? Please send a CV, a letter of motivation and the names and

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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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UCBerkeley ResAssoc EvolutionaryGenetics

Staff Research Associate, PMB (9612C) http://jobs.berkeley.edu Job ID# 21691

About Berkeley The University of California, Berkeley, is one of the world's most iconic teaching and research institutions. Since 1868, Berkeley has fueled a perpetual renaissance, generating unparalleled intellectual, economic and social value in California, the United States and the world. Berkeley's culture of openness, freedom and acceptanceacademic and artistic, political and culturalmake it a very special place for students, faculty and staff.

Berkeley is committed to hiring and developing staff who want to work in a high performing culture that supports the outstanding work of our faculty and students. In deciding whether to apply for a staff position at Berkeley, candidates are strongly encouraged to consider the alignment of the Berkeley Workplace Culture with their potential for success at http://jobs.berkeley.edu/why-berkeley.html . Departmental Overview Plant & Microbial Biology at UC Berkeley provides outstanding academic opportunities to undergraduate and graduate students. Our cutting-edge research by the world's foremost scientists is at the forefront of the latest advances in the biological sciences. Also known as PMB, we are proud of our internationally acclaimed research and teaching programs in both plant and microbial biology. We are regularly ranked as excellent for our academics and research at the top-ranked public university, UC Berkeley, where our mission is furthering scientific exploration for the public good.

The Blackman Lab studies how plants adapt to local environments and how crops were domesticated, with an emphasis on studying how these evolutionary processes alter plant-environment interactions during development.

Responsibilities The Blackman Laboratory in the Department of Plant & Microbial Biology requires a Staff Research Associate II to assist with research in evolutionary and ecological developmental genetics using sunflower and monkeyflower as study systems. Research in the lab focuses on how and why plant developmental responses to environmental cues evolve during domestication, adaptation, and speciation.

The position involves a combination of research and lab management responsibilities. Research duties include plant care and phenotyping, molecular and biochemical work (e.g. DNA/RNA extraction, genotyping, qRT-PCR, sequencing library construction), and coordination of field/greenhouse experimental procedures.

Required Qualifications Knowledge/Skills: - Able to perform sterile techniques, prepare media, carry out basic procedures associated with DNA amplification and sequencing. - Must be able to work in a greenhouse, manage data sets utilizing Excel, and follow research protocols and regulatory guidelines with exactness. - Ability to train and supervise student workers and coordinate student work schedules. - Good baseline knowledge of genetics, plant biology, and evolutionary biology is essential. - Strong organizational, computer, and communication skills, including familiarity with Microsoft Office tools. - Excellent oral and written communication in daily interactions is necessary in order to work independently and as part of a team. Preferred Qualifications - Experience using packages relating to statistics, phylogeny, sequence alignment, and bioinformatics. - Experience building libraries for next-generation sequencing. - Research experience working with sunflower and/or monkeyflower. - Associate's degree and at least 2 years of lab experience which may include student experience; or Bachelor's degree in related science; or an equivalent combination of education and experience.

Salary & Benefits $3,811 - $3,889 Monthly For information on the comprehensive benefits package offered by the University visit:

http://ucnet.universityofcalifornia.edu/compensation-and-benefits/index.html How to Apply

Please submit your cover letter and resume as a single attachment when applying.

Other Information This is a 100% full-time, 5 month limited appointment. Conviction History Background This is a designated position requiring fingerprinting and a background check due to the nature of the job responsibilities. Berkeley does hire people with conviction histories and reviews information received in the context of the job responsibilities. The University reserves the right to make employment contingent upon successful completion of the background check.

Equal Employment Opportunity The University of California is an Equal Opportunity/Affirmative Action Employer. All qualified applicants will receive consideration for employment without regard to race, color, religion, sex, sexual orientation, gender identity, national origin, disability, or protected

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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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UKentucky ArthropodHostPathogenEvol

Subject Job: Assistant Professor - arthropod ecology, including host/pathogen evolutionary ecology In addition to the details listed below in the position advertisement, researchers investigating aspects of vector population dynamics, population genetics, or host/pathogen evolutionary ecology are encouraged to apply for this position. Arthropod Ecologist Department of Entomology, University of Kentucky https://entomology.ca.uky.edu/ Position: Assistant Professor of Entomology, Arthropod Ecology, twelve-month, tenure track appointment, research (70%), teaching (30%)

Description: The Department of Entomology at the University of Kentucky is seeking a broadly trained entomologist or ecologist who will develop an internationally recognized, externally funded research program focused on arthropod ecology or ecologically-based pest management. We are particularly interested in candidates with expertise in biology of arthropod vectors that affect public health, vector-host-pathogen relationships, vector distribution and abundance, epidemiology or emerging diseases. Candidates with experience in other areas of arthropod ecology are encouraged to apply. The individual is expected to develop an independent and innovative research program employing integrative approaches that complement, enhance, and interact with existing efforts within the Department, University (e.g., Colleges of Arts and Sciences, Medicine or Public Health) and at a national or international level (e.g., the One Health Initiative).

This position includes a 30% teaching responsibility, which may include a graduate course in Insect Ecology. The individual will be expected to participate in other areas of undergraduate and graduate education, including developing a course in their area of expertise and mentoring graduate students.

Qualifications:The successful applicant must have a PhD in Entomology, Biology or related discipline with a strong record of publication. Candidates will be evaluated based on their potential for both independent and collaborative research. Post-doctoral research, grant writing, and teaching experience are highly desirable.

Salary and Benefits: Salary commensurate with background and experience; overview of benefits: http://www.uky.edu/professors/benefit.htm Application Procedure: Applicants should submit a packet including cover letter, research statement, teaching philosophy, CV, names and addresses of four individuals who may be contacted for letters of reference, copies of undergraduate and graduate transcripts. Questions should be directed to Kenneth F. Haynes, Chair of the Search Committee, khaynes@uky.edu, PH 859-257-1618. Applications must be submitted electronically to the Integrated Employment System at the University of Kentucky https://ukjobs.uky.edu/postings/109184 Application Deadline: July 31 2016, however the position will remain open until filled

Date Position is Available: January 1, 2017 or as mutually agreed upon

The University of Kentucky is an Equal Opportunity Employer and encourages applications from veterans, individuals with disabilities, women, African Americans, and all minorities

Clare C. Rittschof, Ph.D. Assistant Professor Department of Entomology University of Kentucky S-225 Agricultural Science Center North Lexington, KY, 40546 clare.rittschof@uky.edu Website: clarerittschof.blogspot.com Office: S-307C Agricultural Science Center North 859-218-3343 405 Plant Sciences Building Lab: 437 Plant Sciences Building

Clare Rittschof <clare.rittschof@uky.edu>

UOttawa PlantEvolution

Title of the position: Assistant professor, a higher rank will be considered under exceptional circumstances.

Duties: The functions of a member of the academic staff include: a) teaching b) scholarly activities revealed by research; c) academic service activities, d) supervision of graduate students. Preference will be given to plant scientists with research expertise in one or more of the following areas: plant physiology, plant molecular biology, genetics and plant genomics, plant-microbe interactions.The candidate will join an active department of over 40 professors working in the fields of biodiversity, cell and molecular biology, developmental and evolutionary biology, comparative physiology, and ecotoxicology. The department engages in collaborations with plant scientists at Agriculture and Agri-Foods Canada, the Canadian Museum of Nature and Carleton University. The department includes research and teaching greenhouses as well as several core laboratory facilities for analyses in molecular biology, microscopy and chemistry. The successful candidate would be expected to teach plant science courses at the undergraduate (e.g. introduction to plant biology, plant physiology, plant molecular biology) and graduate level.

Terms: Tenure-track position

Wage: Assistant professor salary scale

Benefits package: The University of Ottawa provides a complete compensation package, which includes long-term disability, basic group life insurance, supplementary health insurance, University of Ottawa Pension Plan and optional life insurance.

Location of work: Department of Biology, University of Ottawa, 30 Marie Curie, Room 160, Ottawa, ON K1N 6N5

Contact information: Chair, Department of Biology, 30 Marie Curie, Room 160, Ottawa, ON K1N 6N5. Email: biochair@uottawa.ca .Telephone: 613-562-5729, fax: 613-562-5486

Skills requirements:

o Education: Ph.D. or equivalent in plant sciences.

o Work experience: A demonstrated excellent research record in plant sciences. A commitment to teaching and graduate training. Priority will be given to candidates with strong communication skills in both French and English.

Application deadline: Review for applications will begin January 1, 2017 and will continue until the position is filled.

Interested candidates should submit an application consisting of:

o A letter of application formally expressing interest in the position, summarizing research objectives, and outlining teaching experience and philosophy.

o A full curriculum vitae.

o Three recent peer-reviewed publications.

o Contact information for three references.

All qualified candidates are invited to apply; however, preference will be given to Canadian citizens and permanent residents. The University of Ottawa is an equal opportunity employer. We strongly encourage applications from women, Aboriginal peoples, persons with disabilities and members of visible minorities. If you are invited to continue the selection process, please notify us of any particular adaptive measures you might require by contacting the Office of the Associate Vice-President, Faculty Affairs at 613-562-5958. Any information you send us will be handled respectfully and in complete confidence.

The University of Ottawa is proud of its 160-year tradition of bilingualism. Through its Official Languages and Bilingualism Institute, the University provides training to staff members and to their spouses in their second official language. At the time of tenure, professors are expected to have the ability to function in a bilingual setting.

Risa Sargent <rsargent@uottawa.ca>

USouthampton 2 EvolutionaryCompSci

Hello all -

Please see below the advert for two positions in the AIC group at Southampton. We are a multidisciplinary group in a top ranked computer science department with eclectic interests including Theoretical/Computational Evolutionary Biology, Evolutionary Systems Biology. e.g. see http://www.ecs.soton.ac.uk/people/raw Feel free to get in touch - best, Richard.

Please distribute widely (and responsibly) -

Lecturer*/Associate Professor (*USA translation = Assistant professor) https://jobs.soton.ac.uk/-Vacancy.aspx?ref=3D3D744016FP Agents, Interactions & Complexity research group Location: Southampton, UK Salary: £36,672 to £60,081 per annum Full Time Permanent Closing Date: Sunday 10 July 2016 Interview Date: Thursday 28 July 2016 Reference: 744016FP

The Agents, Interaction and Complexity (AIC) group within Electronics and Computer Science, at the University of Southampton, welcomes applications for a full time post at either Lecturer or Associate Professor level.

Electronics and Computer Science (ECS) is the largest and most distinguished School of its kind in the UK, with a worldwide reputation for its research,enterprise and research-lead teaching.

The AIC group undertakes world-leading, interdisciplinary research into the science and engineering of computing systems, in particular those that connect people and technology. We are interested in complex socio-technical, socio-economic and socio-ecological systems that underpin the most pressing challenges currently facing society. Problems as diverse as engineering resilient and sustainable smart infrastructure, or refactoring health-care systems to cope with demographic change, understanding voting patterns, or anticipating and mitigating the impacts of climate change, all involve building and analysing complex systems comprising many interacting agents, including people and other organisms, hardware robots and autonomous software agents.

AIC is a highly interdisciplinary group, not only collaborating across areas in Electronics and Computer Science, but across disciplines from physics and maths to psychology and the humanities. We are therefore actively seeking colleagues with excellent research track records and demonstrated ability to build collaborations, especially across disciplinary boundaries, and to engage in and to lead exciting, innovative work.

Applications are welcome in any of the group's key areas of interaction, complexity and agent-based systems as well as other areas that support the research themes and ongoing projects in the group. Information analytics and visualisation, serious games/play, machine learning are examples of areas of particular additional interest.

Further info, w. links to research areas, group members and application procedures etc:

https://jobs.soton.ac.uk/Vacancy.aspx?ref=-3D3D744016FP – Dr. Richard A. Watson Associate Professor Institute for Life Sciences/Electronics and Computer Science, University of Southampton http://www.ecs.soton.ac.uk/people/raw R.A.Watson@soton.ac.uk

R.A.Watson@soton.ac.uk

UToronto DiseaseEcolOrEvol

Assistant Professor - Ecology and Evolution of Disease

The Department of Ecology and Evolutionary Biology at the University of Toronto invites applications for a tenure-stream appointment in the field of ecology and evolution of disease. This appointment will be at the rank of Assistant Professor, with an expected start date of July 1, 2017.

We seek a candidate who conducts conceptually driven research, using either empirical or theoretical approaches to study issues related to ecology and evolution of disease. We seek applications from candidates whose research program fits with the research programs of the highly collaborative faculty currently in the department. The appointee will be expected to build an active, externally funded and internationally recognized research program. The successful candidate will demonstrate excellence in teaching and contributions to the education and training of undergraduate and graduate students. Evidence of demonstrated excellence in research and teaching should be documented through the applicant's CV, publications, research and teaching statements, letters of reference and where appropriate, course evaluations.

The successful applicant will have a PhD by July 1, 2017 or soon thereafter, with an outstanding academic record. Salary to be commensurate with qualifications and experience.

The University of Toronto is a leading academic institution with over 60 faculty members specializing in ecology and evolution. Strong links exist between the Department of Ecology and Evolutionary Biology and the Royal Ontario Museum, the Centre for Global Change, Dalla Lana School of Public Health, the University network of leading academic research hospitals (www.uhn.ca, sunnybrook.ca/) and the School of the Environment. The University owns a nearby field station dedicated to ecological research (the Koffler Scientific Reserve; www.ksr.utoronto.ca). Toronto is a vibrant and cosmopolitan city, one of the most desirable in the world in which to work and live.

All qualified candidates are invited to apply at https://utoronto.taleo.net/careersection/10050/-jobdetail.ftl?job=1600709 .Applications must include a CV and statements of research and teaching interests combined into a single PDF file, plus three representative publications. Applicants should arrange to have three confidential letters of recommendation (signed and on letterhead) sent directly to: Professor Donald Jackson, Chair of Search Committee, Department of Ecology and Evolutionary Biology, 25 Willcocks Street, University of Toronto, Toronto, Ontario, M5S 3B2 Canada. Letters of reference may be e-mailed to chairsec.eeb@utoronto.ca. Deadline for receipt of applications is September 28, 2016.

For further information on the Department of Ecology and Evolutionary Biology, please visit our website at www.eeb.utoronto.ca. Questions regarding this position can be directed to Liz Rentzelos at chairsec.eeb@utoronto.ca or (416-946-3340).

The University of Toronto is strongly committed to diversity within its community and especially welcomes applications from visible minority group members, women, Aboriginal persons, persons with disabilities, members of sexual minority groups, and others who may contribute to the further diversification of ideas.

All qualified candidates are encouraged to apply; however, Canadians and permanent residents will be given priority.

Aneil Agrawal <a.agrawal@utoronto.ca>

UUppsala SpeciationGenomics

A tenure track position as Assistant Professor (Associate Senior Lecturer) is available at the Department of Ecology and Genetics, program in Evolutionary Biology, at the Evolutionary Biology Centre of Uppsala University, Sweden. Reference number: UFV-PA 2016/1228.

World-leading research in the interface of ecology, evolution and genomics is conducted in the Department. One particular area of strength is speciation and its genetic basis, with several research projects in this area financed by the European Research Council (ERC) and other major funding bodies. This recruitment is aimed to complement existing research in the Department for the study of genome differentiation and divergence, and speciation. There is an excellent infrastructure available for large-scale genomic, proteomic and bioinformatic analyses through the SciLifeLab initiative (https://-www.scilifelab.se).

The program in Evolutionary Biology has a strong record in fostering and supporting young group leaders. We offer a vibrant research environment with excellent possibilities for interactions along with scientific independence. The position will come with adequate start-up funding. A presentation of the program can be found at http://www.ieg.uu.se/evolutionary-biology/ and of the Department at http://www.ieg.uu.se Appointment Period: The position can be held for a maximum of four years. An Associate Senior Lecturer has the opportunity to apply for promotion to Senior Lecturer (Associate Professor). If the Associate Senior Lecturer is deemed suitable and fulfills the criteria for promotion established by the Faculty Board, he/she shall be promoted to and permanently employed as Senior Lecturer. Subsequently, the successful candidate has the opportunity to apply for promotion to Professor.

Qualifications Required: According to the Swedish Higher Education Ordinance those qualified for appointment as Associate Senior Lecturer are persons who have obtained a doctoral degree or achieved the equivalent competence. Applicants who have obtained a doctoral degree in seven years or less (excluding time for parental leave etc) prior to the end of the application period will be given priority.

Assessment Criteria/Ranking: The ranking of eligible applicants will be based primarily on research and teaching expertise, which will be given equal importance. Research expertise comprises research merits as well as the applicantÂs potential to contribute to the future development of both research and teaching. In assessing research expertise special weight will be attached to large-scale genomic studies of speciation, population differentiation and/or local adaptation in eukaryotic systems. Special weight will also be paid to scientific independence and the ability, or expected ability, to attract funding in strong competition. The planned research of the applicant shall complement on-going research in the Department by bringing in new angles and/or study systems. The research may be mainly empirical or theoretical, or both.

For further information about the position please contact Professor Hans Ellegren (Hans.Ellegren@ebc.uu.se).

For further information about Uppsala University appointment regulations see http://regler.uu.se/-digitalAssets/144/144568_appointment-regulations-for-uppsala-university.pdf For further information about Faculty appointment regulations see http://www.teknat.uu.se/digitalAssets/395/-395576_1guidelines-appointment-promotion-2014-12-03.pdf Uppsala University is an international research university focused on the development of science and education. The University has 40,000 students, 7,000 employees and a turnover of SEK 6,5 billion. Uppsala University aims for gender balance and diversity in all activities in order to achieve a higher quality at all levels of the organization. We therefore welcome applicants of any gender and with different birth background, functionality and life experience. Within this category a majority of the employed are men, and we would therefore particularly like to see female applicants for employment.

Application must be submitted through the central job search system of Uppsala University (starting page: http://uu.se/en/about-uu/join-us/jobs/) (direct link to this position: http://uu.se/en/about-uu/join-us/-details/?positionId=107246) and no later than August 21, 2016. Starting date is as agreed upon.

Hans Ellegren <hans.ellegren@ebc.uu.se>

UVirginia ResAssoc PlantFungalEvolution

The Taylor Lab in the Department of Biology at the University of Virginia is searching for an exceptional scientist to fill a Research Scientist position. The intended project is to explore how extinction and re-colonization events drive the evolutionary process in natural populations. The research is supported by the NSF Long-Term Research in Environmental Biology (LTREB) Program. The work will involve field and molecular population genetics in the plant, Silene latifolia, and its associated fungal pathogen, Microbotyum violaceum. We are specifically interested in how gene flow and founder effects influence genetic diversity in different regions of the genome, and the work will involve maintaining and disseminating long term genetic data, population genetic analysis and demographic studies in the field.

Candidates will have a PhD in Biology or related field. The candidate will also have at least 1 year of experience using plants as a model with experience in some combination of molecular population genetics, analysis of population genetic data, and computational skills necessary to maintain and disseminate long-term data. Candidates will have experience working as a member of an interdisciplinary research team at the post doctoral fellow level or above, and excellent communication skills. This is a nine month appointment; however appointments may be renewed for an additional two, one-year increments, contingent upon available funding and satisfactory performance

Our lab is located in the Gilmer Hall at UVa in Charlottesville, Virginia and is within a 10 minute walk to the Medical Center, which provides exceptional opportunities for collaboration among basic and clinical scientists. Our scientific community is heavily invested in training, and we work hard to help trainees develop the skills necessary for successful independent careers.

To apply, candidates must complete a candidate profile through Jobs@UVa (hhttps://jobs.virginia.edu) and electronically attach the following: cover letter, curriculum vitae, and the contact information for three professional references; search on posting number 0618766.

Review of applications will begin June 20, 2016; however, the position will remain open until filled.

Questions regarding the position and application process should be directed to Rich Haverstrom at rkh6j@virginia.edu.

The University will perform background checks on all new hires prior to making a final offer of employment.

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

Douglas Taylor <taylordouglasr@gmail.com>

UZurich FieldAssist BirdsLapland

Expenses paid field assistant positions to study the foraging ecology of Siberian Jays in Swedish Lapland

For the upcoming field season (15 August-31 October 2016) we are looking for a highly motivated expenses paid field volunteer to join our field project (main responsible Dr. Michael Griesser, University of Zurich, Switzerland) investigating life-history evolution in Siberian jays. The study site is located near Arvidsjaur, Swedish Lapland.

Our current project investigates the influence of habitat quality on the foraging and food storing behaviour of Siberian jays. The work of the field volunteers will be to help with field experiments, behavioural observations, catching birds, and data management. This work will give insight into exciting experimental fieldwork and will be carried out partly in managed forests and partly in scenic pristine boreal habitats. We will work 5-6 days per week in the field depending on the workload of the experiments. Observe that temperatures in the end of the season can be as low as -10C. The work is physically strenuous at times. The team will vary in size depending on the weeks, but at least two other people will be present during the whole field season.

Qualifications: (1) BSc/MSc in Biology, Ecology, Evolution or similar qualification (2) Previous field experience (3) Ability to work in small teams and sociable personality (4) Knowledge in observing (5) bird ringing and mist-netting experience (6) Driving licence (7) Fluent in English

We will cover for the accommodation, travel expenses from and to the study site (in total up to 300 Euros), as well as the living expenses.

Applications - including a CV, a letter of motivation (1 page) and the name of two referees - should be send to Michael Griesser michael.griesser@uzh.ch, preferably in a single PDF.

Applications received until 10 July 2016 will be given full consideration.

For further information on the project, see:

http://www.aim.uzh.ch/de/research/birdfamilies/-JayResearch.html Michael Griesser Anthropological Institute & Museum University of Zurich - Campus Irchel Winterthurerstrasse 190 8057 Zürich Switzerland

http://www.aim.uzh.ch/research/birdfamilies/-mgriesser.html michael.griesser@uzh.ch michael.griesser@uzh.ch

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Other

ConservationBiology grants

Hi Everyone,

We added many, many more grants to our lists of conservation/ environmental grant lists.

- Marine Grants – 35 grants < https://t.yesware.com/tt/662c6da5514e1e190020486b7cbdcf056fa8d716/eb3c50f29588a5d3b5dbfd1f5954d57f/18126d5367096956993c2acdb5dca4ea/www.instrumentl.com/summer-marine-grants?utm_source=summermarine615&utm_medium=email&utm_campaign=aess >

- Wildlife Grants - 75 grants < https://t.yesware.com/tt/662c6da5514e1e190020486b7cbdcf056fa8d716/eb3c50f29588a5d3b5dbfd1f5954d57f/f1b3f88bb21f741c109a3bee00abc79f/www.instrumentl.com/summer-wildlife-grants?utm_source=summerwildlife615&utm_medium=email&utm_campaign=aess >

- Plant Grants - 45 grants < https://t.yesware.com/tt/662c6da5514e1e190020486b7cbdcf056fa8d716/eb3c50f29588a5d3b5dbfd1f5954d57f/7c19d216da850a83ca69f9a0b0094fbe/www.instrumentl.com/summer-plant-grants >

I hope this info helps you out this season. Please share with colleagues, friends and students if you think they could use it.

Best of luck!

Katharine

– Katharine Corriveau Co-founder Instrumentl (510) 684-4978

Follow us on Facebook < https://www.facebook.com/Instrumentl >

and Twitter < http://twitter.com/BeInstrumentl >

Visit us at: www.instrumentl.com Katharine Corriveau <katharine@instrumentl.com> Katharine Corriveau <katharine@instrumentl.com>

ESEB2017 CallSymposia

ESEB 2017 Groningen - CALL FOR SUBMISSION OF SYMPOSIUM PROPOSALS

The 16th Congress of the European Society for Evolutionary Biology (ESEB) will take place in Groningen (The Netherlands), August 20-25, 2017. Submissions for symposium proposals are now open. Information about the symposia can be found at http://www.eseb2017.nl/ . Symposium proposals should be proposed via http://www.eseb2017.nl/scientific-programme/symposium/ You will be asked to provide:

(1) The names and email addresses of the primary organiser (for all communication) and max. two co-organiser(s) (as a replacement), who 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 and timely subject for the ESEB Congress.

(4) The names of two invited speakers (please check beforehand whether they are indeed available).

The deadline for submission is June 30, 2016.

Proposals will be evaluated by the Scientific Committee, and the selected list will be communicated in September 2016.

Ute Friedrich Office Manager European Society for Evolutionary Biology

ESEB Office: office@eseb.org ESEB Website: www.eseb.org office@eseb.org

Fungal Melampsora strains

Dear EvolDir members,

I am Olaya Mediavilla, a PhD student on Forestry at the University of Valladolid (Spain).

Our research group is going to develop a study of pathogenicity of the species Melampsora larici-populina in Populus sp. We want to perfom some assays with the pathotypes E4 and E5 and we are currently seeking for them, so if any of you had these strains and is willing to share them, I'd highly appreciate it!

Please feel free to contact me if you need more details about the project itself or if you have any other kind of questions.

Thank you very much in advance!

Yours sincerelly,

Olaya

PhD student Olaya Mediavilla

University of Valladolid Sustainable Forest Management Research Institute. Department of Vegetal Production and Natural Resources Avda. Madrid 57; E-34071 Palencia (Spain)

E-mail: olaya.mediavilla@uva.es

Olaya Mediavilla <olayamediavillasantos@gmail.com>

Hangzhou StudentTravelGrantsGenomicsSymposium Aug15-21

Limitedtravel grant awards are still available for graduate students orpostdoctoral students interested in presenting at talk at the symposium“Amphibian & Reptile Genomics: Recent Success, Current Progress,and Future Challenges”, as part of the 8th World Congress of Herpetologyto be held in Hangzhou, China, August 15â€21, 2016. Regularregistration fees will increase after June 15th. For more informationabout the event, please see:

http://wch8.worldcongressofherpetology.org/ http://wch8.worldcongressofherpetology.org/WCH8-Announce.pdf Travelawards made possible by the American Genetic Association (http://www.theaga.org/index.htm). Graduate students have priority, andsymposium organizers would like to encourage interested female scientiststo apply, as well as students from countries not yet representedin the symposium.

Confirmedspeakers include: TonyGamble, Marquette University, USA. ArthurGeorges, University of Canberra, Australia. DanielLee Jeffries, Université de Lausanne, Switzerland. KenroKusumi, Arizona State University, USA. JohnH. Malone, University of Connecticut, USA. RachelLockridge Mueller, Colorado State, USA. EvanMcCartney-Melstad, UCLA, USA. RasmusNielsen, UC Berkeley, USA. YongShao, KIZ, China. YanboSun, KIZ, China. Symposiumco-organizers are: JingChe, Kunming Institute of Zoology, Chinese Academy of Sciences. AndrewJ. Crawford, Universidad de los Andes, Colombia, and Smithsonian TropicalResearch Institute, Panama. RobertW. Murphy, Royal Ontario Museum, Toronto, Canada, and KIZ GuojieZhang, University of Copenhagen and BGI-Shenzhen. Ya-PingZhang, KIZ, Chinese Academy of Sciences.

Symposiumsummary: Genomicstouches nearly all aspects of evolutionary and organismal biology,and allows powerful laboratory and analytical methods to be applyto virtually an organism, regardless of previous genetic work. Therapid rate of technological advancement in the field of genomics inspiredthe Genome 10K project, and audacious proposal to genome sequence10,000 vertebrate species (Haussler et al., 2009). Relative to othervertebrates, however, reptiles and especially amphibians have laggedbehind due in part to the large size and complexity of their genomes.Under the umbrella of the WCH8, the year 2016 is the ideal timefor a first worldwide appraisal of current success and future prospectsfor WGS of amphibians and reptiles, and China is an ideal site.Our goal is to bring together leaders in the fields of herpetologyand genomics to share experiences, propose solutions, and developa road map for advancing genomic studies of amphibians and reptiles.

Talksare welcome in areas such as whole genome assembly, evolutionary andcomparative genomics, molecular evolution, transcriptomics, and relatedtopics in evolutionary genetics.

Studentsinterested in applying for travel support may contact as soon aspossible:

AndrewJ. Crawford Email: crawfordaj@gmail.com AssociateProfessor Director,Museo de Historia Natural ANDES, M-101 Departmentof Biological Sciences, Edif. Ip-204 Universidadde los Andes Bogotá,Colombia Tel.+57 1 339-4949 x3270 Web:http://dna.ac ResearchAssociate SmithsonianTropical Research Institute Balboa,Ancón

PanamaCity, Republic of Panama

"AndrewJ. Crawford" <crawfordaj@gmail.com>

HermannMullerAward CallNominations

Hermann J. Muller Award for Contributions to Our Understanding of Genes and Society: Call for Nominations

This annual award and lecture series was established in 2016 to honor Professor Hermann Joseph Muller - renowned geneticist, Nobel Laureate, and social activist. The award is meant to recognize luminary international geneticists whose discoveries in genetics, like Muller's, have or are making a significant impact on human society in the broad sense (e.g., understanding the basis of genetic disorders, disease prevention, and innovations in agricultural genetics). In addition to a $10,000 cash award, the recipient will receive a commemorative medal, will attend an awards ceremony, and will present a public scholarly presentation of his/her work. Further information about the award and Muller himself can be found at: http://www.bio.indiana.edu/events/lectures/-muller.shtml We are now calling for nominations for the 2017 award, which must be submitted as a one-page letter by 1 August 2016, noting the nominee's most significant accomplishments relative to joint issues of genetics and society. Nominations must be sent by email to: jenjones@indiana.edu. Selection of the awardee will be made by a committee composed of senior faculty at Indiana University - Bloomington.

The Hermann J. Muller Award for Contributions to Our Understanding of Genes and Society and lecture series is funded by Indiana University Bloomington, the College of Arts and Sciences, and the IU Department of Biology.

Michael Lynch, Distinguished Professor

Class of 1954 Professor

Department of Biology

1001 East Third Street

Indiana University

Bloomington, IN 47405

Phone: 812-855-7384

Fax: 812-855-6705

www.bio.indiana.edu/faculty/directory/-profile.php?person=milynch "Lynch, Michael" <milynch@indiana.edu>

ID Norway spruce from photos

Hi EvolDir folks:

I recently had a request from a citizen to identify two trees recently purchased from a horticultural supplier as they should both be Norway spruce but look quite different. The owners have photos of the trees or could supply branch cuttings if needed.

The morphological question is outside my training, so I am looking for an expert in Picea taxonomy who may be willing to help, and potentially provide a letter stating conclusions.

If you are able and willing to help, please contact me at the info below.

Thanks and best, Jenn

Jennifer DeWoody, PhD Geneticist Forest Service National Forest Genetics Lab p: 530-621-6883 jadewoody@fs.fed.us 2480 Carson Road Placerville, CA 95667 www.fs.fed.us/NFGEL/ Caring for the land and serving people

"DeWoody, Jennifer A -FS" <jadewoody@fs.fed.us>

OxfordNanopore MinION platform

Has anyone had any experience with this platform? I would like to chat about its realized capabilities. Email off-list to rjdyer@vcu.edu

Rodney

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

SabbaticalFellowship UToronto

EEB Visiting Fellow

This fellowship is meant to support world-class researchers wishing to visit Toronto for periods of 6-12 months during their sabbatical. The value is up to $25K per year of expenses paid for the Fellow (e.g., travel, accommodation, etc.). During their stay, Fellows are expected to become active members of the Department of Ecology and Evolutionary Biology (St. George Campus), University of Toronto. This includes regularly attending departmental seminars, discussion groups and socials. In addition, in collaboration with EEB faculty and graduate students, Fellows will organize an international workshop on an agreed upon topic. Costs of the workshop will be supported up to $5K.

Applicants should provide a cover letter (maximum of two pages) identifying the faculty member(s) with whom she or he will undertake her/his sabbatical, the period of time when the sabbatical will occur within our department, an overview of the proposed research to be undertaken, and a general topic for the workshop to be developed. Applicants should include their CV with the cover letter and submit applications (as Adobe PDF files) to Don Jackson, Chair, Department of Ecology and Evolutionary Biology (chairsec.eeb@utoronto.ca <mailto:chairsec.eeb@utoronto.ca>). The department will typically fund one Visiting Fellow each year, but this practice may vary depending on the applications received. The application deadline is September 30, 2016 for the 2017-2018 Fellowship.

More information on EEB at U of Toronto: http://www.eeb.utoronto.ca/ “a.agrawal@utoronto.ca” <a.agrawal@utoronto.ca>

Seminar Participation Survey

Dear EvolDir community,

My colleagues, Alecia Carter, Gillian Sandstrom, Alyssa Croft, and I would like to understand why academics choose to participateâquestions or notâacademic seminars. If you are a student or an academic at any stage of your career and would like to help us out, please take part in our quick survey here: http://goo.gl/xida3O. It will take 5-10 min to complete some quick questions and your answers will be completely anonymous.

Please participate, and please forward the survey far and wide!

If you would like more information about our study, please contact any of us with these contact details:

Dr Alecia Carter: ac854@cam.ac.uk Dr Gillian Sandstrom: gsands@essex.ac.uk Dr Alyssa Croft: alyssac@email.arizona.edu Dr Dieter Lukas: dl384@cam.ac.uk

Thanks,

Dieter Lukas

Department of Zoology University of Cambridge Downing Street Cambridge CB2 3EJ

http://people.pwf.cam.ac.uk/dl384/ Dieter Lukas <dl384@cam.ac.uk>

SouthAfrica 2VolResAssist SocialMoleRats

SouthAfrica.VolResearchAssistant.SocialMoleRats

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

2 Voluntary research assistants

Position 1 (Starting between July and September 2016, 6 month minimum stay required):

This position entails assisting in several studies on hormonal effects on social behaviour of mole-rats (Fukomys damarensis). We are interested in the effects of cortisol and testosterone on allo-parental care in non-reproducing mole-rats and in the effects of these hormones on developing offspring during gestation. The research assistant will be involved in all steps of the experiments and will mainly work in the laboratory with our captive mole-rats which are housed in large semi-natural tunnel systems. The responsibilities include behavioural observations, hormonal measures (blood sampling, urine sampling), morphological measurements (using X-ray) and hormonal manipulations. The laboratory is situated in the Kuruman River Reserve in the southern Kalahari, Northern Cape province of South Africa.

The successful applicant will work in a team of 5-10 persons. The research station is also the home of several other projects studying meerkats (www.kalahari-meerkats.com), pied babblers, forktailed drongos, bat-eared foxes 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, blood and urine sampling and how to operate X-rays technique for research purpose.

Position 2 (Starting August 2016, 3 months minimum stay):

This project investigates the group augmentation hypothesis and how benefits of living in large groups can generate selection for altruism in animals. We are currently conducting a large scale capture-mark and recapture experiment running over more than one year in which the voluntary research assistant would play an important role. Field work takes place in the southern Kalahari, Northern Cape province of South Africa in a private game reserve. Entire groups of mole-rats will be captured and individually marked. Morphological measurements and tissue samples will be obtained before the release of the animals. The work is physically demanding (digging to capture mole-rats) and weather conditions are challenging (heat during the day, cold during the night). Field work will make trapping during the night necessary. The assistant will mostly be working along one more experienced scientist but will need to work independently at times.

Applicants for both positions should be enthusiastic, willing to work hard and keen to get involved in an ecological research project in the African bush. The research assistants are expected to work at night when trapping schedules require it and need to be fit as capturing mole-rats requires the capacity to do hard physical work (digging) in a challenging environment. A zoology related degree and/or previous field experience will be considered an asset. The successful applicant needs to be a team player and generally a person that enjoys collaboration and team work.

Accommodation is provided, and research assistants are paid a monthly allowance to cover their personal costs and food. The bus fare from Johannesburg to the field site can be covered but we do not provide an international airfare, travel insurance, or visa fees for applicants from overseas.

Applications received until the 15th of June 2016 are ensured full consideration. Later applications can be considered if the position(s) have not been filled.

Please apply to Markus Zoettl: mz338@cam.ac.uk; Including a CV and a cover letter explaining why you would like to participate in our research project.

Please indicate whether you are applying for position 1 (mainly lab-based) or position 2 (mainly field based) or both.

http://www.zoo.cam.ac.uk/directory/dr-markus-zottl
Markus Zoettl <mz338@cam.ac.uk>

YoungScientist prize

Science/AAAS and SciLifeLab, a coordinated effort of four universities, have joined forces in creating the Science & SciLifeLab Prize for Young Scientists. Each year, the grand prize winner will receive a prize of US$30,000; each of the three category winners will receive US$10,000.The grand prize winner will have his/her essay published in Science and the three category winners will be published online. The topic of the entrant's thesis research (and the subject of the essay) must be in one of the following categories: Ecology and Environment, Cell and Molecular Biology, Genomics and Proteomics, Translational Medicine. The deadline for entry is August 1. For further information, see http://www.sciencemag.org/site/feature/data/prizes/scilifelab/index.xhtml Barbara Jasny <bjasny@aaas.org> Barbara Jasny <bjasny@aaas.org>

PostDocs

ArizonaState EvolutionaryGenomics2

Postdoctoral Research Associate — Genomics/Bioinformatcs

URL: http://cartwrig.ht/jobs/2016/05/19/Postdoc-Opening/ PDF: http://cartwrig.ht/postdoc-2016.pdf

A Postdoctoral Research Associate position is available at the Biodesign Institute at Arizona State University (ASU). This new Postdoctoral Research Assocate will be part of the Cartwright lab (http://cartwrig.ht/) located in the Biodesign Center for Personalized Diagnostics. The lab is focused on evolutionary research related to mutation and population variation, as well as developing statistical software to process large, genomic datasets to identify and study somatic and germline mutation patterns. A successful candidate will participate in two NIH funded research programs: (1) analysis of mutation accumulation lines from the ciliate, Tetrahymena thermophila, and (2) development of DeNovoGear (https://github.com/denovogear/denovogear), a general toolkit for the study of mutation rates from next-gen sequencing of related individuals and cells. Corresponding projects in the lab involve the study of somatic and germline mutations in humans, chimps, trees, bacteria, bees, mice, and cancer.

In particular, under guidance from Dr. Cartwright, the candidate is expecte= d to:

1. Work both independently and closely with other members of the lab 2. Map and/or assemble next-generation sequencing data 3. Adapt existing genomic techniques to non-model organisms 4. Develop novel, high-throughput methodologies to identify de novo mutations by comparing related individuals and somatic samples. 5. Present the results of research at meetings, in publications, etc.

Requirements

- PhD in bioinformatics, computational biology, biostatistics, genomics, molecular biology or related fields - Proficiency in scientific computing and programming/scripting languages in UNIX platforms (e.g. Bash, Python, C/C++) - Experience in statistical computing (e.g. R/Bioconductor and Biopython)

Desired Qualifications

- Experience in development/maintenance of scientific software - Experience in next-generation sequencing data processing and analysis - Experience in statistical analysis and method development - Experience in high-performance parallel computing - Experience in collecting and processing large-scale scientific data

Instructions to Apply

The position will remain open until filled. To apply, please send cover letter, CV, summary of past work, and the names and email addresses of three references to Dr. Cartwright at cartwright@asu.edu by **June 30, 2016**. Please put "Postdoctoral Research Associate" in the subject line of your email.

The Cartwright Lab (http://cartwrig.ht/) offers a productive environment, in which researchers are given the freedom to explore new ways of solving scientific problems. There are opportunities to work with a large number of collaborators at both ASU and worldwide. We are located in the Valley of the Sun (Phoenix, AZ, USA), home to 4.5 million people, and short driving distances from numerous outdoor activities in the Sonoran Desert. Biking, hiking, mountain climbing, and bird watching are all popular activities in the area.

The Biodesign Institute Mission

The Biodesign Institute at ASU addresses today$B!G(Bs critical global challenges in healthcare, sustainability and security by developing solutions inspired from natural systems and translating those solutions into commercially viable products and clinical practices.

Arizona State University is a VEVRAA Federal Contractor and Equal Opportunity/Affirmative Action Employer. All qualified applicants will be considered without regard to race, color, sex, religion, national origin, disability protected veteran status, or any other basis protected by law.

ASU's full non-discrimination statement: https://www.asu.edu/aad/manuals/acd/acd401.html Title IX statement: https://www.asu.edu/titleIX/ Reed A. Cartwright, PhD Barrett Honors Faculty Assistant Professor of Genomics, Evolution, and Bioinformatics School of Life Sciences Human and Comparative Genomics Laboratory The Biodesign Institute Arizona State University

Availability: http://links.asu.edu/CartwrightCalendar Address: The Biodesign Institute, PO Box 875301, Tempe, AZ 85287-5301 USA Packages: The Biodesign Institute, 1001 S. McAllister Ave, Tempe, AZ 85287-5301 USA Office: Biodesign A-224A, 1-480-965-9949 Website: http://cartwrig.ht/ "rcartwri@asu.edu" <rcartwri@asu.edu>

AustNatlU BirdMatingPatterns

Postdoctoral Researcher in Evolutionary Quantitative Genetics at the Research School of Biology, Australian National University

Evolution of mating patterns in a cooperative songbird

A 36-month postdoctoral position is available to study the evolutionary quantitative genetics of mating systems in a wild bird population. The project would investigate the evolutionary processes that shape mating and breeding systems, and in particular the evolution of mate choice, the dynamics of sexual selection and the interaction of these factors with the social environment. It will use data from a long-term study of superb fairy-wrens, a cooperatively-breeding passerine bird with exceptionally high levels of extra-pair paternity. The data-set comprises detailed records on individual life histories, mating patterns, relatedness and population spatial structure. The aim of the project is to address fundamental evolutionary questions about patterns of variation in breeding success and the role of indirect genetic effects and inclusive fitness.

The post constitutes an exciting opportunity for a highly-motivated postdoctoral researcher with experience in evolutionary ecology and/or quantitative genetic analyses. It will involve statistical analyses of a long-term data-set as well as fieldwork, in collaboration with Loeske Kruuk and Andrew Cockburn in ANU's Division of Evolution, Ecology and Genetics.

Applicants should possess (or be nearing completion of) a PhD in a relevant area of evolutionary ecology or genetics. They should have strong skills in complex statistical analyses; in particular, whilst familiarity with quantitative genetic mixed models is by no means essential, it would be a strong advantage. They should also be able to demonstrate excellent writing skills and a strong track record of publication in academic journals.

The position is available for 36 months. Start date could be as soon as possible dependent on red tape, and the salary would be $81,122 p.a. plus 17% superannuation.

For informal enquiries or further information, please contact Loeske.Kruuk@anu.edu.au.

To apply: http://internaljobs.anu.edu.au/cw/en/job/508972/postdoctoral-fellow Closing date 31 July 2016.

Professor Loeske Kruuk Division of Evolution, Ecology & Genetics Research School of Biology The Australian National University Canberra, ACT 2601 Australia Loeske.Kruuk@anu.edu.au www.biology.anu.edu.au/Loeske_Kruuk Loeske Kruuk <loeske.kruuk@anu.edu.au>

AustralianNationalU EvolQuantGen

Postdoctoral Researcher in Evolutionary Quantitative Genetics at the Research School of Biology, Australian National University

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To apply: http://internaljobs.anu.edu.au/cw/en/job/508972/postdoctoral-fellow Closing date 31 July 2016.

Professor Loeske Kruuk Division of Evolution, Ecology & Genetics Research School of Biology The Australian National University Canberra, ACT 2601 Australia Loeske.Kruuk@anu.edu.au www.biology.anu.edu.au/Loeske_Kruuk Loeske Kruuk <loeske.kruuk@anu.edu.au>

Berlin Metabarcoding

Postdoc:Berlin.Metabarcoding

We are looking for a postdoc interested in preparing an application for the International IGB Fellowship Program in Freshwater Science (1-year position) for the next call (30 June 2016): http://www.igb-berlin.de/igb-fellowship-812.html We are currently using metabarcoding approaches to assess evolutionary and ecological changes in our model lake: Müggelsee (Berlin, Germany). This lake has been intensively studied since the 1970s and phytoplankton and zooplankton communities are responding to global stressors including climate change or eutrophication. This project will involve implementation of genomics approaches into our lake monitoring program and analyses of existing metabarcoding data.

The project will be carried out in Berlin, at the Leibniz Institute of Freshwater Ecology and Inland Fisheries (IGB) and the Berlin Center for Genomics in Biodiversity Research (BeGenDiv):

http://www.igb-berlin.de/ http://begendiv.de/

Applicants must have experience in metabarcoding or metagenomic analysis (prokaryotes or eukaryotes) and interest in applying these tools to evolutionary and ecological questions. Preference will be given to candidates with a strong publication record.

The successful applicant will then prepare, together with us, a fellowship application (1 page + CV) to be submitted 30 June 2016. Recipients are notified within 4-6 weeks of application and can start one month after notification. Please note that applicants who currently reside in Germany are not eligible for the International IGB Fellowship Program. In keeping with the IGB's policy regarding gender equality, female applicants are particularly encouraged. Severely disabled applicants with equal qualification and aptitude are given preferential consideration.

If you have a strong CV and are interested in the research topic, please send an email (including a CV) with NGS lake project in the subject line to both PIs by 11 June 2016:

Prof. Justyna Wolinska (wolinska@igb-berlin.de)

Michael T. Monaghan (monaghan@igb-berlin.de)

Justyna Wolinska

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

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

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

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

Berlin Zurich Genomics

Postdoc:Berlin.Zurich.Genomics

Eawag, the Swiss Federal Institute of Aquatic Science and Technology (Dübendorf, Switzerland), and IGB, the Leibniz-Institute of Freshwater Ecology and Inland Fisheries (Berlin, Germany), are internationally recognized institutes that are committed to the ecological, economical and social management of water. They offer excellent laboratory and field facilities for interdisciplinary research, large-scale experimental facilities, and long-term research programs and data sets. These institutions share common goals towards education, research, and technology transfer at the highest international level.

The Department of Aquatic Ecology (Eawag) and the Department of Ecosystem Research (IGB) seek Postdoctoral Researcher in Genomics (2-year position) Project title: Hostâparasite interactions in hybridizing Daphnia, from correlations to experiments

The postdoctoral researcher will participate in a collaborative research project with PD Dr. Piet Spaak (Eawag) and Prof. Justyna Wolinska (IGB), financed by the Swiss and German Science Foundations (SNF & DFG).

Eutrophication is a worldwide environmental problem accelerated by global warming, affecting the stability of aquatic ecosystems and having longâconsequences. We will investigate if and how eutrophication affects two interacting evolutionary processes: disease spread and interspecific hybridization. We will use water fleas (Daphnia), a well-established model in both host-parasite and hybridization research. This project is a combination of field surveys of two eutrophic lakes, a large scale mesocosm experiment (where trophic conditions will be manipulated), the transcriptional profiling of Daphnia exposed to stressful eutrophic conditions, and the development and application of molecular markers to study parasite evolution in eutrophic environments. Overall, through the unique combination of expertise and methods, this project will improve our understanding of disease spread and biodiversity loss under different trophic conditions and, consequently, might provide tools for management of aquatic ecosystems.

This is a collaborative project involving a team of five researchers: both PI's, a PhD student in Germany, a PhD student in Switzerland as well as this postdoctoral researcher (one year in Germany and one year in Switzerland). The PhD students will be primarily responsible for processing samples in a molecular lab (as well as for experimental- and field-work), whereas the postdoctoral researcher will work on the bioinformatics of the project. The first task will be the sequencing of the genome of our model parasite species, and the use of this information to develop molecular markers to study parasite evolution in the hybridizing host (Daphnia). Second, Daphnia will be transcriptionally profiled (RNA-seq) under various stressful conditions (including parasitism), in order to explore the mechanisms underlying immunity and synergistic interactions between the stressors. Third, depending on skills and interests, the postdoctoral researcher might also get involved in a large genomic project, which involves an annotation of several Daphnia lineages, belonging to either parental species or interspecific hybrids.

The position will be for a period of two years and should start in January 2017 or soon thereafter (negotiable). Generous funds are available to cover attendance at national and international conferences and for stays in collaborating institutions. The postdoctoral researcher will have an opportunity to participate in several research training exercises and workshops to facilitate career building: http://www.igb-berlin.de/postdocs-at-igb-kopie.html In Berlin, the postdoctoral researcher will additionally be affiliated with the Berlin Center for Genomics in Biodiversity Research (BeGenDiv): http://begendiv.de/ The ideal candidate should have a strong background in bioinformatics and genomics, and interest in applying these tools to evolutionary questions. In particular, experience with genome annotation, development of SNP markers, and/or analyses of RNA-seq data would be advantageous. In addition, some lab experience would be beneficial (but this is not a must).

We are seeking a highly motivated person who has an ambition to stay in academia. A record of successful publication is anticipated. We expect strong analytical and data handling skills, and the ability to communicate within a cross-disciplinary research environment. Excellent writing skills in English, good work ethic, and creative thinking are desired. The working language of the group is English. In keeping with the IGB's policy regarding gender equality, female applicants are particularly encouraged. Severely disabled applicants with equal qualification and aptitude are given preferential consideration.

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BrighamYoungU CottonGenomeEvolution

A postdoctoral position is available at Brigham Young University, Department of Plant and Wildlife Sciences. The postdoctoral person will be coordinate a project to sequence the existing genetic diversity with cotton germplasm collections. A large number of domesticated and wild cotton accessions will be sequenced from multiple species. They will analyze of large amounts of whole-genome shotgun data from tetraploid and diploid cotton species to identify loci under selection during domestication. The ideal candidate would have a thorough understanding of genetics, DNA sequencing, bioinformatics, and experience on a supercomputer. All are not required. A Ph.D. in bioinformatics, 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. (< https://yjobs.byu.edu/hr/postings/10114 >)

*The application and start date are flexible, but preferably the postdoc would be hired during the 2016-2017 academic year. 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). To receive consideration, please send all application materials as soon as possible.*

Joshua Udall (5133 LSB) Brigham Young University 701 E. University Parkway Plant and Wildlife Science Depart. Provo, UT 84602

Office: 801-422-9307

jaudall1@gmail.com

BrooklynCollege EvolutionaryBiol

Job Title: Research Associate (Post-Doctoral) - Biology

Job ID: 14984

Location: Brooklyn College

Full/Part Time: Full-Time

Regular/Temporary: Regular

Under the mentorship and guidance of Dr. Jeremy Draghi, Assistant Professor of Biology (Principal Investigator), the post-doctoral fellow will assist with research activities and train and supervise student researchers. Research projects will focus on the PIs areas of interests: evolutionary theory, eco-evolutionary feedbacks, and epistasis & gene interactions, and evolution of microbes. See www.jeremydraghi.com for more information about activities in the lab.

The post-doctoral fellow will:

- Develop plans, collect and analyze data based on projects prepared by the Principal Investigator.

- Prepare reports of completed projects for publication in scientific journals, academic presentations or for further applied or theoretical research activities.

- Develop, plan, and conduct new research projects.

- Assist the Principal Investigator with managing laboratory budgets and research supplies.

- Train and supervise undergraduate and graduate researchers.

MINIMUM QUALIFICATIONS

Doctoral Degree in a related field and demonstrated research ability.

OTHER QUALIFICATIONS

- A doctoral degree in biology or quantitative fields such as physics, mathematics or computer science is preferred.

- Published research in evolutionary biology.

- Experience with one or more programming environments, especially C, R, and Mathematica.

- Experience with the mathematical analysis of models.

- Outstanding communication and writing skills.

- A history of successful collaborative work and mentoring.

COMPENSATION

$44,849; All appointments are subject to financial availability.

BENEFITS

CUNY offers a comprehensive benefits package to employees and eligible dependents based on job title and classification. Employees are also offered pension and Tax-Deferred Savings Plans. Part-time employees must meet a weekly or semester work hour criteria to be eligible for health benefits. Health benefits are also extended to retirees who meet the eligibility criteria.

HOW TO APPLY

Applicants must upload their cover letter (referenced Job ID # 14984), resume, and contact information (name, phone number, and email address) for three references in rtf, doc or pdf format.Please visit www.brooklyn.cuny.edu/adminjobs and click on the job title's link.

CLOSING DATE

July 22, 2016

EQUAL EMPLOYMENT OPPORTUNITY

CUNY encourages people with disabilities, minorities, veterans and women to apply. At CUNY, Italian Americans are also included among our protected groups. Applicants and employees will not be discriminated against on the basis of any legally protected category, including sexual orientation or gender identity. EEO/AA/Vet/Disability Employer.

Jennifer Tsui <JTsui@brooklyn.cuny.edu>

CIBIOInBIO Portugal 3 EnvironmentalMetagenomics

1. Two research positions for PhD holders

Ref: ICETA 2016-52

Link to the call

Job description:

Two research positions for PhD holders (References ICETA 2016-52) are available to work on a range of projects that employ analysis of environmental DNA to address ecological questions. The post-doctoral positions will be contracted under the scope of the project "EnvMetaGen - Capacity Building at InBIO for Research and Innovation Using Environmental Metagenomics" (Reference No 668981), funded by the European Commission under the call H2020-WIDESPREAD-2014-2. The project aims to expand the research and innovation potential of InBIO, supporting emerging research areas in environmental metagenomics for applications in biodiversity surveys, invasive species control, ecosystem services assessment, and environmental (bio)monitoring. The successful candidates will work on one or more potential projects that will be determined by their interests and skills and the research areas that are developed at CIBIO-InBIO associated with the EnvMetaGen project. Examples of current research at CIBIO-InBIO that are employing environmental metagenomics include analysis of diet of bats and birds by DNA metabarcoding of faecal DNA; analysis of invertebrate species composition of rivers, lakes and estuaries; researching critical components of the diet of endangered species; and biodiversity surveying by analysis of the diets of multiple high trophic level species. Similar research topics will be developed as the EnvMetaGen project progresses and the post-doctoral researchers will be expected to take a role in directing research in these areas. The successful candidates should be flexible in working both independently on their own projects and being involved in current and future projects as part of the overall EnvMetaGen team.

Research field:

Biological sciences

Admission requirements: The research positions are suitable for candidates of any nationality holding a PhD degree based on research in an area that includes the use of modern molecular biological methods to answering environmental or ecological questions. The candidates should have skills and experience in:

1. Laboratory research in molecular biology applied to environmental or ecological research. 2. Publication of their own research in international, peer-reviewed journals. 3. Data analysis methods including: statistical analyses; scripting in R, Python or similar languages; bioinformatic methods for analysis of high throughput DNA sequencing in DNA metabarcoding applications; and high quality data presentation for publication. 4. Experimental planning and working effectively both independently and as part of a multi-disciplinary team. 5. Fieldwork and organisation of sample collection with non-scientific project affiliates.

Project overview: The goal of the project is to expand the research and innovation potential of InBIO - Research Network in Biodiversity and Evolutionary Biology, through the creation of a European Research Area (ERA) Chair in Environmental Metagenomics and recruitment of a team of researchers and support staff to work with the ERA chair. The project aims to strengthen the research potential of human resources, lab facilities and next-generation genome sequencing equipment funded by a FP7 CAPACITIES project, supporting an emerging research line in environmental metagenomics for applications in biodiversity conservation, invasive species control, ecosystem services assessment, and environmental (bio)monitoring. The project will contribute to the regional and national smart specialisation strategies, by developing tools and approaches to foster environmentally sustainable development, and strengthening innovation and knowledge transfer activities in close collaboration with local and global industrial partners, as well as with governmental agencies. In addition, the project will contribute to the advanced training of new scientists to expand the locally available expertise in this area, and to the communication, dissemination and exploitation of InBIO's research and innovation. These two post-doctoral positions are a key component of the EnvMetaGen team. These two positions will upgrade InBIO's research capacity, improve its innovation potential and through peer reviewed publication and other knowledge dissemination mechanisms and better integrate InBIO within the ERA.

Benefits:

- Initial appointment for 4 years; - Internationally competitive salary commensurate with qualifications and experience; - Significant opportunities for travelling, training, conference attendance and networking.

Work place: The work will be mainly conducted at the Vairao campus of the Centro de Investigacao em Biodiversidade e Recursos Geneticos (CIBIO-InBIO), Universidade do Porto. However, the candidates may be required to do some field work and spend some time in other labs, both in Portugal and elsewhere, in the scope of research, training and

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CIBIO-InBIO Portugal Archaeogenetics

Post-doctoral Fellowship

Ref: ICETA 2016-48

Link to the call

Description

One post-doctoral fellowship (Reference ICETA 2016-48) is opened at CIBIO-InBIO, funded by the Fundacao para a Ciencia e a Tecnologia, I.P., (FCT) Project

"ARCHAIC - The archaeogenetics of Iberian cattle: investigating their origins, evolution and improvement" (PTDC/CVT-LIV/2827/2014).

Main research field

Biological sciences

Scientific areas

Biological Sciences / Archaeogenetics

Admission requirements

The post-doc fellowship is suitable for candidates of any nationality holding a PhD degree in biology, genetics, animal science or related fields. The candidate must have research experience in genetics, including laboratory skills in DNA extraction, sequencing and genotyping of molecular markers. It is desirable that the candidate has experience in ancient DNA methodologies (or in the genetic analysis of degraded specimens) and in preparation of DNA libraries for next-generation sequencing. Analysis of genetic data and bioinformatics knowledge will be valued. The candidate is expected to be able to work independently, to show initiative, perseverance and to have excellent verbal and written communication skills. Excellent speaking and written knowledge of English is required. A proven publication track record is required.

Project overview and workplan

The candidate will work in collaboration with the other team members to achieve the objectives of the project. Iberian domestic animal breeds show a vast range of morphological and genetic variation. This is due to strong artificial selection, however what fraction results from local domestication and/or post-domestication introgression from wild ancestors has not been investigated. The major aim of the ARCHAIC project is to perform a phylochronological study, by using cutting-edge molecular biology methods, to capture ancestral variation and to unveil the origins and modes of improvement of Iberian and North African cattle. A multidisciplinary approach - merging zooarchaeology and genomics - will be employed, which is critical to capture the temporal and geographical dimensions of the history that shaped the genetic composition of cattle.

The selected candidate will collaborate with zooarchaeologists to collect Bos specimens for ancient DNA (aDNA) analysis, and will be responsible for extracting aDNA from archaeological specimens (i.e. bones and teeth), for preparing genomic libraries for next-generation shotgun and targeted sequencing. The candidate will have an active role in the statistical analysis of the genetic data collected and in drafting manuscripts for publication. The aDNA analyses will be conducted in dedicated facilities offered by foreign partners (e.g. AFL-Stockholm University), thus the candidate must be available to travel and live abroad for up to 6 months. The candidate will participate in informal meetings among project partners. Participation in national and international seminars is also expected.

Keywords

Archaeogenetics; phylochronology; domestication; hybridization; animal improvement

Legislation framework

A fellowship contract will be celebrated according to the regulations defined by FCT "Regulations for Advanced Training and Qualification of Human Resources", in accordance with Law 40/2004, of 18 August, as amended and republished by Decree-Law No. 202/2012 of 27 August, and as amended by Decree-Law No. 233/2012 of 29 October and by Law No. 12/2013, of 29 January, and Decree-Law No. 89/2013 of 9 July, to Fellowships Regulation of FCT (www.fct.pt/apoios/bolsas/docs/-RegulamentoBolsasFCT2015.pdf), and to Fellowships Regulation of ICETA approved by FCT.

Work place

The work will be mainly conducted at CIBIO-InBIO Campus Agrario de Vairao, Portugal under the scientific supervision of Doctor Catarina Ginja.

Fellowship

The duration of the fellowship is 12 months, renewable up to a maximum of two years.

Salary

Monthly stipend is euro1495 according to the stipends established by FCT, I.P. in Portugal (http://-alfa.fct.mctes.pt/apoios/bolsas/valores). Payment will be made by bank transfer on a monthly basis. During the time spent in a foreign laboratory travel and accommodation expenses will be covered by the project. The grant holder will have a personal accident insurance and, if not covered by any social protection scheme can ensure the right to social security through adherence to the voluntary social insurance scheme, pursuant to Codigo dos Regimes Contributivos do Sistema Previdencial de Seguranca Social.

Application

The call for applications is open between 08/06/2016 and 22/06/2016 (24:00 GMT).

Applications must be submitted by email to bolsas@cibio.up.pt with the fellowship reference in the subject area, and the following documents attached:

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CIBIO-InBIO Portugal Archaeogenetics 2

Post-doctoral Fellowship

Ref: ICETA 2016-48

Link to the call: http://www.eracareers.pt/opportunities/index.aspx?task=3Dglobal&jobId=3D76115

Description

One post-doctoral fellowship (Reference ICETA 2016-48) is opened at CIBIO-InBIO, funded by the Fundacao para a Ciencia e a Tecnologia, I.P., (FCT) Project "ARCHAIC - The archaeogenetics of Iberian cattle: investigating their origins, evolution and improvement" (PTDC/CVT-LIV/2827/2014).

Main research field

Biological sciences

Scientific areas

Biological Sciences / Archaeogenetics

Admission requirements

The post-doc fellowship is suitable for candidates of any nationality holding a PhD degree in biology, genetics, animal science or related fields. The candidate must have research experience in genetics, including laboratory skills in DNA extraction, sequencing and genotyping of molecular markers. It is desirable that the candidate has experience in ancient DNA methodologies (or in the genetic analysis of degraded specimens) and in preparation of DNA libraries for next-generation sequencing. Analysis of genetic data and bioinformatics knowledge will be valued. The candidate is expected to be able to work independently, to show initiative, perseverance and to have excellent verbal and written communication skills. Excellent speaking and written knowledge of English is required. A proven publication track record is required.

Project overview and workplan

The candidate will work in collaboration with the other team members to achieve the objectives of the project. Iberian domestic animal breeds show a vast range of morphological and genetic variation. This is due to strong artificial selection, however what fraction results from local domestication and/or post-domestication introgression from wild ancestors has not been investigated. The major aim of the ARCHAIC project is to perform a phylochronological study, by using cutting-edge molecular biology methods, to capture ancestral variation and to unveil the origins and modes of improvement of Iberian and North African cattle. A multidisciplinary approach - merging zooarchaeology and genomics - will be employed, which is critical to capture the temporal and geographical dimensions of the history that shaped the genetic composition of cattle.

The selected candidate will collaborate with zooarchaeologists to collect Bos specimens for ancient DNA (aDNA) analysis, and will be responsible for extracting aDNA from archaeological specimens (i.e. bones and teeth), for preparing genomic libraries for next-generation shotgun and targeted sequencing. The candidate will have an active role in the statistical analysis of the genetic data collected and in drafting manuscripts for publication. The aDNA analyses will be conducted in dedicated facilities offered by foreign partners (e.g. AFL-Stockholm University), thus the candidate must be available to travel and live abroad for up to 6 months. The candidate will participate in informal meetings among project partners. Participation in national and international seminars is also expected.

Keywords

Archaeogenetics; phylochronology; domestication; hybridization; animal improvement

Legislation framework

A fellowship contract will be celebrated according to the regulations defined by FCT "Regulations for Advanced Training and Qualification of Human Resources", in accordance with Law 40/2004, of 18 August, as amended and republished by Decree-Law No. 202/2012 of 27 August, and as amended by Decree-Law No. 233/2012 of 29 October and by Law No. 12/2013, of 29 January, and Decree-Law No. 89/2013 of 9 July, to Fellowships Regulation of FCT (www.fct.pt/apoios/bolsas/docs/RegulamentoBolsasFCT2015.pdf), and to Fellowships Regulation of ICETA approved by FCT.

Work place

The work will be mainly conducted at CIBIO-InBIO Campus Agrario de Vairao, Portugal under the scientific supervision of Doctor Catarina Ginja.

Fellowship

The duration of the fellowship is 12 months, renewable up to a maximum of two years.

Salary

Monthly stipend is euro1495 according to the stipends established by FCT, I.P. in Portugal (http://alfa.fct.mctes.pt/apoios/bolsas/valores). Payment will be made by bank transfer on a monthly basis. During the time spent in a foreign laboratory travel and accommodation expenses will be covered by the project. The grant holder will have a personal accident insurance and, if not covered by any social protection scheme can ensure the right to social security through adherence to the voluntary social insurance scheme, pursuant to Codigo dos Regimes Contributivos do Sistema Previdencial de Seguranca Social.

Application

The call for applications is open between 08/06/2016 and 22/06/2016 (24:00 GMT).

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CIBIO Portugal DiseaseEvolution

Post-doctoral Fellowship

Ref: ICETA 2016-41

Link to the call

Job description:

Applications are invited for a Postdoctoral Fellowship (Reference ICETA 2016-41) in the context of the project “Modelling and inference for population and ecosystem health” (IF/01346/2014), funded by FCT/MCTES (PIDDAC) and co-funded by FEDER through COMPETE (POFC).

Research field:

Infectious disease epidemiology

Eligibility:

Candidates must hold a PhD in mathematical, biomedical or social sciences. Preference will be given to candidates with research experience in mathematical/statistical modelling of biomedical systems.

Work plan: Statistical analysis of the social and biologic determinants of tuberculosis in Portugal, and development of mathematical and computational models of the disease in a heterogeneous population. Impact studies for intervention strategies targeting high risk groups.

Legislation and regulations:

Estatuto do Bolseiro de Investigacao CientÃfica, aprovado pela Lei n.o 40/2004, de 18 de Agosto, alterado e republicado pelo Decreto-Lei n.o 202/2012, de 27 de Agosto, alterado ainda pelo Decreto-Lei n.o 233/2012, de 29 de Outubro, pela Lei n.o 12/2013, de 29 de Janeiro, e pelo Decreto-lei n.o 89/2013, de 9 de Julho; Regulamento de Bolsas e Investigacao da Fundacao para a Ciencia e a Tecnologia, IP (FCT), em vigor (www.fct.pt/apoios/bolsas/docs/RegulamentoBolsasFCT2015.pdf) e de acordo com os Estatutos de Bolsa do ICETA aprovados pela FCT.

Work place:

The candidate will be affiliated to CIBIO-InBIO - Centro de Investigacao em Biodiversidade e Recursos Geneticos do ICETA - Instituto de Ciencias, Tecnologias e Agro-Ambiente, and will spend periods at the Liverpool School of Tropical Medicine, United Kingdom, under the supervision of Dr Gabriela Gomes.

Duration of fellowship:

The fellowship will have the duration of 12 months, starting on September 01, 2016.

Monthly stipend:

The fellowship stipend will be euro1.495/month, according to the regulations of the FCT Postdoctoral Fellowships in Portugal (http://alfa.fct.mctes.pt/apoios/bolsas/valores), paid monthly by bank transfer.

Selection procedures: Applications will be evaluated based on Curriculum Vitae (25%), motivation letter (15%) and references (10%). The best candidates will be selected for an interview (50%).

Selection Jury:

Prof. Dr. Gabriela Gomes (Chair)

Prof. Dr. Raquel Duarte

Prof. Dr. Rita Gaio

Prof. Dr. Gertrude Thompson

Notification of results:

The results of this call will be published in CIBIO-InBIO, and sent by email to all candidates and to the FCT.

Application period and documents:

The call will be open from 10 May 2016 until 10 July

2016.

Applications must include Curriculum Vitae (CV), motivation letter, and contact details of two references, sent to: bolsas.cibio@cibio.up.pt

CIBIO - Centro de Investigacao em Biodiversidade e Recursos Geneticos/ InBIO Laboratorio Associado, Universidade do Porto

Campus Agrario de Vairao

Rua Padre Armando Quintas

4485-661 Vairao

Portugal

t: +351 252 660 411 Ext. 285

f: +351 252 661 780

e: divulgacao@cibio.up.pt

w: http://cibio.up.pt | http://inbio.pt

f: https://www.facebook.com/cibio.inbio CIBIO-InBIO Divulgação

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FloridaIntlU MarineEvolutionaryGenomics

PostDoc: Evolution of Bioluminescence and Vision in the Deep Sea

The Bracken-Grissom Lab at Florida International University in the Department of Biology and Marine Sciences Program is looking for a postdoctoral fellow to work on a NSF-funded project to study the evolution of bioluminescence and vision in deep-sea shrimp. This position is for 1-year with possible extension dependent on performance.

The CRUSTOMICS Lab is fundamentally interested in using genomic techniques to study the evolution and adaptation of marine invertebrates with a focus on crustaceans. We are searching for a postdoc to lead a recently funded NSF project aimed to test several hypotheses addressing the evolution of bioluminescence and light detection in the deep sea. As part of this project the postdoctoral fellow will use phylogenomic methods to trace the evolution of different bioluminescence modes across deep-sea shrimp. In addition, RNA-Seq will be used to characterize the visual systems and bioluminescence organs within a comparative framework. Experience with wet-lab molecular techniques, phylogenomics, transcriptomics (RNA-Seq), large data matrices, associated analyses and software, and bioinformatics is required. Additional experience with visual system ecology and opsin evolution is a plus. In addition to research, mentoring of graduate and undergraduate students and lab manager duties are expected as part of this position. The successful candidate must have completed her/his doctoral degree before taking the position. Our work requires good organizational and computational skills and the ability to work collaboratively as part of a team. Occasional physically demanding fieldwork (research cruises) may also be required to support research.

Additional information on the lab's research, the biology department, and marine sciences program can be found here: and *www.brackengrissomlab.com, *http://biology.fiu.edu/ and www.fiu.edu/~marine.

Requirements: As a *single PDF*, applications must include a 1) cover letter briefly outlining the candidate's fit to the position 2) curriculum vitae 3) research statement, 4) contact information (email and phone) for three references, preferably including doctoral advisor and/or postdoctoral advisor (if relevant) and 5) three relevant PDFs and 5) All information may be sent directly to Dr. Heather Bracken-Grissom at hbracken@fiu.edu. If you attending SMBE 2016 and are interested and qualified for the position please contact me so that we can meet.

Due Date: To receive full consideration, applications and required materials should be received by July 5th, 2016. Review will continue until position is filled. The position may be taken as early as late August 2016 (if search is complete), but start date is flexible (+ a few months). A competitive salary and benefits package will be included. This position will be based on the Biscayne Bay Campus.

Contact Information

Heather Bracken-Grissom, PhD Assistant Professor Dept. of Biological Sciences Florida International University-Biscayne Bay Campus

3000 NE 151 Street, MSB-353

North Miami, Florida 33181, USA

305 919-4190 (Phone)

– Heather Bracken-Grissom, PhD Assistant Professor Dept. of Biological Sciences Florida International University-Biscayne Bay Campus 3000 NE 151 Street, MSB-353 North Miami, Florida 33181, USA 305 919-4190 (Phone) 305 919-4030 (Fax)

CRUSTOMICS: Crustacean Genomics and Systematics Lab *http://www.brackengrissomlab.com/ < http://heatherbracken.wix.com/brackengrissomlab > * heather.brackengrissom@fiu.edu

<Valerie.Hall@fiu.edu> www.fiu.edu/~marine Heather Bracken-Grissom <heather.bracken@gmail.com>

Halifax ModelingFishPopulations

Postdoctoral Fellow Position with Fisheries and Oceans Canada on modeling the impacts of Atlantic salmon aquaculture on wild Atlantic salmon populations.

Overview: Fisheries and Oceans Canada is seeking applicants for a full-time postdoctoral fellow position on modeling relationships between wild and farm escaped Atlantic salmon in the North Atlantic. This is a 24-month position that will be based at the Bedford Institute of Oceanography, Halifax Nova Scotia, beginning in the fall of 2016. The position may be extended contingent upon performance and funding. The PDF will be mentored by Dr. Ian Bradbury, and directly collaborate with both students and fellows in the lab as well as an international modeling team working on the topic. The successful candidate will undertake analyses and modelling to investigate the genetic and ecological impacts of escaped farmed salmon on wild populations. This project will directly inform management and conservation efforts of Atlantic salmon in Atlantic Canada.

Requirements: Candidates must have a Ph.D. in fisheries science, population genetics, genomics, oceanography or a related field. The position requires strong mathematical, and computational skills, and previous experience with individual based models, or population dynamics models would be an asset. Candidates should have experience in the R and/or MATLAB programming languages. In addition, candidates are expected to have a demonstrated ability to work independently and possess strong organizational and communication skills. The successful applicant will be expected to lead and contribute to journal articles, reports, and presentations to both stakeholders and scientific audiences. As this position will collaborate with an international team, the candidate should be willing and able to travel domestically and internationally on a regular basis.

To apply: Please submit a CV, and letter of interest to Dr. Ian Bradbury - ibradbur@me.com, Review of applications will begin on July 30th, 2016, but the position will remain open until filled. Questions should be referred to ibradbur@me.com.

Ian Bradbury <ibradbur@me.com>

Hannover EvolutionaryBiology

Department: Institute of Zoology, University of Veterinary Medicine, Hannover, Germany Position title: Postdoctoral Research Associate for Evolutionary Biology Full-time, starts on July 18, 2016

Position summary: Responsibilities will include research (65% time) in the field of molecular genetics and evolutionary biology as well as teaching of basic zoology courses for veterinary students in German, further research-oriented teaching, and general tasks at the institute (35% of time).

The position will be temporarily filled as replacement for a maternal leave but can be extended. Professional qualification (habilitation) on this position is supported.

Required skills: Extensive knowledge of molecular techniques, and bioinformatics skills. Strong publication and communication skills, and high capacity for teamwork. Experience in teaching of undergraduate and graduate students, as well as in obtaining external funding.

Major duties: Genetic laboratory analyses. Organisation and Management of large genetic data sets. Preparation of scientific papers for publication in peer-reviewed journals and for presentation at scientific conferences. Development and submission of research proposals. Supervision and teaching of undergraduate, master and graduate students.

Job Requirements: Ph.D. in the field of molecular biology, genetics, ecology and/or related disciplines, Fluency in German and English, international publication record.

Applicants with disabilities will be employed preferentially if equally qualified.

Full applications shall be sent to: Institute of Zoology, University of Veterinary Medicine, Bünteweg 17, 30559 Hannover, Germany or as email attachments to sandra.hamacher@tiho-hannover.de with copy to jasmin.ouakidi@tiho-hannover.de.

Applications have to include: application letter, curriculum vitae, copy of PhD transcript, publication and teaching record, contact information of 2 academic references.

Application deadline: June 20, 2016

Further information will be provided by Apl. Dr. Heike Pröhl: Phone: +49-511-9538431, Email:

heike.proehl@tiho-hannover.de

"Pröhl, Heike" <Heike.Proehl@tiho-hannover.de>

INRAFrance EvolQuantGenetics

Post doc position in Evolutionary Quantitative Genetics, INRA, Bordeaux, France

Job description: The general goal of the research is to predict evolutionary changes of trees, particularly European white oaks, to environmental changes using diachronic approaches. These predictions will be based on observations conducted in situ in age structured cohorts of different ages (from 360 to 5 years), and in common garden experiments. Populations that have experienced the little ice age (360 years ago) will be compared with more recent and modern populations. A major goal of the project will be to estimate components of evolutionary change (selection gradients, heritability, elements of the G matrix), by analyzing existing genomic, genetic and phenotypic data in wild populations.

Scientific environment: The post doc position is part of the ERC project Treepeace (http://www.treepeace.fr/). The working location will be at the BIOGECO research unit (20 km south-west of Bordeaux, France: https://www4.bordeaux-aquitaine.inra.fr/biogeco_eng/). BIOGECO is a joint research unit between INRA and the University of Bordeaux and has long standing experience in studying evolution of forest trees by assembling contributions of different disciplines (ecology, genetics, genomics and evolution).

Expected profile: We seek for a scientist with a PhD degree and experience in the field of evolutionary quantitative genetics and/or proficiency in statistical modeling. Knowledge of tree ecology and practice of computer programming will be helpful. Candidates should be fluent in English.

Application: Application with CV, a brief statement of research interests, contact information for two professional references and publication list should be submitted in an electronic form to Dr. Antoine Kremer (antoine.kremer@pierroton.inra.fr). Review of applications will begin on August 1st 2016 and continue until the position is filled. Do not hesitate to contact us for further details or questions. The position is open for 2 years.

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Examples of recent publications: Alberto F., J.Derory J, et al. (2013). "Imprints of natural selection along environmental gradients in phenology-related genes of Quercus petraea". Genetics 195, 495-512.

Kremer, A., B. M. Potts, et al. (2014). "Genetic divergence in forest trees: understanding the consequences of climate change." Functional Ecology 28(1): 22-36.

Kremer, A., O. Ronce, et al. (2012). "Long-distance gene flow and adaptation of forest trees to rapid climate change." Ecology Letters 15(4): 378-392.

Soularue, J. P. and A. Kremer (2014). "Evolutionary responses of tree phenology to the combined effects of assortative mating, gene flow and divergent selection." Heredity 113(6): 485-494.

cyril.firmat@pierroton.inra.fr

INRA QuantitativePopulationGenomics

We are looking for a highly motivated, creative and enthusiastic young scientist to join our team "prediction and management of genome and population diversity in forest trees" at INRA Orléans, France. Our ideal starting date is October 2016, but there is some flexibility.

Project description

Lignocellulosic biomass is a renewable resource of interest for biorefinery. However, current poplar varieties have not been selected for this specific purpose. The factors affecting biomass yield and chemical properties need thus to be studied. This is the main objective of the ANR funded project SYBIOPOP, within which we have initiated a systems biology approach, integrating genomic, transcriptomic and phenotypic data in natural populations of black poplar (Populus nigra). More specifically, we are focusing on 240 genotypes originated from 10 populations representative of the species range in Western Europe. These genotypes have been evaluated for the target traits in a common garden experiment located at Orléans. They have also been genotyped with a 12k Infinium array yielding around 8,000 reliable SNPs (Faivre-Rampant et al., MolEcolRes 2016). Additionally, RNA sequencing (RNAseq) of pools of young differentiating xylem and cambium has been carried out on 2 biological replicates of each of the 240 genotypes in order to simultaneously provide reliable expression profiles and sequence variants transcriptome wide. Within this context, the ultimate goal of the postdoc project will be to integrate these readily available genomic and transcriptomic data to better explain and predict the genetic variability of the phenotypes under study. This could be achieved through the following - not necessarily exhaustive - steps: * Quantitative genetics of transcriptomic data, including marker based heritability and Qst estimates; * Identification of polymorphisms associated with phenotypes (QTN) and transcripts (eQTN); * Identification of transcripts associated with phenotypes (QTT); * Gene network inference from transcripts co-expression.

Research environment

Our team has long research experience in genetics and genomics, biometry and tree physiology, as well as in conducting breeding programs for several of the main commercial tree species in France, including the model species of the project, black poplar. The successful candidate will interact with a multidisciplinary team of geneticist and physiologists, and will find readily local support on key issues like bio-informatics, if revisiting genomic data is eventually required, or high performance computing where the host has all required resources. We believe our team will make a great scientific environment for a young scientist. Moreover, Orléans is attractively situated by the beautiful Loire River, offering rich culinary, cultural, and outdoor possibilities.

Required qualifications & skills

We are looking for candidates with a Ph.D in quantitative genetics or statistical genomics, with experience in genetic analysis involving sequencing, and programming skills. Experience with biometrical analysis involving transcripts is a definite plus. The candidate will be encouraged to contribute to the scope and reach of the project by own ideas and approaches. An eventual extension of the grant will be highly conditioned to this holder's input. We expect from the successful candidate to be independent, creative, and with strong collaborative skills.

Terms & salary

Salary before taxes is 2,310.52, the same level as a junior permanent researcher. Duration could eventually be extended at least one extra year depending ultimately on the level of fulfilment and holder's involvements. Application instructions To apply, please send the following items to Vincent Segura (vincentDOTseguraATorleansDOTinraDOTfr) and Leopoldo Sanchez (lsanchezrodATorleansDOTinraDOTfr): * Letter of motivation complemented by a text where you will briefly introduce one of your best published works; * Curriculum Vitae; * Publication list; * Contact details of at least 2 referees. Deadline for applications: 22 August 2016. Decisions will be made available on 23 September 2016, the latest.

– Vincent Segura UR0588 Amélioration, Génétique et Physiologie Forestières INRA Val-de-Loire 2163 avenue de la Pomme de Pin CS 40001 - Ardon 45075 ORLEANS CEDEX 2 France Tel : +33(0)238417811 Fax : +33(0)238417879 https://sites.google.com/site/vincentosegura/ http://www6.val-de-loire.inra.fr/uragpf

visegura <Vincent.Segura@orleans.inra.fr>

IPasteur Paris EpiStatGenomics

POSTDOCTORAL RESEARCH ASSOCIATE IN EPIGENETICS AND STATISTICAL GENOMICS, Institut Pasteur A Postdoctoral Research Associate position in epigenetics and statistical genomics, funded by the Labex Milieu Interieur (www.milieuinterieur.fr/en), is available in the Human Evolutionary Genetics Unit (Quintana-Murci's Lab) at Institut Pasteur in Paris. The lab combines large empirical datasets and computation approaches to study epigenetic variation, population genetics and the human immune response, for more information see http://www.pasteur.fr/research/heg . The current project focuses on the dissection of the genetic and non-genetic factors affecting DNA methylation variation and its impact on immune response heterogeneity. Genetic, epigenetic and transcriptional data have been obtained in 1,000 healthy donors - stratified by age (5 decades of life, from 20 to 70 years old) and gender - and detailed socio-demographic and biological parameters have been defined. The goals of this project will be (i) to quantify how non-genetic factors, including sex, age, lifestyle habits, latent infections, etc, influence the levels of genome-wide DNA methylation, (ii) to dissect how genetic factors impact DNA methylation patterns, and (iii) to understand the (causal) relationships between genetic, epigenetic, and environmental factors accounting for by immune response heterogeneity. Our consortium benefits from the large and outstanding community of researchers in genomics, population genetics, microbiology, immunology and computational biology at the Institut Pasteur and Paris Universities, providing a working interdisciplinary research environment.

Postdoctoral applicants should have (i) a PhD in bioinformatics, computational biology, biostatistics, genomics, or population genetics, (ii) a quantitative background and/or extensive experience with genomic data analysis, and (iii) strong programming and bioinformatics skills (R and Perl/Shell scripting) are essential.

The position will remain open until filled. To apply, please send a cover letter, CV, summary of past work, and the names and email addresses of three references (in a single pdf file) to Lluis Quintana-Murci at <quintana@pasteur.fr> by **July 31, 2016**. Please put "Postdoctoral Research Associate" in the subject line of your email. Interviews, via Skype, will be held soon after this date. The starting date can be any time but not later than November 2016 (negotiable).

Lluis QUINTANA-MURCI <lluis.quintana-murci@pasteur.fr>

LiverpoolU DaphniaEvolution

Postdoc: Liverpool University, U.K. - limits to rapid evolution in Daphnia https://www.liverpool.ac.uk/working/jobvacancies/currentvacancies/research/r-590834/ s.plaistow@liverpool.ac.uk

LundU EvolutionaryEcology

Postdoc position in Evolutionary Ecology open i Lund.

Coevolution in metacommunities.

The following problems will primarily be addressed:

- Adaptive radiations and trait evolution in co-evolving metacommunities
- Ecological speciations and extinctions driven by trophic interaction in space
- The biogeography of sister species in two trophic levels.
- The importance and evolution of specialization in co-evolving communities

This is a theoretical project. We are also using published data on the spatial phylogenetic signal and sister species distributions from a wide range of organisms, e.g. small rodents and birds, fish, birds and mammals and their parasites, and plant-insect mutualistic interactions.

Project description, qualifications, application procedure and other info found here: https://lu.mynetworkglobal.com/en/what:job/jobID:106260/ Per Lundberg Jörgen Ripa

Per Lundberg, Professor (Theoretical Ecology) Theoretical Population Ecology and Evolution Group Department of Biology Ecology Building Lund University SE-223 62 LUND; SWEDEN

per.lundberg@biol.lu.se

Jörgen Ripa <jorgen.ripa@biol.lu.se>

LundU EvolutionMulticellularity

Dear colleagues, We are looking to recruit a postdoc for 2+1 years to work on the evolution of multicellularity in algae. I would be very grateful if you could alert potential candidates to the position.

Many thanks,

Charlie

Subject area

Evolutionary Biology: predicting the evolution of multicellularity

Description of the project

A postdoctoral fellowship position is available to work on a project examining the major evolutionary transitions led by Charlie Cornwallis. The fellow will work with researchers in the molecular ecology and evolution lab and the aquatic ecology group at the Department of Biology, Lund University.

Over evolutionary time there have been several major transitions that have shaped contemporary patterns of organismal complexity. In each of these transitions a group of individuals that previously replicated independently joined together to form a new, more complex life form. For example, unicells joined together to form multicellular bodies, asexual organisms combined to reproduce sexually and individual organisms have foregone independence to live in groups.

The position will focus on understanding what predisposes some species to undergo a major evolutionary transition, with particular focus on predicting why species go from being unicellular to multicellular. The project will use a combination of experimental evolution on target groups (e.g. green algae), and comparative analyses of the independent transitions to multicelluarity across the tree of life using genomic, ecological and life-history data. This position will provide the opportunity to explore social evolutionary theory and develop skills in experimental design, bioinformatics, phylogenetic comparative methods and meta-analysis.

The Department of Biology has a number of research units studying a range of ecological and evolutionary topics including aquatic ecology, microbial evolution, speciation, sexual selection, and host-parasite coevolution, and the post-doctoral fellow will be integrated across these different units.

Description of the qualifications that are required of the candidate

Qualifications:

Applicants should have completed a PhD in Evolutionary or Molecular Biology within four years from application deadline. Candidates should have a keen interest in general evolutionary theory and demonstrate an ability to be work both independently and in teams with other researchers, including co-supervising PhD and MSc students. Experience and skills in the following areas is essential: experimentation using algal and/or other microorganisms, molecular genetic analyses and laboratory work. Experience and skills in the following areas is desirable: bioinformatics, experimental evolution, linear mixed modeling and phylogenetic comparative analysis. Complementary training will be provided where needed.

Fluent written and spoken English is essential with a strong record of publishing in internationally recognized scientific journals. The scientific aptitude and the ability to develop and carry out high-quality research within the subject area will be given special attention in the assessment of the candidate. Importance will be attached to the potential of the candidate to develop as an independent researcher.

Salary will be set according to the general regulations for postdoctoral positions at Lund University in relation to the number of years research experience and achievements. Applicants should send a cover letter explaining their background, research interests and motivation for applying to this position, and a CV that includes publications and the contact information for two referees.

Additional Information For more information and informal discussion about the position candidates can contact Charlie Cornwallis (charlie.cornwallis@biol.lu.se).

Link to position and information about application procedure: https://lu.mynetworkglobal.com/en/what:job/jobID:103762/ Charlie Cornwallis <charlie.cornwallis@biol.lu.se>

LundU SocialEvolution

A postdoctoral fellowship is available for 3 years to work on the evolution of multicellularity

The fellow will work with researchers in the molecular ecology and evolution lab and the aquatic ecology group at the Department of Biology, Lund University.

The position will focus on understanding what predisposes some species to undergo a major evolutionary transition, with particular focus on predicting why species go from being unicellular to multicellular.

Over evolutionary time there have been several major transitions that have shaped contemporary patterns of organismal complexity. In each of these transitions a group of individuals that previously replicated independently joined together to form a new, more complex life form. For example, unicells joined together to form multicellular bodies, asexual organisms combined to reproduce sexually and individual organisms have foregone independence to live in groups.

The project will use a combination of experimental evolution on target groups (e.g. green algae), and comparative analyses of the independent transitions to multicelluarity across the tree of life using genomic, ecological and life-history data. This position will provide the opportunity to explore social evolutionary theory and develop skills in experimental design, bioinformatics, phylogenetic comparative methods and meta-analysis. The post-doc will also be supported by a technician.

The Department of Biology at Lund has a number of research units studying a range of ecological and evolutionary topics including aquatic ecology, microbial evolution, speciation, sexual selection, and host-parasite coevolution, and the post-doctoral fellow will be integrated across these different units.

Description of the qualifications that are required of the candidate

Applicants should have completed a PhD within the fields of Evolution, Ecology or Molecular Biology within four years from application deadline. Candidates should have a keen interest in general evolutionary theory and demonstrate an ability to be work both independently and in teams with other researchers, including co-supervising PhD and MSc students. Experience and skills in the following areas is essential: experimentation using algal and/or other microorganisms, molecular genetic analyses and laboratory work. Experience and skills in the following areas is desirable: bioinformatics, experimental evolution, linear mixed modeling and phylogenetic comparative analysis. Complementary training will be provided where needed.

Fluent written and spoken English is essential with a strong record of publishing in internationally recognized scientific journals. The scientific aptitude and the ability to develop and carry out high-quality research within the subject area will be given special attention in the assessment of the candidate. Importance will be attached to the potential of the candidate to develop as an independent researcher.

Salary will be set according to the general regulations for postdoctoral positions at Lund University in relation to the number of years research experience and achievements. Applicants should send a cover letter explaining their background, research interests and motivation for applying to this position, and a CV that includes publications and the contact information for two referees.

Additional Information

Deadline 15th July 2016

For more information and informal discussion about the position candidates can contact Charlie Cornwallis (charlie.cornwallis@biol.lu.se). Link to position and information about application procedure: https://lu.mynetworkglobal.com/en/what:job/jobID:103762/
Charlie Cornwallis <charlie.cornwallis@biol.lu.se>

MaxPlanckInst Plon TheoEvolutionaryGenomics

The Max Planck Institute for Evolutionary Biology in Plön (Schleswig-Holstein) is an internationally oriented research institute and is looking for a

Postdoc in Theoretical evolutionary biology and evolutionary genomics

A postdoctoral position is available for two years in the field of theoretical biology and evolutionary genomics with the Max Planck research group “Environmental Genomics” headed by Prof. Eva H. Stukenbrock. The Max Planck group is affiliated with the Max Planck Institute for Evolutionary Biology in Plön and the Christian-Albrechts University of Kiel in the North of Germany. The position is funded by the German Research Foundation, DFG, in the framework of the Priority Program “Rapid Evolutionary Adaptation - Potentials and Constraints”. The project will be conducted in close collaboration with Prof. Wolfgang Stephan, Museum für Naturkunde, Berlin, Germany.

Background Antagonistic co-evolution between pathogens and their hosts can drive rapid adaptive changes in both partners. In this project we aim to understand the underlying mechanisms that drive rapid adaptation in two closely related fungal plant pathogenic species Zymoseptoria tritici (pathogen of cultivated wheat) and Z. ardabiliae (pathogen of wild grasses). These two species differ not only in terms of host and environment (agro-ecosystem versus natural grassland) but also in terms of demography. Our previous analyses have documented a high effective population size in Z. tritici and a strong impact of natural selection on genome evolution.

In this project we aim to investigate the role of recombination in rapid adaptation of Z. tritici and Z. ardabiliae. Comparing patterns of genome evolution in the two species that exist in contrasting environments will allow us to address the impact of ecological constraints on evolution of pathogens. We have used a population genomic approach to infer the genomic recombination landscape in the two species and show the presence of dynamic recombination hot spots in coding sequences in both species. In this project we aim to identify signatures of positive selection in the genomes of Z. tritici and Z. ardabiliae using composite likelihood ratio (CLR) statistics and modeling. A particular goal is to infer the genome-wide distribution of selective sweeps accounting for demography in the two species and we will correlate this information with recombination maps to assess the importance of recombination to adaptive evolution. The development and application of appropriate models will be conducted with Prof. Wolfgang Stephan.

Relevant Literature - Wilches R, Voigt S, Duchen P, Laurent S, Stephan W (2014) Fine-mapping and selective sweep analysis of QTL for cold tolerance in Drosophila melanogaster. G3: Genes| Genomes| Genetics 4(9):1635-1645 - Stukenbrock EH, Bataillon T, Duthei JY, Hansen TT, Li R, Zala M, McDonald BA, Wang J, Schierup MH (2011). The making of a new pathogen: Insights from comparative population genomics of the domesticated wheat pathogen Mycosphaerella graminicola and its wild sister species. Genome Research 21.12 (2011): 2157-2166 - Stukenbrock EH, Banke S, Javan-Nikkhah M, McDonald BA. 2007. Origin and domestication of the fungal wheat pathogen Mycosphaerella graminicola via sympatric speciation. Molecular Biology and Evolution 24: 398-411 - Kim Y, Stephan W (2002).? Detecting a local signature of genetic hitchhiking along a recombining chromosome. Genetics 160: 765-777

Description The candidate should have a PhD in the field of population genetics with expertise in population genomics analyses and theoretical modeling. Proficiency in Linux scripting, in a major programming language and in handling large datasets are needed. The selected candidate will have the opportunity to collaborate with a team of biologists (molecular biologists, evolutionary biologists and population geneticists) as well as to pursue unique research in the fields of population genomics and evolutionary genomics of pathogenic fungi as well as theoretical population genetics. For further information please contact Eva Stukenbrock (stukenbrock@evolbio.mpg.de).

This position requires a highly self-motivated candidate with excellent oral communication skills and great interpersonal skills. Interested candidates should send a motivation letter including a description of current research directions, an up-to-date CV, together with the names and the contact information of two references to Eva H. Stukenbrock as pdf. Application deadline is August 1st, 2016, however the position will remain open until filled by a qualified candidate.

The Max Planck Society is committed to increasing the number of individuals with disabilities in its workforce and therefore encourages applications from such qualified individuals. The Max Planck Society seeks to increase the number of women in those areas where they are underrepresented and therefore explicitly encourages women to apply.

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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

McGill MathPopulationGenetics

PhD and postdoc projects in mathematical and population genetics are available at McGill University in Montreal, Canada. The projects aim to develop mathematical, statistical, or computational models to better understand human genetics, human history, and disease. Sample projects are outlined below.

Candidates should have:

- a strong background in mathematics, statistics, programming, or related fields;

- demonstrated interest in biology, evolution, or medical research;

- a curious and creative mind.

Experience in genetics, stochastic processes, or machine learning are assets.

The fully-funded positions offer an exceptional opportunity to develop theoretical and computational ideas and apply them to cutting-edge data in a supportive and thriving research environment.

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

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Project 1: Genetics and Human history

The student will develop mathematical models of human genetic diversity to refine our understanding of human history, demography, and disease risk, especially in non-European populations.

Project 2: Tumor heterogeneity

The student will model heterogeneity in primary and metastatic tumors through simulation and mathematical models. She will seek to answer fundamental questions about cancer progression and resistance to treatment, and to help interpret the latest generation of sequence data.

Project 3: Genetics, Genealogies, and Evolution The student will develop statistical models that combine genetic and genealogical data to learn about the transmission history of alleles over generations and identify evidence for selection or disease-causing alleles. He will work with some of the largest and most complete genealogical datasets available, as well as with cutting-edge biological datasets.

Simon gravel <gravellab@gmail.com>

MichiganStateU EvolutionaryGenetics

Postdoc opportunity: Evolutionary & Landscape Genetics plus Sensory Evolution

With Jenny Boughman, Michigan State University

Postdoctoral scientist wanted for evolutionary and landscape genetics projects funded by NSF. Experience in genomic analysis (admixture mapping, fitness mapping, landscape genomics) highly desirable. Additional experience in quantitative genetics (G matrix) and evolution of sensory systems a definite plus. Good writing and communication skills highly prized. Opportunities for independent research. Initial position for 1 year with possibility of renewal.

MSU provides a dynamic intellectual environment for motivated evolutionary biologists.

If interested, send CV, letter of interest and 1 or 2 papers to: Jenny Boughman at boughman@msu.edu.

I will be attending the Evolution meeting in Austin and can arrange an interview there.

"boughman@msu.edu" <boughman@msu.edu>

Montpellier CoevolvedNetworks

Post-doc position in Ecological networks (ISEM Montpellier and MNHN Paris, France)

"Stability of coevolved interaction networks"

A two-year postdoctoral position is available in the research group of Sonia Kefi (ISEM, BioDICee team, Montpellier, France) in collaboration with Colin Fontaine (MNHN, Paris, France). Applications will be assessed from June 6.

Project description

The postdoc applicant will work in the context of a wider project funded by the ANR (the French National Research Agency) called ARSENIC, "Adaptation and Resilience of Spatial Ecological Networks to human-Induced Changes" (2015-2019). The general aim of ARSENIC is to contribute to the understanding of how ecological networks are shaped by evolution.

Using modeling, this postdoc will investigate how network properties which have emerged from evolutionary dynamics affect the dynamics and stability (resilience, robustness) of ecological networks. Theoretical predictions will be confronted to data, taking advantage of existing databases on species traits and interactions.

Requirements

* PhD in (theoretical) ecology, applied mathematics, physics, or similar background * Strong modeling skills * Programming skills (R, C++ and/or Matlab) * Statistics and data analysis skills * Interest in linking models with data * Fluent in English * Good scientific writing skills

The ideal candidate will have experience with network approaches (modeling and/or data analysis) and an interest in linking models and data.

Appointment

The postdoc position should ideally start in the fall 2016, no later than the summer of 2017. Salary will be based on work experience according to University of Montpellier regulations (e.g., about 2200euro two years after PhD).

Job application

Applications should include a detailed CV with a list of publications, a letter of interest, a short description of research experience and interests (1 page maximum), and the names and contact addresses of two academic references from whom information about the candidate can be obtained. Combine all these items into a single PDF file.

Applications should be sent by email only to Sonia Kefi (sonia.kefi@univ-montp2.fr) and Colin Fontaine (cfontaine@mnhn.fr).

Applications will be assessed from June 6 and until the position is filled. Interviews, possibly via Skype, will be held soon after this date.

Sonia Kefi <sonia.kefi@univ-montp2.fr>

NHM Denmark PopulationPalaeogenomics

Postdoc of Population Palaeogenomics

A computation genomic postdoctoral position is available in the Megafauna Palaeogenomics project, a recently funded Villum foundation Young Investigator Programme Grant based at the Natural History Museum of Denmark. The successful candidate will be required to undertake evolutionary genomic analyses of population-level palaeogenomic data.

Thus mandatory skills include demonstrated experience in computational genomic analysis of whole-genome NGS data and of palaeogenetic/genomic data, as well as expertise in population genomic theory and computational methods.

The postdoc's duties will primarily include research within genomics, as well as teaching. The post may also include performance of other duties.

Further information on the Department is linked at http://snm.ku.dk/english/research/sections/-evolutionary_genomics/ . Inquiries about the position can be made to Associate Professor Eline Lorenzen (elinelorenzen@snm.ku.dk).

The position is open from 1st September 2016 or as soon as possible thereafter, and is time limited for two years, with the possibility of extension for one year.

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

More information can be found here:

http://jobportal.ku.dk/videnskabelige-stillinger/-?show=3D828722 Best regards / Venlig hilsen Eline Associate Professor Eline LORENZEN, PhD Curator of Mammals Villum Young Investigator

Natural History Museum of Denmark ÃËster Voldgade 5-7 1350 Copenhagen K Denmark

Email elinelorenzen@snm.ku.dk Tel: +45 2670 1024

Eline Lorenzen <elinelorenzen@snm.ku.dk>

NOAA Seattle MarineFisheriesPopulationGenomics

POSTDOCTORAL FELLOWSHIP OPPORTUNITY

NOAA Fisheries, Northwest Fisheries Science Center

TITLE: Population genetics of marine fish species to inform assessment and management efforts

The Fisheries Resource, Assessment, and Monitoring (FRAM) and Conservation Biology (CB) Divisions at the NOAA Fisheries, Northwest Fisheries Science Center seek a shared National Research Council (NRC) postdoctoral research associate in marine genetics and genomics. The two division have long been involved in collaborative efforts, including, but not limited to the genetic identification of cryptic rockfish species, and now embark on large-scale, Pacific Coast-wide population genetic studies aimed at understanding genetic connectivity of marine fishes, including lingcod, rockfishes, and hake. The research will involve building genomic DNA libraries, bioinformatics processing of sequencing data, and analyses to evaluate population structure, as well evaluating associations between environmental and life history parameters and genetic diversity. A theoretical population genetics background with extensive computational/bioinformatic experience is essential along with experience in computing languages and programs that facilitate population genomic and seascape genomic studies.

The National Research Council Research Associateship Program is administered by the National Academies of Sciences, Engineering and Medicine. The initial funding period for the award is for one year, renewable for up to three years pending funding. NRC research associates receive a competitive stipend, health insurance and travel allowance. Details on eligibility, terms, and application for the award may be found at http://bit.ly/1Ze78WG, research opportunity number 26.03.39.B8369. The online application period begins 1 June, with applications due 1 August 2016, for a start date as early as fall or winter 2016-2017. Applications include a research proposal, which will be developed by the applicant in discussing the project with the research advisers. Applications and supporting documents are to be submitted by the deadline to the NRC WebRAP system (https://nrc58.nas.edu/nrcwebrap/rap/-login/login.asp). For more information on the specific associateship opportunity, please contact prospective co-advisers Dr. Krista Nichols (krista.nichols@noaa.gov) or Dr. Michelle McClure (michelle.mcclure@noaa.gov).

Krista M. Nichols, PhD Supervisory Research Molecular Geneticist NOAA, National Marine Fisheries Service Northwest Fisheries Science Center Conservation Biology Division Genetics and Evolution Program 2725 Montlake Blvd E Seattle, WA 98112 206.302.2470 (o) 206.860.3335 (f)

krista.nichols@noaa.gov

Norwich UK EvolutionaryGenomics

Postdoctoral Scientist (Evolutionary Genomics) Starting salary range: 30,500 - 33,750 Duration: 3 years Location: Norwich, UK Reference: 1002991

We are currently seeking to appoint an enthusiastic and highly motivated Postdoctoral Scientist to work on comparative and population genomics studies, with a focus on evolutionary and molecular mechanisms of mammalian environmental adaption. The successful candidate will be responsible for developing computational methods and analysing primary genomic resources, in order to study genomics signatures of environmental adaptation, with a particular focus on the adaptation to aridity. The post holder will work in a highly collaborative and interdisciplinary environment and interact with other group members and external collaborators coming from a variety of backgrounds, to include; Experimental Biologists, Field Ecologists and Computational Biologists.

To be considered for this post you will hold a PhD in Computational Biology or Population Genetics and already have experience with large-scale genomic data analysis in at least one of the following areas; (i) population genomics, (ii) molecular evolution, (iii) gene expression regulation. The successful candidate will also have extensive knowledge in R and other script languages such as Perl or Python, be autonomous, organised and collaborative and also possess strong problem solving skills.

TGAC is a vibrant, contemporary research institute and actively explores and implements new applications of DNA sequencing technologies and acquired a world-class expertise in genomic and computational biology. The Institute is located in Norwich (http://www.visitnorwich.co.uk) and is part of the Norwich Research Park (NRP), which includes world leading research institutions such as John Innes Centre (JIC), The Sainsbury Laboratory (TSL) and the University of East Anglia (UEA). The NRP has a vibrant multidisciplinary scientific community in the field of environmental science, genomic, plants, food diet, microbes and health (http://www.norwichresearchpark.com/home.aspx).

At TGAC we offer competitive salaries, excellent defined contribution pension scheme, life assurance, tailored learning and development and onsite sports facilities that are available to all staff and their guests.

As a user of the disability symbol, we guarantee to interview all disabled applicants who meet the minimum essential criteria for this vacancy.

Should you have any informal questions about the project, please contact David Thybert at David.Thybert@tgac.ac.uk.

For further information, including details of how to apply, please visit http://jobs.tgac.ac.uk/ .

David Thybert, PhD

The Genome Analysis Centre Norwich Research Park NR4 7UH - Norwich - UK Tel: 0044 (0)1603 452782 Email: David.Thybert@tgac.ac.uk

"David Thybert (TGAC)" <David.Thybert@tgac.ac.uk>

OregonStateU FuncGenomicsSalmonMateChoice

The Coastal Oregon Marine Experiment Station at Oregon State University invites applications for a Research Associate (Post-Doc) in Functional Genomics applied to salmon behavior. Candidate will conduct genome wide association studies to resolve functional mechanisms underpinning fitness differences between hatchery and wild salmon, recommend strategies to overcome for those differences, and use their research innovations and findings to attend overall goals of maximizing Oregon's fishery and conservation objectives. Strong collaborative skills working with OSU and agency colleagues (Oregon Department of Fish and Wildlife, NOAA Northwest Fisheries Science Center, and USFWS Abernathy Fish Technology Center) are expected. Initial responsibilities will be to use total lifetime fitness estimates and concordant genome wide analysis of a previously established coho salmon genetic pedigree to determine if fitness differences between hatchery and wild salmon can be explained by inference on additive and/or non-additive effects of mate choice. This coho salmon pedigree involves fish of known hatchery and or wild ancestry that spawned in a natural context in Calapooya Creek, Oregon with previous studies including Theriault et al (2011) Molecular Ecology 20(9):1860-9 and Whitcomb et al 2014 CJFAS 71(7):1000-1009.

To apply go to https://jobs.oregonstate.edu/postings/-26317 Applicant Closing date: June 27th, 2016

Enquiries: Michael Banks michael.banks@oregonstate.edu

"Banks, Michael" <michael.banks@oregonstate.edu>

Oslo Norway FungalMicrobialMolEvol

Two year position as a researcher (post doc) is available at the University of Oslo, Department of Biosciences, Section for Genetics and Evolutionary Biology (EVOGENE).

Soil fungi play important functional roles in forest ecosystems. While saprotrophic taxa are essential for organic matter decomposition, mycorrhizal root-associated fungi mediate the link between living plants and the belowground community. The goal of this project, which is funded by the Norwegian Research Council, is to make fundamental progress in the understanding of the community ecology and functions of fungi in boreal forest soils, how they are organized spatiotemporally and how they influence on carbon sequestration processes. We will take advantage of linking the project to two long-term surveys of boreal forests. State-of-the-art DNA metabarcoding and metatranscriptomics approaches will be used to analyze spatiotemporal variation in the soil fungal communities. The appointed researcher will work closely with another post doc fellow.

Good collaborative skills are highly desirable. The researcher will be involved in DNA metabarcoding and metatranscriptomics analyses and must have a strong background within these fields, including high throughput sequence analyses. We are especially looking for a person with a strong background in bioinformatics analyses of environmental sequence data and/or strong skills in wet-lab work and/or high expertise in statistical analyses.

For more information about the position and for applying, go to the following homepage: http://uio.easycruit.com/vacancy/1650741/96323?iso=-3D3Dno Deadline for applying is 22. June.

havard.kauserud@ibv.uio.no

Paris-Sud StramenopilePhylogenomics

Postdoct University Paris-Sud - Stramenopile phylogenomics

A postdoctoral contract of 2 years is available in the "Microbial diversity, ecology and evolution" team (http://www.ese.u-psud.fr/rubrique7.html?lang=en) at the institute of Ecology, Systematics and Evolution starting from October 2016 (dates are negotiable). The institute belongs to the French Research Council (CNRS) and the University of Paris-Sud, and is located at the pleasant university campus of Orsay, a botanical garden 25 km south of Paris, 30 min by direct train (RER B line).

The scientific project aims at exploring the evolution of stramenopiles using comparative genomics and phylogenomic approaches, with special emphasis on heterotrophic species to better understand their adaptations to very diverse environments.

The postdoc will be funded by the French ANR Agency. The net salary will be of ca. 2000 euros depending on the candidate experience and includes social security and medical assistance. We are looking for highly motivated candidates with interest in protistology and strong knowledge on genomics and bioinformatics.

Candidates should send a CV, a cover letter and the names of at least two referees to:

David MOREIRA (david.moreira@u-psud.fr) Unite d'Ecologie, Systematique et Evolution Orsay, FRANCE http://www.ese.u-psud.fr/rubrique7.html?lang=en
David Moreira <david.moreira@u-psud.fr>

Tuebingen Germany GenomicsBehavior

Postdoc Position in evolutionary genomics of behaviour

The application deadline for below postdoctoral position has been extended till July 8, 2016

University of Tübingen, Institute of Evolution and Ecology, Group of Comparative Zoology

We have an open position (2 years) for a PostDoc with a strong interest in the genetic/genomic basis of phenotypic traits. In a project related to the genetic basis of behavior, we will use already available phenotypic data on personality and cognitive traits from a captive population of European harvest mice to search for genetic variation that correlates with behavioral profiles. We seek a candidate with strong molecular lab skills, including Sanger and next generation sequencing, and strong bioinformatics skills, preferably with training in genome wide association studies. A theoretical background in the evolutionary genetics of behaviour would be an asset.

Tübingen University offers a large community of researchers working in the field of evolution and ecology of model and non-model systems, joined together in the Institute for Evolution and Ecology (https://www.uni-tuebingen.de/en/faculties/faculty-of-science/departments/bi ologie/institute/evolutionecology.html). The successful candidate will join the Comparative Zoology group of Katharina Foerster. We offer molecular lab facilities within the group and through collaborations with the Max Planck Institute Tübingen. Further lab support and computational facilities are available through the Quantitative Biology Center on campus (http://www.uni-tuebingen.de/en/facilities/zentrale-einrichtungen/quantitati ve-biology-center-qbic.html).

The working language in the group is English. However, for teaching and everyday life at the University and in Tübingen, some knowledge of German or the willingness to learn the language will be advantageous.

Founded in 1477, Tübingen University has influenced the historical town significantly. Tübingen today remains a place of research and teaching. In addition to the 85.500 inhabitants, there are some 28.300 German and international students. 450 professors and 4.400 other academic staff teach at the University's seven faculties. Tübingen offers a lively mix of shops, bars, and restaurants. Urban parks, nearby nature reserves, as well as the Swabian Jura and the Black Forest offer outdoor recreation. Tübingen is well connected via bus and local trains to Stuttgart and its airport. The Welcome Center of the university provides service and support for international researchers: https://www.uni-tuebingen.de/en/-international/international-scholars.html Applications are being accepted immediately. Review of applications submitted before the initial deadline has started; the extended deadline for applications is July 8, 2016. Intended starting date is September 1, 2016. Applications should include a current CV (specifying training in relevant methods and applications), along with a cover letter that provides a short statement of research interests (maximum three pages) and contact information for three references. Applications should be submitted by email as a single file attachment to henri.thomassen@uni-tuebingen.de, with the subject line: Postdoc. Informal inquiries can be sent to katharina.foerster@uni-tuebingen.de.

Henri Thomassen <henri.thomassen@uni-tuebingen.de>

UAlabamaHuntsville EcologicalGenomicsBehavior

Postdoctoral position on Ecological Genomics and Behavior in cactophilic Drosophila

The Matzkin Lab at the University of Alabama in Huntsville is currently recruiting a postdoc to work on a recently awarded NSF project on the genetic analysis and life history consequences of variation in larval behavior in cactophilic Drosophila. I am seeking a highly motivated and creative individual with strong quantitative & evolutionary genetics, molecular and/or computational biology skills to join our evolutionary and ecological genomics lab. Good writing and communication skills will be required for this position. Prior experience working with Drosophila is not necessary, but a plus. Postdoc will be based at the University of Alabama in Huntsville and will have the opportunity to interact with investigators at the HudsonAlpha Institute < http://hudsonalpha.org/ >.

The funded three year project aims to examine the genetic basis and evolution of alternative larval behaviors and ultimately in the long term to understand how local ecological adaptation can lead to the divergence of populations, potentially leading to the formation of new species. The four specific aims of this proposal are:

Assess the transcriptomic nature of the distinct larval behavior strategies among the D. mojavensis populations. Determine the genetic architecture of larval activity by performing a quantitative trait loci (QTL) mapping study. Generate knockouts and transgenics (exchange alleles between populations) of candidate QTLs using CRISPR-Cas9 genome editing. Use the CRISPR-Cas9 knockouts and transgenics to quantify the functional role of the candidate behavior QTLs in an ecological context and examine the life history consequences of variation at these loci. Additionally, the postdoc will have the opportunity to collaborate on other Matzkin lab projects on the genomics of adaptation and the evolution of reproductive incompatibilities.

The initial appointment will be for one year with the possibility of renewal for a second and third year contingent on satisfactory performance. The position is available now and I will be accepting applications until filled.

To apply please submit as a *single PDF*, a 1) cover letter briefly outlining the candidate's fit to the position and future goals 2) curriculum vitae 3) contact information (email and phone) for three references, preferably including doctoral advisor and/or postdoctoral advisor (if relevant) and 4) no more than three relevant publication PDFs. Link to application site is https://uah.interviewexchange.com/-jobofferdetails.jsp?JOBID=3D73238 Please contact Dr. Luciano Matzkin (lmm0015@uah.edu) for more information regarding the project and position.

About The University of Alabama in Huntsville:

The University of Alabama in Huntsville is a Tier 1 research university that prepares students for demanding positions in Engineering, the Sciences, Business, Nursing, Education, and the Arts, Humanities, and Social Sciences. Located within one of the largest research parks in the United States, UAH is considered one of the nation's premier research universities, and is listed in "America's 100 Best College Buys" and "The 150 Best National Doctoral Universities" by US News and World Reports. Approximately 7,350 students from almost all of the 50 states and 80 countries currently pursue degrees in over 100 areas of study.

Dr. Luciano M. Matzkin Assistant Professor Director of the Graduate Program Department of Biological Sciences The University of Alabama Huntsville Adjunct Faculty Investigator - HudsonAlpha Institute for Biotechnology Office (256) 824-4326 Lab (256) 824-6968 http://www.uah.edu/biology/LAB/matzkin/

"lmm0015@uah.edu" <lmm0015@uah.edu>

UAustralDeChile ExptEvolBiol

Postdoctoral fellow in Experimental Evolutionary Biology

(Valdivia, Chile)

(pre-proposal to be submitted to the Fondecyt National postdoc competition, see http://www.conicyt.cl/-fondecyt/2016/06/10/concurso-de-postdoctorado-201 7)

Contact: Roberto Nespolo, robertonespolorossi@gmail.com

Universidad Austral de Chile (UACh), Instituto de Ciencias Ambientales y Evolutivas

Universidad Austral de Chile is located in Southern Chile in the Los Rios Region, which is characterized by native forest and rivers (https://-en.wikipedia.org/wiki/Valdivia). The Sciences Faculty is one of the largest in UACh and is located in Campus Teja (https://www.uach.cl/sedes-y-campus/-informacion-general/campus-isla-tej a). Our Department, Instituto de Ciencias Ambientales y Evolutivas develops research projects in ecology and evolutionary biology, with emphasis in genomics, phylogeography, and evolutionary mechanisms at the level of species, populations and organisms.

Project description

Our ongoing research program is funded by Fondecyt grant 1130750, and is primarily aimed at studying essential constraints to adaptive evolution using experimental evolution (Kawecki et al. 2012), particularly experimental phylogenies of yeasts. We work in close collaboration with Dr. Michael Travisano, from University of Minnesota (Travisano and Shaw 2013, Ratcliff et al. 2015). We experimentally evolve populations of Saccharomyces cerevisiae in the laboratory from a single, known, diploid ancestor and induce population divergence periodically, producing an experimental phylogeny of lineages, about 600 generations later. Every experimental phylogeny is, in this sense, a replicate. Using a combination of laboratory (plating), spectrophotometric and flow-cytometer method we compare performance (fitness) and morphology among the resulting lineages and also with the ancestor. We store every generation at -80oC so we can go "back in time" and compare evolved versus ancestral populations. These data are analyzed with modern comparative phylogenetic methods that permit to test the effects of selection and other evolutionary forces (Hansen or "OU" models)(Butler and King 2004) on the pattern of experimental divergence in traits and fitness. Thanks to the small and well-known genome of yeasts, we aim also at combining these approaches with next-generation population genetics methods (restriction-site associated DNA sequencing, RADSeq)(Baird et al. 2008), to identify genes, markers (SNPs) that constraint or permit diversification, and contribute to adaptation. Using these approaches, we are interested in answering the following general questions:

How the environment constraint adaptive diversification?

How micro-evolutionary processes (processes at the level of a population or lineage) impact macro-evolutionary patterns (patterns above lineage level)?

Does the classic distinction among trait-types (i.e., physiology, morphology, fitness) have analogous consequences at the level of an experimental phylogeny?

What are the most important genetic constraints to evolution?

ALTERNATIVELY, we also seek a research associate who can address these kinds of questions using phylogenetic comparative methods and data compilations/phylogenies from literature or large public databases such as megatrees (Hedges et al. 2015).

Required qualifications To have a PhD degree in Biological Sciences, obtained after Jan, 1, 2013 and before Nov 30^th, 2016.

Experience and skills in the following areas is essential:

Experience in laboratory work using microorganisms OR advanced skills in trait-based comparative methods.

Experience and skills in the following areas is desirable:

Statistical procedures based on the R-platform, knowledge in evolutionary theory, basic tools of comparative analysis (e.g., ape and phytools packages).

Salary & Conditions

According to the Fondecyt competition (2017), the salary corresponds to about 2487 USD per month, and funds for travels and operational costs for about 6500 USD. It includes installation costs (flight tickets).

See details in http://www.conicyt.cl/fondecyt/files/2016/06/Bases-Postdoctorado-2017.pdf Pre-proposals deadline

Please send a pre-proposal (two pages maximum) to robertonespolorossi@gmail.com, delineating questions, predictions and a short Mat & Methods, before July 7th. Please include a short CV, including the publication list as can be seen in the Web of Science.

The project should start in March, 15th 2017.

References

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UBath MicrobialGenomics

Research Associate (fixed-term)

Biology & Biochemistry Salary: Starting from £31,656, rising to £37,768 Placed On: Thursday 16 June 2016 Closing Date: Sunday 17 July 2016 Interview Date: To be confirmed Reference: FY4064

Postdoctoral position in Microbial Genomics

A NERC-funded postdoctoral research associate position is available for a highly motivated research scientist to analyses a wide range of genomic data related to population structure and evolution of pathogenic bacteria.

The successful candidate is expected to have (or about to obtain) a PhD degree in a relevant area of biology (microbiology, genetics or bioinformatics), a good publication record and strong interest in microbial genomics and evolution. Applicants must be familiar with Unix environments, proficient in scripting languages, and with experience in high throughput sequence analysis of microbial genomes and metagenomic data.

The position is offered on a full-time, fixed-term (up to 17 months) contract in the laboratory of Dr Jaime Martinez-Urtaza (J.L.Martinez-Urtaza@bath.ac.uk) at the Milner Center for Evolution, Department of Biology and Biochemistry, University of Bath. Informal enquires are welcome and should be directed to Dr Jaime Martinez-Urtaza (J.L.Martinez-Urtaza@bath.ac.uk).

The University of Bath and our Department are committed to equality of opportunity. We particularly encourage applications from under-represented groups, including women. Key Responsibilities include:

Manage and analyse large-scale whole-genome sequencing datasets Perform analysis on datasets generated by next generation sequencing platforms Integrate sequence data with environmental/epidemiological data

Liaise with collaborators and coordinate projects Train group members Develop new methods to analyse sequence data Essential Skills:

PhD in microbiology, population genetics, molecular evolution, computer science, or bioinformatics Experience working with next generation sequence data and/or large datasets Ability to program in either Perl or Python Experience with bacterial genomics, genome annotation, phylogeny and metagenomics Outstanding personal initiative and communication skills Strong publication record in peer-reviewed journals A desire to learn, to innovate and to move out of their comfort zone

Interviews are expected to be held on Friday 22nd or Monday 25th July 2016.

Application: https://www.bath.ac.uk/jobs/-Vacancy.aspx?ref=3DFY4064 Ronnie Gavilan <ronniegavilan@gmail.com>

UBristol PopulationModellingGenomics

A Postdoctoral position in Population Modelling and Lepidoptera Genomics is available at the University of Bristol, UK, working with Dr Jon Bridle and Prof Mark Beaumont, along with researchers at the Universities of Liverpool and York.

This position forms part of a consortium research grant funded as one of NERC's Highlight Topics to test how evolutionary responses determine the resilience of butterfly populations to climate change, using historical and contemporary ecological, genomic, geographical and climatic information.

This three-year PDRA will model the population genomics and spatial population ecology of populations and apply these models to genomic and ecological data of c. 30 species of UK Lepidoptera derived from museum samples, and population surveys from the 1930s to the present day by PDRAs working in Liverpool and York respectively. This ambitious project includes collaborations with the Universities of Melbourne and Stockholm, as well as the UK Centre for Ecology and Hydrology, Butterfly Conservation, and the Natural History Museum.

The researcher is expected to have a background in statistical modeling and Bayesian inference, and will develop an integrated population model that can simulate range changes and evolutionary responses, and will enable model outputs to be compared to genomic, ecological and demographic data using a variety of statistical approaches. The project represents a fantastic opportunity to gain experience and expertise in linking novel empirical genomic and ecological data with the latest techniques in modelling and inference in order to test the ecological consequences of climate change for biodiversity.

For more details and informal enquires, please contact Jon Bridle (jon.bridle@bristol.ac.uk) or Mark Beaumont (m.beaumont@bristol.ac.uk) in the first instance, or see http://www.jobs.ac.uk/job/ANW540/researcher-in-population-modelling-and-genomics-of-lepidoptera/ Closing date for applications is 10th July.

Best wishes

Jon Bridle

Dr Jon Bridle School of Biological Sciences 2A03, Life Sciences Building University of Bristol, BS8 1TQ

Tel. (+44) 117 394 1174 (internal 41174) jon.bridle@bristol.ac.uk

http://www.bristol.ac.uk/biology/people/jon-r-bridle/ Jon Bridle <Jon.Bridle@bristol.ac.uk>

UCalgary AdaptationGenomics

Postdoctoral positions: Genomics of local adaptation Yeaman Lab

Department of Biological Sciences, University of Calgary

I am looking to hire two postdoctoral fellows to collaborate on projects studying how patterns in the genome evolve during local adaptation:

1. Genomic rearrangements and local adaptation: This project will develop and use comparative genomic approaches to study whether rearrangements have contributed to the evolution of clusters of functionally related genes (genomic islands, metabolic clusters, etc.). We are currently working on an assembly of the tubesnout genome (a relative of stickleback) as a means of studying if/where/when rearrangements have contributed to the evolution of clustered architectures observed in the stickleback. We will also be exploring patterns in a range of already-assembled genomes, and there is some budget flexibility to play around with new ideas. Good bioinformatics and R-scripting skills will be very important, ideally with experience in comparative genomics.

2. Genomics of local adaptation to abiotic stress in sunflower: For this project, we will be studying whole genome sequence data from over 600 individuals, searching for associations with environment and signatures of selection, and developing new methods for data analysis. It is a large-scale collaboration with Loren Rieseberg and John Burke, funded by Genome Canada. Experience managing and analyzing NGS data, GWAS, and related approaches would be ideal, coupled with strong R & unix skills.

Positions will run for 2+ years (CAD $50k salary).

TO APPLY: Please send a CV and a short description of your interest in the position to samuel.yeaman at ucalgary.ca, along with the names and emails of three people I could contact for reference letters. I will begin reviewing applications on July 1st, 2016, but please contact me to check in if you need to make a quick decision. I will be at SSE and CSEE this summer, so please get in touch if you'd like to chat with me about it then!

Sam Yeaman <yeaman@zoology.ubc.ca>

UCalifornia Merced ConservationGenomics

Conservation Genomics Postdoc

Under the University of California, President's Office Catalyst program, a three-year award has been made for 1.75 million dollars to establish a conservation genomics network among 6 campuses. The goal of the program is to support research, develop new analytical tools, educate graduate and post-graduate students via workshops, and interface with conservation managers and planners as well as the general public.

We have support for a two-year post-doc beginning January 2017 at the University of California, Merced to work on (1) adaptation to seastar wasting disease and (2) conservation and adaptation to vernal pools in invertebrates and plants. We are looking for a researcher with keen interest in conservation genetics and with experience in relevant wetlab protocols and strengths in bioinformatics. The postdoc also will liaise with other conservation genetics network members (https://ucconservationgenomics.eeb.ucla.edu/-affiliations/) and assist in project workshops and the educational mission of the program. Interested researchers should have a recent PhD and contact mdawson@ucmerced.edu. After obtaining approval from the UC Merced team, the post-doc candidate should submit a short one-page project plan, including discussion of their qualifications, at https://-ucconservationgenomics.eeb.ucla.edu/positions/hiring-postdocs/ . More information is available at: https://-ucconservationgenomics.eeb.ucla.edu/projects/ochre-seastar/ https://ucconservationgenomics.eeb.ucla.edu/-positions/hiring-postdocs/ PIs for the projects are: Mike Dawson -:- http://mnd.ucmerced.edu Jay Sexton -:- http://sextonlab.ucmerced.edu/ Andy Aguilar -:- http://andresaguilar.weebly.com/ p.s. If you're in Austin for the Evolution conference and are interested in the position - Mike or Jay would be happy to chat ... (if not, drop us an email)

Michael N Dawson Associate Professor University of California, Merced

Michael Dawson <mdawson@ucmerced.edu>

UCBoulder FlowerColorEvolution

The Smith Lab at the University of Colorado, Boulder is looking to hire a postdoctoral fellow to join an NSF-funded project on the macroevolution of flower color. Research in the lab encompasses phylogenetics, evolutionary genomics, biochemistry, and comparative methods. Our questions are centered on understanding phylogenetic patterns of floral trait evolution and identifying the mechanisms that underlie changes in floral traits (http://www.colorado.edu/smithlab/research).

The postdoc will lead research aimed at testing the predictability of genetic changes associated with the macroevolution of flower color in Solanaceae (the tomato family). This project builds on previous research suggesting that, for a given pigment pathway, color evolution proceeds through a predictable subset of possible mutations. Testing this hypothesis at a phylogenetic scale will involve a combination of biochemical analysis of pigments, floral transcriptomics, and statistical comparative methods. The postdoctoral fellow will also have the opportunity to participate in field trips to South America to sample new taxa, and is expected to take part in several local evolution outreach activities.

Qualified candidates will have a PhD in biology or related disciplines and a strong publication record. Experience in plant biochemistry (including HPLC) and/or analysis of next-generation sequence data is a plus. To apply for the positions, please send a brief letter of interest (1-2 paragraphs), a CV, and the names and contact information for three references to Stacey D. Smith, stacey.d.smith@colorado.edu. Each position is available for 1 year with the possibility of renewal for up to two additional years depending on research progress. The start date is flexible, but could be as early as September 1st, 2016. Review of applications will begin on June 24, 2015 and will continue until the positions are filled. I encourage interested candidates to meet with me in person at the Evolution meetings in Austin.

dewitt832@gmail.com

UChicago HumanGenetics

I am looking for a postdoc to join us in the Department of Human Genetics at the University of Chicago. We are not looking for someone to work on the specific projects we are already engaged in. Rather, we are looking for a new postdoc to join us when their scientific interest and ours are well aligned, with the goal of developing a new research focus together. Typically the postdoc would then use their tenure with us to build the foundation for an independent research program.

To apply, please email me a cover letter describing your research interests, and your CV. Only candidates who have played a major role in at least one published study (as preprint or traditional publication) will be considered. Candidates who wish to focus on scientific questions that require the application of single cell technology are especially encouraged to apply.

Yoav Gilad Chief, Section of Genetic Medicine Professor of Medicine Professor of Human Genetics

University of Chicago 920 E. 58th st. CLSC 325c Chicago, IL 60637, USA Office: 773-702-8507 Lab: 773-834-1984 Fax: 773-834-8470 WWW: http://giladlab.uchicago.edu Yoav Gilad <gilad@uchicago.edu>

UChile HumanPopulationGenetics

We are seeking candidates for a Postdoctoral position in Genetics to study the demographic history of settlers of Patagonia. The postdoc will work in a genomics and bioinformatics laboratory and will have available microarray genotyping data and whole genome sequence data from modern and ancient DNA from Patagonia (Chile and Argentina). He/she will also be responsible for generating and analyzing new data. Travel opportunities to our collaborator's laboratory, Carlos Bustamante in Stanford University.

Requisites: * PhD in Genetics, Evolution, Bioinformatics or related field obtained between January 2013 and July 2016. * A motivation letter * Writing fluency in English * CV or resume

Desired skills: * Strong background in quantitative or population genetics * Bioinformatic skills at user level * Spanish or willingness to learn

Funding: * Through a FONDECYT Postdoctoral fellowship < http://www.conicyt.cl/fondecyt/category/-concursos/postdoctorado/ > (Spanish). * Successful applicants will apply for funding with the sponsorship and assistance of the laboratory PI (application will be in English).

Deadline: * June 30 2016

Postdoc start date: * November 2016

Interested should inquiries and application material to Dr. Ricardo Verdugo (raverdugo@u.uchile.cl).

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Ricardo A. Verdugo S., M.V., Ph.D. Assistant Professor Human Genetics Program, ICBM Faculty of Medicine, University of Chile Independencia 1027, Santiago, Chile Phone: +56 (2) 2978 9527 raverdugo@u.uchile.cl http://genomed.med.uchile.cl "Ricardo A. Verdugo" <raverdugo@u.uchile.cl>

UCLondon ExcellenceFellowships

UCL Excellence Fellowships Department of Genetics, Evolution, and Environment University College London

UCL's Department of Genetics, Evolution and Environment (GEE) is a world class department with a broad research portfolio. We are currently recruiting promising early-career researchers via UCL's Excellence Fellowship programme. We aim to expand our current strengths by encouraging applications from outstanding applicants in the main research areas within the department:

- Comparative 'omics' and deep evolutionary analysis (newly proposed Centre for Life's Origins and Evolution, contact Prof. Max Telford, m.telford@ucl.ac.uk)

- Research at the interface between biodiversity and environmental change (Centre for Biodiversity and Environmental Research, contact Prof. Georgina Mace, g.mace@ucl.ac.uk) - Statistical and computational biology (R.A. Fisher Centre for Computational Biology, contact Prof. Ziheng Yang, z.yang@ucl.ac.uk) - Genetics of health and disease (UCL Genetics Institute, contact Prof. François Balloux, f.balloux@ucl.ac.uk) - Biology of ageing (Institute for Healthy Ageing, contact Prof. Linda Partridge, l.partridge@ucl.ac.uk)

The UCL Excellence Fellowship scheme is run by the School of Life and Medical Sciences and is open to the full range of disciplines in basic and applied life sciences. The fellowship offers salary and research funding, as well as generous funding supplements for individuals transferring existing, externally funded fellowships to UCL. Excellence Fellows who are not already holding awards are expected to apply to externally funded schemes, including ERC, Royal Society, NERC, BBSRC, and Wellcome Trust. This requires that Excellence Fellowship applicants are eligible and competitive for these awards. For more information on the Excellence scheme and application process, seehttp://www.ucl.ac.uk/slms/-research/excellence-fellowship/ Candidates are required to identify a sponsor in GEE by contacting a relevant member of staff. GEE runs a pre-selection to identify candidates for departmental support. Preliminary applications, including a one-page proposal, full CV and the name of the sponsor, should be submitted for internal review by July 15. Documents should be sent to Prof. Anjali Goswami (a.goswami@ucl.ac.uk) or Dr Max Reuter (m.reuter@ucl.ac.uk), who are in charge of fellowship support for GEE. They can also provide assistance with identifying a potential sponsor if contacted in advance of the deadline. Based on the preliminary applications, a shortlist of applicants will be selected for departmental support and invited to submit a full application by the scheme deadline of August 29.

The Department has had great success supporting fellowship applicants from initial application to securing subsequent permanent employment within UCL. You can find more information about the department and its research centres and institutes at http://www.ucl.ac.uk/gee . A note for non-UK applicants: Fellowships allow early- and mid-career scientists to concentrate on their work unhindered by teaching and administrative loads. They are an integral part of the UK academic system and are the preferred and privileged route towards permanent academic positions. Schemes covering salary and research expenses from a range of funding agencies are open to non-UK applicants. Please see http://www.ucl.ac.uk/-gee/fellowships for more details.

"Goswami, Anjali" <a.goswami@ucl.ac.uk>

UCLondon SexChromEvolutionaryGenomics

2 Postdoctoral positions available in Evolutionary Genomics of Sex Chromosome Evolution and Sexual Selection

The Mank Lab in the Department of Genetics, Evolution and Environment at University College London is looking for up to two talented evolutionary biologists to work on cutting edge projects at the interface of sex chromosome evolution, sexual selection and genome biology. The positions are available initially for 2 years with the possibility of extension.

We work at the intersection of evolutionary genetics and genomics and organismal biology, with the aim of understanding the 1) molecular basis of sexual dimorphic variation and 2) sex-specific genome evolution, including the causes and consequences of sex chromosome evolution.

The lab has just been awarded a second consecutive European Research Council grant to study sex chromosome evolution, sexual conflict and sexual selection in guppies and related species. We are looking to recruit talented and motivated team members to work on this project. Project specifics will depend on the skills and interests of the post-holder, and may include both wet-lab and computational components, as well as experimental evolution and phenotyping. In addition, there is significant opportunity and funding for the successful applicant to develop their own projects and interests within the broader goals of the grant.

Requirements: We invite applications for the above positions at the postdoctoral level. You will have obtained or close to completing your PhD in the near future. You will have experience handing genomic data or in statistical genetics, as well as demonstrated expertise in one or more of the following areas:

1) handling and analysis of NGS datasets (whole genome, RNASeq, etc)

2) advanced skills in statistical genomics

3) de novo genome and/or transcriptome assemblies and comparative genomics.

4) empirical and theoretical population genetics

5) Sexual selection and/or sex chromosome evolution

Experience or desire to learn programming languages is essential (R, Python, Perl, etc). Wetlab skills and experience in other types of data analysis (e.g., image processing) will be an advantage.

We are interested in candidates who are keen to apply new and innovative statistical approaches. Passion for research, team spirit and enthusiasm are essential.

The Lab Team: You will work with an enthusiastic multidisciplinary team that focuses on applying genomics approaches to understand the basis of intra-specific phenotypic diversity. More about the lab, including current members and research projects, is available at http://www.ucl.ac.uk/mank-group/ The Host Institute: The Department of Genetics, Evolution and Environment at UCL hosts world-class research groups, and is located in the vibrant centre of London. More about the department is available at http://www.ucl.ac.uk/gee The post: Positions at the postdoc level will be initially offered for 2 years, with the possibility of extension. Positions will be supported by contracts with salary and benefits based on the UCL pay scale and are commensurate with training and experience.

To Apply: Consideration of applications will begin in mid July, 2016, and will remain open until filled. Please apply through the UCL Human Resources website, https://goo.gl/QPIJSk, with the reference number 1556179. Enquiries can be sent to Prof. Judith Mank (Judith.mank@ucl.ac.uk).

Judith Mank University College London Department of Genetics, Evolution and Environment The Darwin Building Gower Street London WC1E 6BT

http://www.ucl.ac.uk/mank-group/ Judith Mank <judith.mank@ucl.ac.uk>

UFlorida HumanEvolGeneticsEpigenetcs

Post-doctoral position in Human Evolutionary Genetics and Epigenetics, Laboratory of Connie Mulligan, Department of Anthropology, University of Florida, Gainesville, FL, USA

Post-doctoral position to work on two ongoing projects: 1) Investigation of an epigenetic mechanism to mediate the effects of maternal stress on maternal and infant health in the Democratic Republic of Congo (DRC). We are testing for associations between maternal stress exposures, newborn health outcomes and changes in DNA methylation and/or gene expression in mothers and their infants. More broadly, we are interested in the idea that mechanisms may have evolved to allow the genome to respond to psychosocial stressors, specifically behavior and complex phenotypes may be shaped by early life experiences that alter gene expression through epigenetic alterations. See http://www.tandfonline.com/doi/pdf/10.4161/epi.21180 and http://onlinelibrary.wiley.com/doi/10.1111/cdev.12487/epdf .2) Investigation of genetic, epigenetic, and biological signatures of war trauma exposures and impact of a program intervention in Syrian refugees. This is a collaboration with Catherine Panter-Brick (Anthropology, Yale University) to integrate genetic and epigenetic analyses into an ongoing study to measure the health effects of a program intervention to reduce psychosocial stress in Syrian refugees. Genetic variants will be assayed to predict the impact of past stress exposures and effects of the program intervention on self-reported mental health. Epigenetic variants will be tested as possible mediators of the effect of stress on mental health outcomes. See project website at http://www.elrha.org/map-location/yale-psychosocial-call2/ . Qualifications: A PhD, good publication record, and strong background in the generation of genetic data (microarray, NGS, SNP detection, etc.) and data analysis (gene association analysis, regression analysis, genetic ancestry estimation, linkage analysis, etc) are essential. A background in evolutionary genetics and experience with methylation data (Illumina chips, pyrosequencing, etc), RNA sequence/transcriptome data and/or additional computational or bioinformatics experience (e.g. computer programming, simulation analysis, etc) is a plus. Candidates who speak French or Swahili are encouraged to apply. In addition to the projects listed above, there are excellent opportunities for the successful candidate to develop new lines of research as well as productive collaborations outside the lab.

The University of Florida is a leading research institution with a university-wide commitment to genetics research. The Department of Anthropology (www.anthro.ufl.edu) has 30 full-time faculty with diverse interests and is one of the top rated programs in the country (6th among public institutions, 11th overall). The University of Florida Genetics Institute (www.ufgi.ufl.edu) is an inter-college institute with a dedicated research building intended to enhance opportunities for collaboration. Gainesville is located in north central Florida (away from the hurricanes!), with average temperatures ranging from 45F to 90F. Beaches on the gulf and Atlantic coast are ~ 1.5 hours away.

To apply: via email, send a CV, statement of research interests, and names and contact information for three references. Applications and inquiries should be addressed to Connie Mulligan at cmulligan@ufl.edu.

Review of materials will begin July 15 and will continue until the position is filled. Start date is flexible and successful candidate can begin as early as August, 2016. Salary is commensurate with experience. Position may be extended for a total of three years. Informal inquiries prior to submitting a formal application are welcome. AA/EOE.

— Connie J. Mulligan, PhD Professor and Associate Chair, Department of Anthropology 2033—Mowry Rd, PO Box 103610 | University of Florida | Gainesville, FL 32610-3610 Office: 409 Genetics Institute | Telephone: 352-273-8092 | Fax: 352-273-8284 Website: http://www.clas.ufl.edu/users/mulligan/Webpage/index.html "Connie J. Mulligan" <cmulligan@ad.ufl.edu>

ULausanne MicrobialEvolution

Postdoctoral position in microbial genomics/evolution at the University of Lausanne, Switzerland

Starting date: from September 1st 2016

Contract: 1 year. This contract can be renewed for a max. length of 5 years.

Work percentage: 100%

Workplace: University of Lausanne, Department of Fundamental Microbiology

Qualification:

PhD. Postdoctoral applicants should have one or more first-author publications in major peer-reviewed international journals and a strong background in a least one of the following fields: computational biology, microbial genomics/evolution, microbial community ecology, microbiota research. Prior research experience with large-scale sequencing datasets and programming experience is needed. A good command of the English language, a high personal motivation to excel in science and a curious mind are required. We offer a stimulating environment in a young international research group combining computational (i.e. genomics) and experimental approaches to study microbial symbiosis.

Work description:

We are looking for an outstanding and highly motivated candidate to join our research group. The project will be part of a collaborative effort funded by a HFSP grant to understand the impact of horizontal gene transfer (HGT) on gut microbiota evolution. HGT is a key mechanism for bacteria to exchange genetic information. However, its role and frequency in natural populations of multispecies communities remains elusive. Our model system is the gut microbiota of honey bees, a simple, yet highly specific, bacterial community of eight species. Each species is represented by a multitude of divergent strains, which can exchange DNA by HGT. The project aims at detecting and quantifying HGT in this community using cutting-edge sequencing technologies and bioinformatics tools. As the project is part of an international collaboration, the prospective postdoctoral researcher will have the opportunity to interact with scientists in the US and Japan.

For recent publications from the lab, please visit the lab webpage at unil.ch/engellab.

How to apply:

Please send your full application including motivation letter, CV, list of publications and the names and addresses of two to three referees to: Philipp.Engel@unil.ch

Application deadline:

July 1st, 2016.

Philipp Engel Assistant Professor Department of Fundamental Microbiology University of Lausanne Biophore Building CH-1015 Lausanne Switzerland Phone: +41 (0)21 692 56 32 Mobile: +41 (0)78 679 96 36 Email: philipp.engel@unil.ch Web page: http://www.unil.ch/engellab Philipp Engel <Philipp.Engel@unil.ch>

UManchester PhylogeneticsPalaeobiology

The University of Manchester is inviting applications for a research associate to work on a project on phylogenetics and evolutionary biology/palaeobiology. The position will ideally start on September 12th 2016 and last for 36 months.

The BBSRC funded project, Overcoming the morphology problem of phylogenetics, is led by Dr. Robert Sansom and aims to directly address the problems and limitations of morphological data in deriving evolutionary relationships. Empirical phenotypic data will be compiled for clades from across the tree of life. Its properties and performance will be assessed through comparison with genotypic data and application of different phylogenetic reconstruction methods. The findings will be used to propose guidelines for best practice and as an assessment of the role of morphology in evolutionary biology. This will be applied to case studies in molecular clock calibration points, human origins, and arachnid evolution.

You will be responsible for data collection, curation and analysis, preparation of a series of publications relating to the project, supervision of some undergraduate projects, dissemination to academic audiences, engaging in outreach activities, and day to day running of the project. You will hold a PhD in evolutionary biology, bioinformatics, palaeobiology or related discipline, have practical experience of phylogenetic research, methodology and analyses, excellent written and spoken English skills, and a track record of publishing high quality peer-reviewed papers. "'It is desirable that you demonstrate familiarity and aptitude with a broad range of phylogenetic software, scripting/coding, and statisical analyses.

The Faculty of Medical and Human Sciences / Life Sciences will form part of a newly created Faculty of Biology, Medicine and Health from 1st August 2016. This post will transfer to the new structure on that date and details of the where the post sits within the new structure will be provided to successful candidates in their letter of appointment.

The School of molecular Systems is committed to promoting equality and diversity, including the Athena SWAN charter for promoting women's careers in STEMM subjects (science, technology, engineering, mathematics and medicine) in higher education. The School received a Silver Award in 2009 for their commitment to the representation of women in the workplace and we particularly welcome applications from women for this post. Appointment will always be made on merit. For further information, please visit http://www.wils.ls.manchester.ac.uk/athenaswanawards/ Enquiries about the vacancy, shortlisting and interviews:

Name: Robert Sansom

Email: robert.sansom@manchester.ac.uk

Tel: 0161 252 1496

General enquiries:

Email: hrservices@manchester.ac.uk

Tel: 0161 275 4499

Technical support:

Email: universityofmanchester@helpmeapply.co.uk

Tel: 01565 818 234

This vacancy will close for applications at midnight on the closing date.

To apply:

https://www.jobs.manchester.ac.uk/displayjob.aspx?jobid=3D11588 charlotte.brassey@manchester.ac.uk

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UMichigan Phylogenetics

Postdoctoral position at the University of Michigan, Ann Arbor in Stephen Smith's lab.

Post-doctoral position to work on ongoing projects including phylogenetics, phylogenomics, and evolution. In particular, there are projects involving work with the Open Tree of Life, phylogenetic dataset construction, large phylogenetic analyses, phylogenomic analyses involving genomes and transcriptomes, orthology and homology searching, analysis of differential gene expression using phylogenies, large comparative analysis, and evolution of plants.

Qualifications: A PhD, good publication record, and strong background in phylogenetics. The candidate will preferably have skills in computational work and computer programming.

Start date: The candidate can start as early as August 2016 (preferable).

Length of position: The position is for one year with review for a second year and possible extension.

Salary: Commiserate with experience.

To apply: via email, send a CV, statement of research interests, and names and contact information for three references. Applications and inquiries should be addressed to Stephen Smith at eebsmith@umich.edu.

Information on the lab can be found at http://blackrim.org . Dr. Stephen A. Smith http://blackrim.org Assistant Professor, Dept. Ecology and Evolutionary Biology University of Michigan 2071A Kraus Natural Science Building 830 North University Ann Arbor, MI 48109-1048

"eebsmith@umich.edu" <eebsmith@umich.edu>

UOldenburg SalpsandKrillBiodiversity

The working group Biodiversity and Biological Processes of polar Seas at the ICBM (Institute for Chemistry and Biology of the Marine Environment), Carl von Ossietzky University Oldenburg in Oldenburg, offers two positions:

3-year Scientist-position in Molecular biology (TVL-E13, 100%) (#1) 3-years PhD-position (TVL-E13/50%) in Molecular biology (#2)

within the project PEKRIS (The PErformance of KRIll vs. Salps to withstand in a warming Southern Ocean), funded by the BMBF (Federal Ministry of Education and Research) from July 1st 2016 to June 30th 2019.

The scientist candidate should perform the work on the tunicate Salpa thompsoni, whereas the PhD candidate should perform the work on Antarctic krill, Euphausia superba.

For detailed project information contact Prof. Dr. Bettina Meyer b.meyer@uni-oldenburg.de

Project aim: The overall goal of the Subproject 1 of the PEKRIS project ("Physiological and genetic traits of krill vs. salps supporting potential adaptation to a warming Southern Ocean"), are to understand the general principles of thermal adaptation of krill and salps defined by their genetic make-up. It is aspired to characterize the thermal window of krill and salps in the Southern Ocean in respect to important physiological life cycle functions (lipid accumulation and utilization, reproduction, growth metabolic activity). The goal of the transcriptomic approach is to identify differentially expressed genes which contribute to these important life cycle functions and new candidate genes of both species, which contribute to their plasticity and adaptation to temperature stress. We aim to identify gene clusters and networks, which define sensitivity and adaptability of both species from which almost no (salps) or only few (krill) essential functional transcriptomic information are available.

Profile of the Candidates: The successful candidates are expected to have an academic university degree (Master or Diploma) and hold a doctoral degree (Scientist position #1) or academic university degree (PhD position #2) in molecular biology, genetics, biology or marine biology. The Scientist candidate must be very well familiar with basic and advanced techniques to investigate cDNA-gene-expression-profiles in invertebrates, for example Real-Time-PCR (SYBR Green und TaqMan Chemie), TaqMan Low Density Arrays, next generation sequencing as well as bioinformatics, analysis and interpretation of next generation sequencing data, multi-variate statistic etc. The PhD candidate must be familiar with basic techniques in molecular biology (RNA isolation, qPCR, bioinformatics) on invertebrates. Both candidates should have skills in experimentation and maintenance of invertebrates. The international nature of the project requires fluency in spoken and written English and good presentation and publication skills. The successful candidates are embedded in the working group of Biodiversity and biological processes in Polar Seas, headed by Prof. Dr. Bettina Meyer. It is expected that both candidates work in close cooperation self reliably on this project. The position requires the ability to manage months-long research expeditions as well as expedition to our cooperative scientific partners at the AAD in Kingston, Tasmania.

The Carl von Ossietzky University Oldenburg is dedicated to increase the percentage of female employees in the field of science. Therefore, female candidates are strongly encouraged to apply. In accordance to Â§21 Section 3 NHG, female candidates with equal qualifications will be preferentially considered. People with disabilities will be given preference if equally qualified.

Please send your application for the specific position (Scientist position #1 or PhD position #2) including a cover letter with motivation, copies of your certificates, a list of your most relevant publications, a CV, and the names and addresses of two referees as a single pdf-file not exceeding 10 MByte via e-mail to Prof. Dr. Bettina Meyer (b.meyer@uni-oldenburg.de) or by mail to the ICBM office c/o Elke Hoxha (Elke.Hoxha@uni-oldenburg.de), Postfach 2503, D-26111 Oldenburg, Carl-von-Ossietzky-Str. 9-11. All applications must be submitted by July 30th 2016. Our ideal starting date would be October 1st 2016.

– Prof. Dr. Bettina Meyer Ecophysiology of pelagic key species Helmholtz Virtual Institute PolarTime

Section Polar Biological Oceanography Alfred Wegener Institute Helmholtz Centre for Polar and Marine Research bettina.meyer@awi.de Am Handelshafen 12 D-27570 Bremerhaven Building E, room 2340 phone: +49 (0)471 4831 1378 fax +49 (0)471 4831 1149

Professor, Biodiversity and Biological Processes in Polar Seas Institute for Chemistry and Biology of the Marine Environment (ICBM)

Carl-von-Ossietzky University b.meyer@uni-oldenburg.de Carl-von-Ossietzky-Straße 9-11 D-26111

Oldenburg Building W3, room 0-025 phone: +49 (0)441-798-3567 fax: +49 (0)441-798-3404

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UOslo AdaptationGeneticArchitecture

CEES, Department of Biosciences University of Oslo

A three year position as postdoctoral research fellow in Evolutionary ecology and quantitative genetics is available at Centre for Ecological and Evolutionary Synthesis (CEES), Department of Biosciences.

Project description Adaptive evolution is driven both by selective forces and trait genetic architectures (evolvability). Additionally, selection itself may alter trait evolvability and simultaneously reshape the adaptive landscape that acts back on phenotypes through so-called eco-evolutionary feedback loops. Integrating this whole suite of gene-to-ecosystem processes into a coherent framework is a major next step in biology. However, to date, this framework remains largely theoretical. The goal of the 3-year postdoc project is to understand whether and how genetic architectures constrain response to selection acting on body size in the medaka (Oryzias latipes). We have been conducting a bi-directional selection experiment during 8 generations. Preliminary results suggest that medaka can evolve larger, but not smaller, body sizes. Additionally, selection on body size induces a response in correlated traits (size at maturity, body shape, behavior). The postdoc will have to manage in parallel (i) continuation of the selection experiment for further 4 generations, (ii) develop and improve phenotyping protocols on the selected lines, and (iii) analyze and model the collected data.

You may also consult the detailed announcement at: http://uio.easycruit.com/vacancy/1656137/96871?iso=no Please, send: - an application letter including a statement of interest, briefly summarizing your scientific work and interest and describing how you fit the description of the person we seek, - CV(summarizing education, positions, pedagogical experience, administrative experience, another qualifying activity), - copies of educational certificates and transcript of records, - a complete list of publications and up to 5 academic works that the applicant wishes to be considered by the evaluation committee, - names and contact details of 2-3 references (name, relation to candidate, e-mail and telephone number),

to Asbjørn Vøllestad (asbjorn.vollestad@ibv.uio.no), Eric Edeline (eric.edeline@upmc.fr), Arnaud Le Rouzic (arnaud.le-rouzic@egce.cnrs-gif.fr) and Finn-Arne Weltzien (finn-arne.weltzien@nmbu.no).

edeline <eric.edeline@upmc.fr>

UOulu PlantEvolutionaryGenomics

Link to jobposting https://www.saimanet.com/certiahome/open_job_view.html?did=5600&jc=1&id=00002550&lang=en Post-doctoral position to study evolutionary genomics of haploid life-stage in conifers in University of Oulu

A postdoctoral position for 20 months is available in the Department of Genetics and Physiology, University of Oulu, Finland to work in Dr Tanja Pyhäjärvi's research group (https://wiki.oulu.fi/x/_DLM).

Environment The Department of Genetics and Physiology has strong expertise and tradition in plant population genetics. Current research topics include genetics of local adaptation both in trees and Arabidopsis, genetics of speciation, conservation genetics and molecular evolution of insects. We offer a scientific environment that is enthusiastic about plant evolutionary genetics, a possibility to develop your genomics and bioinformatics skills and initiate international collaboration. The Pyhäjärvi research group is part of Biocenter Oulu and of the Population and Statistical Genomics Research Consortium which combines different population genomics research groups within the university. Within Europe, we collaborate closely with other forests geneticists via the Horizon 2020 project GenTree.

Finland is one of the most livable countries, with a high quality of life, safety and excellent education system. The successful candidate will receive full benefits provided by the University of Oulu to university employees, including free occupational health care services, and obtain access and high-quality affordable childcare services.

The project This project investigates the evolutionary consequences of haploid selection in plants. For this purpose, we use data from Pinus sylvestris (Scots pine), a widespread coniferous tree. The main objective of the study is to evaluate the effect of haploid phase in gymnosperm evolution using both RNA-seq and genome wide polymorphism data. Gymnosperms are of special interest in understanding evolutionary consequences of different ploidy levels, as they have extensive haploid life stage compared to flowering plants. The project is part of a 5-year Academy Research Fellow project of Dr. Pyhäjärvi funded by the National Research Council of Biosciences and Environment.

Qualifications The applicant should have a doctoral degree, recorded scientific expertise and interest in population and evolutionary genomics. Experience in bioinformatics, gene expression analysis and/or targeted sequencing is an advantage. The successful applicant will contribute to gene expression and population genetic analysis and research questions can be adjusted according to her/his interests and skills. The duties also include a small amount of teaching and supervising students. The work will be conducted in collaboration with Natural Resources Institute Finland (LUKE) and as a part of an international team who are experts in gymnosperm gene expression analysis (Jukka-Pekka Verta, FML of the Max Planck Society) and theoretical plant evolutionary genetics (Yaniv Brandvain, University of Minnesota).

Details Starting time for the position is January 1st 2017. The salary depends on the competence of the applicant, but likely will be level 5 of the national salary scale for teaching and research staff of Finnish universities. In addition, a supplementary remuneration will be given for personal achievement and performance, the sum rising to a maximum of 46.3% of the salary scale. (The total salary is expected to be around 3,200 euro/month).

Applications should consist of (1) a letter of motivation (maximum 2 pages) and (2) a CV that includes a list of publications and the contact details of at least two referees. Applications should be submitted in English using the electronic application form by September 1st, 2016

For further information please contact Academy Researcher Tanja Pyhäjärvi (tanja.pyhajarvi[at]oulu.fi) or Head of Administration Tiina Pääkkönen (tiina.paakkonen[at]oulu.fi).

Tanja_Pyhäjärvi <tanja.pyhajarvi@oulu.fi>

UPennsylvania EvolutionaryDevelGenetics

Post-doctoral position in Evolutionary and Developmental Genetics Laboratory of Yana Kamberov Department of Genetics in the Perelman School of Medicine at the University of Pennsylvania, USA.

Research in our is directed at uncovering the genetic basis of human adaptive traits, with a core focus on the evolution of skin appendages, namely sweat glands and hair follicles. Projects include: dissection of molecular pathways and epigenetic regulation of skin appendage development and regeneration; discovery and modeling of human adaptive variants using transgenic mice; high throughput screening for genetic elements controlling the development and uniqueness of human skin appendages.

The position provides an exciting opportunity to work at the interface of basic and translational research in a collaborative and stimulating environment, and gain experience in a diverse set of technical approaches at the cutting edge of evolutionary and developmental biology.

A doctorate in biology or related field is required. Applicants with a strong background in developmental biology, genetics, genomics or molecular biology are encouraged to apply. Prior experience with mouse genetics and husbandry is preferred.

Interested candidates should provide: 1) your CV 2) A brief letter detailing your interest in the lab and relevant past research experience 3) The contact information for three references who can comment on your research. Application materials and any questions regarding the position should be sent to Yana Kamberov: yana2@mail.med.upenn.edu

yanakamberov@gmail.com

UppsalaU 2
PlantEvolutionaryGenomics
Reminder

Two Postdoctoral Positions in Plant Evolutionary Genomics, Uppsala University

Two postdoctoral positions are available in the research group of Martin Lascoux at the Evolutionary Biology Centre in Uppsala, Sweden (https://lascouxlab.wordpress.com/). Our group works on plant population genetics and evolutionary biology with a special emphasis on local adaptation and related questions. We work on two groups of organisms: forest trees(spruces, birches, larches and poplars) and weeds (mainly the tetraploid weed Capsella bursa-pastoris and its close relatives). For more information please contact Martin.Lascoux@ebc.uu.se

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 is considered one of Europe's leading universities in the subject of biology bridging a broad variety of disciplines. The scientific environment with numerous seminars, journal clubs and social activities offer excellent possibilities for contacts and collaborations. Our lab is part of the Department of Ecology and Genetics and of the program in Plant Ecology and evolution (http://www.ieg.uu.se/), an active environment addressing fundamental evolutionary and ecological 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/). 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.

For both positions the application deadline is June 30, 2016.

1. Postdoctoral position in comparative population genomics of forest trees

The project.

The present position is part of the newly funded EU project Gentree. One of the aims of the project is to infer past population demography and characterize local adaptation in seven tree species across Europe using exome capture. The last large scale multi-species survey of genetic diversity in forest trees is now more than ten years old (Petit et al., Science, 2003) and it was based solely on chloroplast DNA. Patterns of genetic diversity at nuclear and cytoplasmic levels can differ significantly and the project should therefore provide a completely new view on the evolutionary forces, including natural selection, and historical events that shaped genetic diversity across the continent.

The position.

The successful applicant will be responsible for field sampling, gathering genomic data and analyzing them in spruce and birch species. There will also be possibility to participate in other ongoing projects on local adaptation in spruce. The applicant is expected to have a solid background in population gemomics, including associated lab work and be familiar with UNIX environments and have experience in standard bioinformatic approaches using high throughput DNA and RNA sequencing data from platforms such as Illumina. Proficiency in relevant programming languages (e.g. awk, bash, Perl, Python, C) will be a strong advantage.

How to apply.

Applicants with a proven record with and without a PhD degree are encouraged to apply. To apply please go the website of Uppsala University were you can login and submit your application:

http://www.uu.se/en/about-uu/join-us/jobs/ The position is: Postdoctoral fellow in plant genomics (GENTREE).

2. Postdoctoral position on levels of selection in Brassicaceae

The project.

The present position stems from a project funded by the Swedish Research Council on the presence of natural selection at different levels of biological integration (phenotype, gene expression, genome) and is related to our work on Capsella. In the project we will study signature of selection using the whole-genome and the transcriptome of four Capsella species and six more distant Brassicaceae species. More specifically we will address the following questions: How pervasive is adaptive evolution at the genome level? What is the part of neutral, stabilizing and adaptive evolution at the transcriptome level? We will also focus on adaptive evolution within the Capsella genus and in particular the role played by polyploidy in Capsella bursa-pastoris for which genomic and transcriptomic data, as well as large scale, multi-sites common garden data are already available.

The position.

The successful applicant will be responsible for growing plants,

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UppsalaU PlantEvolGenomics 2

Postddoctoral Position in Plant Evolutionary Genomics, Uppsala University

A postdoctoral position is available in the research group of Martin Lascoux at the Evolutionary Biology Centre, Uppsala University, Uppsala, Sweden. The position is for at least two years and is associated to a project recently funded by the Swedish Research Council.

The research group environment. Our group works on plant population genetics and evolutionary biology with a special emphasis on local adaptation and related questions. We study primarily two groups of plants: the tetraploid weed Capsella bursa-pastoris and its close relatives and forest trees (spruces, birches, larches and poplars). The present position stems from a project funded by the Swedish Research Council on the presence of natural selection at different levels of biological integration. For more information please contact Martin.Lascoux@ebc.uu.se

The position. The successful applicant will be responsible for growing plants, gathering genomic data (RNASEQ) and analyzing them. The applicant is expected to have a solid background in population gemomics and be familiar with UNIX environments and have experience in standard bioinformatic approaches using high throughput DNA and RNA sequencing data from platforms such as Illumina. Proficiency in relevant programming languages (e.g. awk, bash, Perl, Python, C) will be a strong advantage.

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 is considered one of Europe's leading universities in the subject of biology bridging a broad variety of disciplines. The scientific environment with numerous seminars, journal clubs and social activities offer excellent possibilities for contacts and collaborations. Our lab is part of the Department of Ecology and Genetics and of the program in Plant Ecology and evolution (http://www.ieg.uu.se/), an active environment addressing fundamental evolutionary and ecological 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/). 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 proven record and with a PhD degree are encouraged to apply. To apply please go the website of Uppsala University where you can login and submit your application:

http://www.uu.se/en/about-uu/join-us/jobs/ The position is: Postdoctoral fellow in plant genomics (VR). The deadline is June 30, 2016.

martin.lascoux@ebc.uu.se

UppsalaU PlantEvolutionaryGenomics

Postdoctoral Position in Plant Evolutionary Genetics, Uppsala University

One postdoctoral position is available in the research group of Martin Lascoux at the Evolutionary Biology Centre at Uppsala university, Uppsala, Sweden. The position is for two years and is associated to a recently funded project on the genetic basis of local adaptation of forest trees.

The research group environment and the project. Our group works on plant population genetics and evolutionary biology with a special emphasis on local adaptation and related questions. We study primarily forest trees (spruces, birches, larches and poplars) but we have also over the last decade worked actively on the tetraploid weed Capsella bursa-pastoris and its close relatives. The present position is part of the newly funded EU project Gentree. One of the aims of the project is to infer past population demography and characterize local adaptation in seven tree species across Europe using exome capture.

The position. The successful applicant will be responsible for field sampling, gathering genomic data and analyzing them in spruce and birch species. THis work will be done in close collaboration with colleagues in Scandinavia. There will be also possibility to participate in other ongoing projects on local adaptation in spruce. The applicant is expected to have a solid background in population gemomics and be familiar with UNIX environments and have experience in standard bioinformatic approaches using high throughput DNA and RNA sequencing data from platforms such as Illumina. Proficiency in relevant programming languages (e.g. awk, bash, Perl, Python, C) will be a strong advantage.

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 is considered one of Europe's leading universities in the subject of biology bridging a broad variety of disciplines. The scientific environment with numerous seminars, journal clubs and social activities offer excellent possibilities for contacts and collaborations. Our lab is part of the Department of Ecology and Genetics and of the program in Plant Ecology and evolution (http://www.ieg.uu.se/), an active environment addressing fundamental evolutionary and ecological 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/). 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 proven record and with a PhD degree are encouraged to apply. To apply please go the website of Uppsala University were you can login and submit your application: http://www.uu.se/en/about-uu/join-us/jobs/ The position is: Postdoctoral fellow in plant genomics (GENTREE). The deadline is June 30, 2016.

Martin Lascoux <martin.lascoux@ebc.uu.se>

UStAndrews ancientDNA

Research Fellow in Ancient DNA - AR1790SB

School of Geography & Geosciences, Department of Geography & Sustainable Development, Salary: 31,656 - 37,768 per annum, Start: As soon as possible, Fixed term for 18 months

The Department of Geography and Sustainable Development at St Andrews is seeking a Postdoctoral Researcher for 18 months to work with Professor Keith Bennett on research with ancient DNA, particularly with DNA from sediments and fossil pollen. The successful applicant will have recently completed or be near to successful completion of a PhD and should, ideally, have expertise with subfossil samples and ancient DNA.

The extraction of ancient DNA from subfossil samples is a rapidly expanding field as new techniques develop. These DNA remains offer the potential to substantially refine the taxonomic level at which fossils can be identified, and enable the discovery of the existence of taxa that are invisible using solely classical palaeoecological techniques. However, results are dependent on understanding the taphonomy of DNA in sediments from lakes and other organic materials. The Postdoctoral Researcher will establish an ancient DNA laboratory, and work on the taphonomy and identification of ancient DNA remains from Holocene sediments from Scotland and elsewhere, as appropriate.

The post is available immediately, for a period of 18 months.

Interested applicants should contact Professor Keith Bennett (kdb2@st-andrews.ac.uk; +44(0)1334 463907).

Applications are particularly welcome from women, who are under-represented in Research posts at the University. You can find out more about Equality & Diversity at https://www.st-andrews.ac.uk/hr/edi/ . The University of St Andrews is committed to promoting equality of opportunity for all, which is further demonstrated through its working on the Gender and Race Equality Charters and being awarded the Athena SWAN award for women in science, HR Excellence in Research Award and the LGBT Charter; http://www.st-andrews.ac.uk/hr/edi/diversityawards/ . To find further details go to https://www.vacancies.st-andrews.ac.uk/Vacancies.aspx and look for vacancy AR1790SB

Closing Date: 29 July 2016

Mike Ritchie Centre for Biological Diversity, School of Biology, University of St Andrews, Fife. Scotland KY16 9TH UK Phone: 0 (44 outside UK) 1334 463495 Some websites: Lab: http://biology.st-andrews.ac.uk/ritchielab/ Uni: http://www.st-andrews.ac.uk/profile/mgr Google: http://scholar.google.co.uk/citations?user=JSkvwMsAAAAJ&hl CBD: http://biodiversity.st-andrews.ac.uk/ Michael Ritchie <mgr@st-andrews.ac.uk>

UToronto BantingFellowship Preapplications

For Banting (NSERC) postdoctoral positions in the Department of Ecology and Evolutionary Biology (EEB) at the University of Toronto, starting between April 2017 and October 2017:

EEB is now accepting brief 'pre-applications' for the prestigious Banting Postdoctoral Fellowships in the areas of Ecology and Evolutionary Biology, broadly defined. Canadians and non-Canadians are eligible for these fellowships that provide 2 years of support at $70,000 per year. For full information on the Banting Postdoctoral Fellowships, including eligibility and evaluation criteria, please see this website: http://banting.fellowships-bourses.gc.ca For applicants wishing to do a postdoc at the University of Toronto, please see the following information. For applicants wishing to do a postdoc at another university, please contact that university.

To begin the application process for the University of Toronto, the applicants should first contact and obtain the agreement of a faculty advisor (or co-advisors) who is a member of EEB's graduate faculty. Please see this list for eligible faculty members: http://www.eeb.utoronto.ca/people/G-faculty.htm Further information on the application process will be available here by June 24: http://www.eeb.utoronto.ca/about-us/employment/postdocs/bantingpostdoc2016.htm The University of Toronto is a leading academic institution in Canada with over 60 faculty members specializing in ecology and evolution. Strong links exist between the Department of Ecology and Evolutionary Biology and the Royal Ontario Museum, the Centre for Global Change, the School of the Environment, and the Faculty of Forestry. The University owns a nearby field station dedicated to ecological and evolutionary research (the Koffler Scientific Reserve,www.ksr.utoronto.ca). The department also has a partnership with the Ontario Ministry of Natural Resources that helps provide access to infrastructure, including lab facilities in Algonquin Provincial Park (www.harkness.ca), funding, and long-term data sets. Genomic analyses are supported by the Centre for the Analysis of Genome Evolution and Function (www.cagef.utoronto.ca) and as well as other facilities.

Asher Cutter <asher.cutter@utoronto.ca>

UUtah EvolutionaryGeneticsCellBiol

Postdoctoral opportunities in the Phadnis Lab.

Department of Biology, University of Utah.

The Phadnis Laboratory is looking for talented and ambitious postdoctoral fellows interested in performing cutting edge research at the intersection of evolutionary genetics, genomics, and cell biology. We enjoy asking unsolved questions in biology, and strongly believe in not being limited by study systems or techniques. Individuals with a record of excellence, and a desire to build an original and impactful research program are strongly encouraged to apply. Postdoctoral fellows in the laboratory are not only encouraged, but expected to develop their own independent scientific trajectories. Cell biologists interested in evolutionary questions, and evolutionary geneticists interested in the molecular questions would make a particularly good fit with the lab.

Current interests in the laboratory include, but are not restricted to 1) Understanding the genetic and molecular bases of hybrid sterility/ inviability and behavioral changes between species. 2) Uncovering the molecular mechanisms of selfish genetic elements such as segregation distorters. 3) Studying the role of genomic conflict in shaping the mechanisms of fundamental cellular processes. Please visit www.flygenetics.com for more information.

Please send an email describing your background and interests, along with your CV to nitin.phadnis@utah.edu. Include contact information for your references as well.

Nitin Phadnis, Ph.D.

Assistant Professor Mario Capecchi Endowed Chair in Biology University of Utah Salt Lake City, UT 84112 801.585.0493 nitin.phadnis@utah.edu www.flygenetics.com NITIN PHADNIS <nitin.phadnis@utah.edu>

UVienna EvolGenomics

Senior Research Staff and Postdoc Positions Available at University of Vienna

Applications are invited for a senior research staff position and a postdoc position in the Department of Molecular Evolution and Development at University of Vienna. Both are supported by the European Research Council (ERC) grant lasting for five years, and planned for at least two years starting from August 1^st, 2016 with possible renewal. The successful applicants will work on the epigenomic evolution of Drosophila sex chromosomes. We will be using Drosophila species with recently born sex chromosome (â-sex') systems to address: How does the Y chromosome become heterochromatic? How does this universal evolution process drive the adaptation of small RNA defense systems? And how does such a male-specific arms race between parasitic transposable elements and small RNAs fuel the changes of the female genome? The candidates are expected to be independent and highly motivated, and are required to have a Ph.D. in molecular biology, genetics or other related field. Essential qualifications include demonstrated experience in Drosophila transgenics, CRISPR/Cas9 mutagenesis, in situ hybridization, next-gen sequencing library preparation (RNA-seq, ChIP-seq & CLIP-seq). Knowledge and skills in bioinformatics (Unix, perl/python programming etc.) and next-gen sequencing data analyses (genome assembly and annotation, ChIP-seq and RNA-seq data analyses) are highly desirable but not mandatory. The senior staff is required to have at least 8 years' postdoctoral research experience.

Successful applicants will receive very competitive salary and benefits and enjoy the diverse and vibrant research environment of the Department and the University. The group members will have frequent interactions with other neighbor labs of Drosophila neurobiology (Prof. Thomas Hummel) and developmental biology (Prof. Ulrich Technau), and have a chance to develop collaborative research projects. The university is located near the city center of Vienna, which also houses numerous world's leading research institutes including Gregor Mendel Institute, Institute of Molecular Biotechnology and Institute of Science and Technology etc. The city has gathered many great scientists in evolutionary biology (http://www.univie.ac.at/evolvienna/-?page_id=3D6), RNA biology (http://www.mfpl.ac.at/-rna-biology/) and there is an encouraging plan to move the biology departments of the University near other institutes of Vienna Biocenter. Vienna has been voted as the world's most livable city for the seventh time, and is famous for its history and culture, and now also a modern and international lifestyle. Interested candidates please send her/his CV and contact information of three referees to Dr. Qi Zhou (muntjaczhou@gmail.com). We will start reviewing the application immediately until the position is filled.

Qi

Qi Zhou <muntjaczhou@gmail.com>

UWarsaw UrbanEvolutionaryGenomics

Postdoc position in Urban Ecological & Evolutionary Genomics We seek a post-doctoral research fellow in ecological and evolutionary genomics to work in the Wild Urban Evolution & Ecology Lab (http://leem.cent.uw.edu.pl) led by Marta Szulkin at the Centre of New Technologies (CeNT), University of Warsaw (Poland) for a period of 2 years, renewable. The position is part of a 5 year grant from the Polish Science Foundation (NCN) entitled: “Ecological genetics of the great tit in a new, long-term population study set along an urbanization gradient”, which started in October 2015. CeNT is a vibrant research-only institute located on the science campus of the University of Warsaw. English is the working language of the group.

Background. Urban areas are predicted to expand 12-fold between 2000 and 2050, yet knowledge on the evolutionary ecology of free-living animals in urban environments is very scarce. To understand the footprint of cities on the phenotype and genotype of a wild bird, we have started a large-scale, long-term study of great tits Parus major and blue tits Cyanistes caeruleus in the city of Warsaw (Poland) in a gradient of urbanization.

Job description. The post-doctoral fellow will develop analytical pipelines to infer the ecological and population genomics of urban great tits. S/he will also participate in fieldwork and in collecting phenotypic and genetic data. The Postdoc will actively participate in co-supervising PhD students and will be involved in group and / or fieldwork management. S/he will also have flexibility to develop his/her own ideas and approaches to the overall research theme. S/he will work in interaction with the PI and all team members, as well as with collaborators in France (Dr Anne Charmantier, CEFE CNRS Montpellier) and other urban evolutionary ecology research groups worldwide.

Job requirements: We seek motivated candidates with a PhD degree, fluent English and a strong interest in population genetics. The candidate should have a background in evolutionary ecology, statistical modelling in R, RADseq and / or population genomic data analysis. Unix / Linux programming skills, lab experience and / or bird ringing experience are desirable. Employment: Post-doctoral full time position.

Salary: 4700 PLN before tax (includes insurance), with a possibility of applying for further research and salary allowance.

How to apply. Your application should include in PDF format: a cover letter, C.V. (including your research experience, conference attendance, a publication list (detailing author contributions of the candidate)), contact information for two referees and scans of your PhD certificate. Please send your applications to marta.szulkin@cent.uw.edu.pl no later than the 30th of June 2016 with the term "Postdoc position" as email subject line. Selected candidates will be asked for reference letters; top candidates will be invited for live interviews or via Skype. Start date: 1st of September-1st of December 2016 (flexible).

Dr hab. Marta Szulkin, Prof. UW Wild Urban Evolution and Ecology Lab Centre of New Technologies (CeNT), University of Warsaw Research Associate, Department of Zoology, University of Oxford http://leem.cent.uw.edu.pl Marta Szulkin <marta.szulkin@zoo.ox.ac.uk>

UWashington Bothell MicrobialEvolution

Postdoctoral position on Microbial Evolution

A postdoctoral research position in microbial evolution and genomics is available in the Hillesland lab at University of Washington Bothell. This position is part of an NSF-funded grant to determine the population genetics governing the evolutionary dynamics of two mutualists during the first 3000 generations of their adaptation to obligate mutualism. In previous work, the Hillesland lab propagated the bacteria Desulfovibrio vulgaris and the archaeon Methanococcus maripaludis for thousands of generations in both conditions requiring their cooperation and in an environment where they could each evolve alone. The postdoctoral researcher will examine the prevalence of coevolutionary processes by pairing each species with past and future mutualist partners. She or he will also acquire and analyze the genome sequences of the entire population of each species at several timepoints to determine the population genetics of adaptation and coevolution in mutualism. The postdoctoral researcher will also contribute to the development and dissemination of a module on microbial population genetics designed for undergraduate microbiology courses, and will be expected to mentor one or more undergraduate researchers.

The successful candidate will have strong background in either evolutionary biology or microbiology and a PhD in a related field, and will demonstrate a strong interest in understanding evolutionary processes in a community context. Candidates that have experience in population genetics, in analyzing next-generation sequencing data, or in anaerobic techniques are strongly encouraged to apply.

This postdoctoral position provides the opportunity to engage in scholarly activities with researchers in the greater Seattle area while living in a thriving metropolitan area in the Pacific Northwest. The Hillesland lab is located in the Division of Biological Sciences in the new School of STEM at University of Washington Bothell, which is about 15 miles (an easy bus ride) from the UW Seattle campus. The Division of Biological Sciences has a highly interactive group of 12 full-time faculty with expertise in ecology, evolution, physiology, computational biology, cellular biology, animal behavior, and neuroscience. The postdoctoral scholar may also participate in regular seminars and research discussions on the Seattle campus. The School of STEM and Division of Biological Sciences values innovative student-centered teaching and high quality research that engages undergraduate researchers. Mentored teaching opportunities are available for postdoctoral researchers that are interested in developing as teacher-scholars.

To apply for this position, please submit a copy of your CV, the names and contact information for three references, and a cover letter that explains i) why you are interested in this particular research project and position, ii) why you are qualified for the position, iii) your career goals, and how you expect this position to help you achieve those goals. Application materials should be sent in a single pdf to Dr. Kristina Hillesland at hilleskl@uw.edu. The appointment is renewable for up to two years with possible extension to a third year.

The position is available immediately but the start date will be flexible contingent on the needs of the preferred candidate.

Best wishes, Kristina Hillesland

Assistant professor Biological Sciences School of STEM University of Washington, Bothell Bothell WA 98011

"Kristina Hillesland" <hilleskl@uw.edu>

WorkshopsCourses

Amsterdam EvoEvol Sep20 CallAbstracts

CALL FOR EXTENDED ABSTRACTS

EvoEvo workshop

Satellite workshop of the 2016 Conference on Complex Systems (CCS16) http://www.ccs2016.org/ Tuesday 20 Sep 2016, Beurs Van Berlage, Amsterdam, The Netherlands

AIMS AND SCOPE Variation and Selection are the two core processes of Darwinian Evolution. Yet, both are directly regulated by many processes that are themselves products of evolution (e.g. DNA repair, mutator genes, transposable elements, horizontal transfer, stochasticity of gene expression, sex, network modularity, niche construction;). This results in the ability of evolution to self-modify its operators, hence its dynamics. We call this process "Evolution of Evolution" or EvoEvo.

Different EvoEvo strategies have been proposed in the literature, including regulation of variability, robustness/evolvability strategies and bet-hedging, but finding traces of these strategies in extant organisms is difficult. Moreover all these strategies are likely to interact one with the others, blurring their respective outcomes.

However, new tools are now available that help understanding EvoEvo. On the one hand, large scale bioinformatic data analysis can be used to recognize signatures of evolution of evolution. On the other hand, large scale computational modelling of multi-level evolution is now becoming feasible, and promises to shed light on the conditions under which evolutionary mechanisms evolve as well as their consequences.

The aim of the EvoEvo workshop is to seek for a unified theory of Evolution of Evolution and bring together researchers from various fields in computational biology to tackle this challenge. The workshop will take place as a satellite workshop of CCS 2016, Amsterdam, NL. The EvoEvo workshop is an initiative of the EvoEvo consortium funded by the FP7 EU-FET grant EvoEvo (ICT-610427).

AREAS OF INTEREST We are seeking submissions that explore all aspects of "Evolution of Evolution", including theoretical and experimental works (including in vivo, in vitro and in silico experiment). Topics include but are not limited to: - Evolution of robustness and evolvability, evolution of pleiotropy - Evolution of mutation rates, regulation of variability, mutators, transposable elements, chromosomal rearrangements - Open-ended evolution - Evolution of the genotype-to-phenotype mapping - Niche construction, evolution of trophic networks, evolution of cooperation - Evolution of genes and metabolic networks, evolution of modularity - Evolution of stochastic gene expression and bet-hedging - Modeling and simulation of EvoEvo, EvoEvo and fitness landscapes/seascapes - Experimental characterization of EvoEvo - Application of EvoEvo to evolutionary computation - Philosophical, theoretical and practical aspects of EvoEvo

SUBMISSIONS EvoEvo will accept extended abstracts of maximum 2000 words in LNCS format. All submissions will be peer reviewed by at least two members of the workshop committee. Accepted papers will be selected for long or short oral presentation during the workshop.

Abstracts should be submitted via EasyChair < https://easychair.org/conferences/?conf=3Devoevo2016 >.

LNCS formatting details can be found at < http://www.springer.com/computer/lncs?SGWID=3D0-164-7-72376-0 >.

IMPORTANT DATES - Abstract Submission: 30 June 2016 - Notification of acceptance: 10 July 2016 - EvoEvo Workshop: 20 September 2016

WORKSHOP CHAIRS - Guillaume Beslon, INSA, Universite de Lyon (FR), LIRIS/Beagle team - Santiago Elena, CSIC and Polytechnic University of Valencia (SP), IBMCP - Paulien Hogeweg, Utrecht University (NL), Bioinformatics group - Dominique Schneider, Universite Joseph Fourier, Grenoble (FR), LAPM - Susan Stepney, University of York (UK), Centre for Complex Systems Analysis

Prof. Santiago F. Elena IBMCP (CSIC-UPV) Campus UPV, CPI 8E, lab. 2.0.4 Ingeniero Fausto Elio s/n, 46022 Valencia, Spain Phone: +34 963 877 895 Fax: +34 963 877 859 E-mail: sfelena@ibmcp.upv.es Web: http://bioxeon.ibmcp.upv.es/EvolSysVir Twitter: @SantiagoFElena The Santa Fe Institute 1399 Hyde Park Road Santa Fe, NM 87501 USA

"Santiago F. Elena" <sfelena@ibmcp.upv.es>

Barcelona PopGeneticsEvol Oct3-5 AbstractDeadline

7 DAYS FOR ABSTRACT SUBMISSION DEADLINE

June 30th is the deadline for submission of abstracts to the XXI SGPE. This workshop will be held October 3-5, 2016 at the Hotel Calipolis in Sitges (Barcelona, Spain). June 30th is also the deadline for early bird registration with reduced fees.

In the workshop webpage:

http://xxisgpe.uab.es You will find a tentative program that includes the basic structure of the workshop. Working sessions will begin on Monday October 3^rd at 15:30 and will end on Wednesday 5th at 20:05. Language is optional for speakers, Spanish or English. Please note that the Conference Dinner will be held on Wednesday 5th October night.

We are already more than 60 attendants. If you did not register yet, don't delay your registration. Remember that space is limited. All the information about registration fees and types of accommodation can be found in the workshop webpage. To register for the workshop, please follow the link.

http://xxisgpe.uab.es/base/base3.asp?sitio=-XXISGPE&anar=inscri We look forward to your participation!

Organizing Committee

Alfredo Ruiz Mauro Santos Antonio Barbadilla Mario Caceres Isaac Salazar-Ciudad

Contact Alfredo Ruiz Departament de Genetica i de Microbiologia Facultat de Biociencies, Edifici C Universitat Aut0noma de Barcelona Tel. +34 93 581 2729 sgpe.sitges@uab.es

Alfredo Ruíz Panadero <Alfredo.Ruiz@uab.cat>

CollegePark MD Bioinformatics Sep15-18

Hi Everyone-

We are offering a Fall Workshop in Introductory Bioinformatics

Where/when: University of Maryland College Park, Maryland September 15-18, 2016

The handling of large datasets has become intractable without some level of bioinformatic literacy. Many biologists find that there is a steep learning curve to develop the confidence required to explore their genomics datasets effectively. This bioinformatics short course includes a rich collection of hands-on instruction and lectures specifically intended to help novice users become comfortable with a range of tools currently used to analyze deep sequencing data. There is no prerequisite for this course other than a willingness to learn and to work hard throughout the week. All workshop exercises will be implemented via VirtualBox and focus primarily on Illumina data; however, we will also include PacBio data during the genome assembly tutorial. Course participation is limited to 25 students to ensure an intimate learning environment. Course tuition is $800 and is open to graduate students, postdocs, staff, faculty, and industry researchers on a first come basis.

Full course information, contact, instructor info and application instructions at https://biodatatraining.wordpress.com < https://biodatatraining.wordpress.com/ >

Please contact us if you have any questions or need additional info. Hope to see you in College Park.

Nic and Ian

biodatatraining@gmail.com

CopenhagenU NGSpopulationGenetics Aug22-26

PhD course in analyses of genotyping and next Â’generation sequencing data in medical and population genetics

When: August 22 - August 26 2016

Where: Department of Biology, University of Copenhagen, Copenhagen Denamrk

Instructors: Brenna Henn, Matteo Fumagalli, Fernando Racimo, Anders Albrechtsen and Ida Moltke

The course is a comprehensive introduction to a number of topics and common research tools used in analyses of genetic data. Topics include: genetic drift, natural selection, population structure, Fst, linkage disequilibrium, association mapping, GWAS, genotyping data, next Â’generation sequencing (NGS) data, 1000 genomes project data. The main focus will be on humans, but the analysis methods are applicable to many other species as well. Lectures will be combined with hands Â’on computer exercises mostly using R and command Â’line Â’based programs. The course is free for all PhD students at Danish universities (KU, AU, AUC, SDU and DTU). For all other PhD students there is a course fee of 200 US dollars. Food and accommodation are not included in the course.

To sign up, please send an email to cphsummercourse@gmail.com

albrecht@binf.ku.dk

Lausanne PopulationGenomicsInR Aug22-26

POPULATION GENOMICS IN R

WHEN? 22-26 August 2016 WHERE? University of Lausanne

FACULTY Prof. Jérôme Goudet, University of Lausanne (CH) Dr. Emmanuel Paradis, Université de Montpellier (FR) Dr. Thibaut Jombart, Imperial College London (UK)

DESCRIPTION In this workshop, we will present a series of R packages tailored for population genomic analyses: ape, adegenet, hierfstat, popr. The teachers are the active developers of these packages, and will illustrate their flexibilities to conduct population genomic analyses in R.

Each of the first four days will be devoted to one package, and the last one will take the form of a mini population genomic conference, showing applications.

Provisional program: Day 1: ape Day 2: adegenet Day

3: hierfstat Day 4: popr Day 5: workshop/conference

INFO & REGISTRATION http://www.cuso.ch/activity/?p=1128&uid=3032 or

https://biologie.cuso.ch/index.php?id=3D1128&tx_displaycontroller[showUid]=3032 or

https://biologie.cuso.ch/ecologie-et-evolution/dpee-activities/ Caroline.Betto-Colliard@unil.ch

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MathVillage Turkey QuantEvolBiol Sep18-25

*Workshop/ Summer school "Quantitative Evolutionary Biology – building bridges between evolutionary theory and empirical approaches to evolution in the genomic era"

*Time and Place September 18-25, 2016, Mathematics Village, Sirince, near Izmir,Turkey.

*Keynote lecturers Nicola Barson (Norwegian University of Life Sciences, As) Laurent Duret (University of Lyon) Pavlos Pavlidis (Institute of Computer Science - FORTH, Heraklion) Judith Mank (University College London)

*Description The workshop is mainly targeted towards advanced graduate students and early post-docs studying evolutionary biology. Our main aim is to bring together researchers and students studying aspects of natural evolution with theoretical, empirical and genomic approaches. Students will get an overview of the state of the art in several fields of evolutionary biology through lectures by established researchers and learn to develop their own scientific ideas by pursuing collaborative short projects. There will also be various short lectures and seminars during the workshop.

*For more information, visit http://qevolution2016.wordpress.com/ *Application deadlines Early: July 8, 2016 (recommended as the number of attendees and fellowships are limited) Late: August 22, 2016

*Other Participating Scientists Tugce Bilgin (University of Zurich) Primrose Boynton (Max Planck Institute, Plön) Gönensin Ozan Bozdağ (Georgia Institute of Technology) Berra Erkoşar (University of Lausanne) Sibel Küçükyıldırım (Indiana University, Bloomington) Sara Mitri (University of Lausanne) İsmail Sağlam (Hacettepe University, Ankara & UC, Davis) Ferran Palero (Centro de Estudios Avanzados de Blanes) Nicolas O. Rode (INRA, Montpellier) Rodrigo Redondo (The Francis Crick Institute, London) Jamie Winternitz (Max Planck Institute, Plön)

*Organizers Ezgi Ã-zkurt (Max Planck Institute, Plön) Hannes Svardal (Wellcome Trust Sanger Institute, Cambridge) Murat Tuğrul (IST-Austria, Klosterneuburg)

*Advisory Board: Tadeusz Kawecki (University of Lausanne) Mehmet Somel (Middle East Technical University, Ankara)

*Sponsor: the Global Training Initiative of ESEB

*Organisational Support: Mathematics Village; the Global Training Initiative of ESEB; Society for Ecology and Evolutionary Biology, Turkey

*Help us spread the word (poster, 1.5 Mb) https://qevolution2016.files.wordpress.com/2014/01/poster_qevolution2016_small.pdf muratugrul@gmail.com

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Minnesota TeachingEvolComputation Oct23-25

Dear Colleagues,

We invite you to the *Teaching Computation in the Sciences Using MATLAB* workshop focused on building students' ability to solve problems with computation using MATLAB in their undergraduate evolutionary biology courses. Quantitative and computational skills are an important component of current biological practice, and this is especially evident in evolutionary research. Faculty are invited to join an interdisciplinary community to explore how their evolutionary applications of MATLAB in the undergraduate classroom can contribute to best practices for the community. By attending the workshop, you will be part of a community effort to bring together best practices and teaching materials that will be made freely available through the SERC website. MathWorks (makers of MATLABÂ) is sponsoring the workshop.

Details

Workshop: Teaching Computation in the Sciences Using MATLAB Location: Carleton College, Northfield, MN

Date: October 23-25, 2016 (5PM Sunday - 2PM Tuesday) Application Deadline: September 2, 2016

Learn more from the workshop website: http://serc.carleton.edu/matlab_computation2016/index.html

Workshop Description:

The *Teaching Computation in the Sciences Using MATLAB *workshop will bring together faculty from the sciences, including Chemistry, Geoscience, Physics, Biology, and allied fields, who teach computation and quantitative thinking skills using MATLAB. Computation is broadly defined as using computers in scientific work to understand and solve problems, or formulating problems in ways that can be computed. Computational skills are critically important for students to understand complex systems, analyze data, and create numerical models and visualizations-all essential aspects of modern science. These skills require students to have comfort and skill with languages and tools such as MATLAB. To achieve comfort and skill, computation and quantitative thinking must build over a 4-year degree program across courses and disciplines. Participants will help build a collection of teaching activities that showcase computation, quantitative thinking, and applied math using MATLAB and design approaches to integrating these skills throughout science degree programs.

This workshop target is 30 college educators (by application).

The application deadline is *September 2, 2016*.

There is no registration fee to attend.

To apply, go to: http://serc.carleton.edu/matlab_computation2016/application.html We hope to see you there!

If you have additional questions, direct them to Rory McFadden (rmcfadden@carleton.edu).

Thank you,

Lisa Kempler

MATLAB Community Strategist, MathWorks

https://serc.carleton.edu/NAGTWorkshops/data_models/toolsheets/MATLAB.html Cathryn A. Manduca

Director, Science Education Resource Center

Executive Director, National Association of Geoscience Teachers

Kristin Jenkins

Executive Director, BioQUEST Curriculum Consortium

Kelly Roos

Professor, Department of Engineering Physics, Bradley University

PICUP Leadership Council

Frederik J. Simons

Associate Professor, Department of Geosciences, Princeton University

Wendy Thomas

Associate Professor, Department of Bioengineering, University of Washington

Kristin P. Jenkins, PhD Director

BioQUEST Curriculum Consortium bioquest.org (608) 622.9394 POBox 126 Boyds, MD 20841-0126

Kristin Jenkins <kristin.jenkins@bioquest.org>

Nantucket Phylogenetic DevelopeR Bootcamp

Nantucket phylogeny developeR bootcamp

We are happy to announce a new graduate-level workshop on phylogenetic method development R. The course will be five days in length and will take place at the University of Massachusetts Boston's Nantucket Field Station from the 22nd to the 26th of August, 2016. This workshop is primarily intended for evolutionary biologists with some prior experience in computer programming who have an interest in participating more fully in the community of method developers for the R statistical computing environment in phylogenetics.

On the first 1.5 days of the workshop, course leaders Drs. April Wright and Klaus Schliep (with Dr. Liam Revell participating remotely) will provide an introduction to the primary data structures and methods of common phylogenetic R packages, the basics of computational algorithms for phylogenies, and an overview of package development in R, along with other essential topics that will depend on the prior experience of the bootcamp participants. Over subsequent workshop days participants will work in groups to develop small R packages on their chosen topics. These projects will focus on adding new functionality to existing R software in phylogenetics, and might range from tree manipulation, to phylogenetic inference, to comparative methods, to phylogenetic simulations, to the visualization of phylogenies or macroevolutionary data on trees.

The workshop is funded by a grant from the National Science Foundation to Dr. Liam Revell, with additional support from the University of Massachusetts Boston. All accepted students will be offered a stipend to cover or defray travel costs to and from Nantucket, and room and board during the workshop will be provided. As the workshop will be held at a field station, accommodation is comfortable, but basic, and participants should be prepared to stay in multiple occupancy rooms.

To apply for the course, please fill the google form (http://goo.gl/forms/4m5ILAGfzRihe9jS2) and submit your CV along with a short (1 page) description of your research interests and your reasons for participating in the workshop. Details of relevant programming background (computer languages, R knowledge, GitHub repositories, ...) should also be provided. Admission is competitive, and preference will go towards students with background in evolutionary biology, basic to moderate experience in computer programming, and a compelling motivation for taking the course. Applications should be submitted the google form (http://goo.gl/forms/4m5ILAGfzRihe9jS2) by July 15th, 2016. Questions can be directed to klaus.schliep@umb.edu.

For an HTML version of this advertisement, please see: http://www.phangorn.org/pages/Nantucket.html Liam J. Revell, Associate Professor of Biology University of Massachusetts Boston web: http://faculty.umb.edu/liam.revell/ email: liam.revell@umb.edu blog: http://blog.phytools.org Liam.Revell@umb.edu

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Oviedo Spain AlertTools

June 14th, 2016.

Dear Colleagues and Friends.

The Deadlines for Early Registrations and Submissions of Communications for the First International Workshop ALERTOOLS: Science & Educational Strategies for Early Detection of Bioinvaders, 2016 have been extended until Sept 5th, 2016.

Dont lose your chance to get involved in such an opportunity to show your work and get in touch with colleagues, students and citizens.

Thanks in advance for your contributions

cheers,

Executive Committee ALERTOOLS 2016. http://alertools.uniovi.es/inicio Alertools - Home alertools.uniovi.es Alertools

Prof. AD Yaisel Juan Borrell Pichs. PhD Dpto Biologia Funcional. Universidad de Oviedo. Calle Julian Claveria s/n. Oviedo. 33006 Asturias. Espana Tel.: +34 661256251 +34 985102746 Fax: +34 985 103534 E-mail address: borrellyaisel@uniovi.es

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Paris ExperimentalEvolution Nov7-11

First Call Experimental Evolution: Theory and Current Practices

The International Graduate Program in Life Sciences and the Interdisciplinary Master in Life Sciences (IMaLis) are now accepting applications for the course “Experimental evolution: theory and current practices”, to be held at the Institute of Biology of the École Normale Supérieure (IBENS), in Paris, November 7-11, 2016.

The course will introduce Master and PhD students in Evolutionary Biology to the experimental approaches employed to test evolutionary theory. It will bring together world-renowned researchers to lecture on topics including the historical development of experimental evolution approaches, experimental design, the evolution of sexuality, origin of multicellularity and sociality, or the genetic basis of adaptation to novel environments. Lectures will be complemented with computer tutorials on the analysis of experimental population genomics data.

The course will be restricted to a maximum of 10 students. Meal and accommodation costs will be fully covered and there is no registration fee. Upon successful completion of the course, European students will be awarded 6 ECTS credits.

Provisional faculty: Charlie Baer (University of Florida); Ivo Chelo (Instituto Gulbenkian de Ciência); Antony Dean (University of Minnesota); Marie-Anne Félix (IBENS) ; Thiago Guzella (IBENS); Steve Proulx (University of California, Santa Barbara); Paul Rainey (ESPCI and New Zealand Institute for Advanced Study); Christian Schlötterer (Institut für Populationsgenetik); Olivier Tenaillon (Université Paris 7); Henrique Teotónio (IBENS); Arjan de Visser (Wageningen UR).

Sponsoring and partner graduate programs: IBENS, Pepiniere interdisciplinaire CNRS-PSL Eco-Evo-Devo, and the Vienna Graduate School of Population Genetics.

We will receive applications until September 30, 2016, and selection results will be available the following week. Applicants should send a letter of motivation and a CV as a single PDF file to: teotonio@biologie.ens.fr.

We also welcome participants at any stage of their careers to attend the lectures. Meals and accommodation costs will not be covered in this case. Registration is required by sending an email to: teotonio@biologie.ens.fr. We will accept applications on a first come first serve basis, to a maximum of 30.

Further information and updates can be found at http://www.gradprog.biologie.ens.fr/ teotonio@biologie.ens.fr

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PortoAlegre Brazil HierarchicalPopModeling Oct9-15

III Porto Alegre Hierarchical Modeling Workshop

Site-Occupancy and Species Distribution Models

Date: October 9-15, 2016 Lecturers: Marc Kéry, Swiss Ornithological Institute, Sempach, Switzerland David Miller, Penn State University, University Park, USA Gonçalo Ferraz, Universidade Federal do Rio Grande do Sul, Porto Alegre, Brazil Teach. Assistants: Ulisses Camargo, University of Helsinki, Finland Courtney Davis, Penn State University, University Park, USA Murilo GuimarÃ£es, UFRGS, Porto Alegre, Brazil Nicolas Strebel, Swiss Ornithological Institute, Sempach, Switzerland Location: Pousada Haras Cambará, Porto Alegre, Rio Grande do Sul, Brazil Language: English Organization: Programa de Pós-GraduaçÃ£o em Ecologia, Instituto de Biociências, Universidade Federal do Rio Grande do Sul (UFRGS), with support from the Swiss Ornithological Institute, Penn State College of Agricultural Sciences, and the Finnish Ministry of Education and Culture. Course Fee: R$1200, covering lectures and handouts, food and accommodation for the whole week. Five bonus slots (reduced fee of R$250) will be available and distributed to graduate students on a merit basis. Attendance: 25 Participants max.

This workshop is the third in a series of Porto Alegre Hierarchical Modeling Workshops for Ecologists, started in 2014. Each year we focus on a particular modeling topic and the theme for 2016 is site-occupancy modeling with particular emphasis on species distribution modeling. The workshop will open with a one-day introduction to linear, generalized linear and mixed models, and their implementation in the Bayesian and likelihood framework. From day two on, we turn our attention to the modeling of species distributions, focusing on the powerful site-occupancy models, which deal explicitly with measurement errors in species detection/non-detection data. We first study the basic MacKenzie et al. (2002) static model, and then develop a range of variations on the basic theme, with particular attention to dynamic occupancy models, mis-identification models, and spatial models of species distribution. A large part of the content will draw on three successful applied statistics books co-authored by Marc Kéry and published by Academic Press (2010, 2012, and 2016). Most models will be implemented in a Bayesian framework, but we will show likelihood implementations, too, especially in the user-friendly R package unmarked. Ample time will be given for solving exercises, which will require some experience in R. We encourage participants to bring their own research problems for discussion during the workshop; both new and returning applicants are welcome.

HOW TO APPLY: Visit http://www.ferrazlab.org/workshops and use the application form link to send us a CV and short letter describing former experience with ecological modeling and R (and possibly with BUGS software). Please also tell us your main reasons for wanting to attend and whether you want to apply for a bonus slot. This course is geared towards an audience of Latin American graduate students but we welcome applications from any background, professional activity and geographic origin. Please send your application no later than June 30th; we will get back to you until July 5th. For more information please visit http://www.ferrazlab.org/workshops or write directly to goncalo.ferraz@ufrgs.br.

Gonçalo Ferraz Professor Adjunto - Departamento de Ecologia Instituto de Biociências Universidade Federal do Rio Grande do Sul

http://ferrazlab.org/ Endereço Postal / Postal Address: UFRGS - Departamento de Ecologia Av. Bento Gonçalves 9500 Porto Alegre RS 91540-000 Brasil

Tel. 55 (51) 3308-6772

"goncalo.ferraz@ufrgs.br" <goncalo.ferraz@ufrgs.br>

PortoAlegre Brazil HierarchicalPopModeling Oct9-15 2

III Porto Alegre Hierarchical Modeling Workshop

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Lecturers: Marc Kery, Swiss Ornithological Institute, Sempach, Switzerland David Miller, Penn State University, University Park, USA Goncalo Ferraz, Universidade Federal do Rio Grande do Sul, Porto Alegre, Brazil

Teach. Assistants: Ulisses Camargo, University of Helsinki, Finland Courtney Davis, Penn State University, University Park, USA Murilo Guimaraes, UFRGS, Porto Alegre, Brazil Nicolas Strebel, Swiss Ornithological Institute, Sempach, Switzerland

Location: Pousada Haras Cambara, Porto Alegre, Rio Grande do Sul, Brazil

Language: English

Organization: Programa de Pos-Graduacao em Ecologia, Instituto de Biociencias, Universidade Federal do Rio Grande do Sul (UFRGS), with support from the Swiss Ornithological Institute, Penn State College of Agricultural Sciences, and the Finnish Ministry of Education and Culture.

Course Fee: R$1200, covering lectures and handouts, food and accommodation for the whole week. Five bonus slots (reduced fee of R$250) will be available and distributed to graduate students on a merit basis.

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HOW TO APPLY: Visit http://www.ferrazlab.org/-workshops and use the application form link to send us a CV and short letter describing former experience with ecological modeling and R (and possibly with BUGS software). Please also tell us your main reasons for wanting to attend and whether you want to apply for a bonus slot. This course is geared towards an audience of Latin American graduate students but we welcome applications from any background, professional activity and geographic origin. Please send your application no later than June 30th; we will get back to you until July 5th. For more information please visit http://www.ferrazlab.org/workshops or write directly to goncalo.ferraz@ufrgs.br.

Gonçalo Ferraz <goncalo.ferraz@ufrgs.br>

Scotland PhylogenticDataAnalysis Oct31-Nov4

Course - “Introduction to phylogenetic analysis with R”

Delivered by Dr. Emmanuel Paradis

http://prstatistics.com/course/introduction-to-phylogenetic-analysis-with-r-phyg/ This course will run from 31st October - 4th November, Millport Field Station, Ilse of Cumbrae, Scotland

The main objectives of the course are to teach the theoretical bases of phylogenetic analysis, and to give the ability to initiate a phylogenetic analysis starting from the files of molecular sequences until the interpretation of the results and the graphics. The introduction will cover a brief historical background and an overview of the different methods of phylogenetic inference. Different kinds of data will be considered, but with a special emphasis on DNA sequences. The software used will be based on R and several specialized packages (particularly ape and phangorn). Other software will be used (e.g., MUSCLE or Clustal) called from R. Overall, the course will cover almost all aspects of phylogenetic inference from reading/downloading the data to plotting the results. This course is intended for PhD and postgraduate students, researchers and engineers in evolutionary biology, systematics, population genetics, ecology, conservation.

Course content is as follows Day 1 - Refresher on R: data structures, data manipulation with the indexing system, scripts, using the help system. - Introduction to phylogenetic inference. - Basics on phylogenetic data (sequences, alignments, trees, networks, "splits") and other data in R. - Reading / writing data from files or from internet. - Matching data. Manipulating labels. Subsetting data. - Main package: ape. Day 2 - Plotting and annotating trees. - Theory of sequence alignment. Comparing alignments. Graphical analyses of alignments. - Main packages: ape (with MUSCLE and Clustal). Day 3 - Theory and methods of phylogeny reconstruction. - Parsimony methods. - Evolutionary distances. - Distance-based methods: General principles and the main methods (NJ, BIONJ, FastME, MVR). - Methods for incomplete distances matrices (NJ*, BIONJ*, MVR*). Methods for combining several matrices (SDM). - Main packages: ape, phangorn. Day 4 - Theory of maximum likelihood estimation. - Application to phylogeny reconstruction. - Substitution models. - Tree space and topology estimation. - Main packages: ape, phangorn. Day 5 - Tree comparison, consensus methods. - Topological space and distances. - Bootstrap. - Bayesian methods.

Please email any inquiries to oliverhooker@prstatistics.com or visit our website www.prstatistics.com Please feel free to distribute this material anywhere you feel is suitable

Upcoming courses - email for details oliverhooker@prstatistics.com 1. ADVANCES IN SPATIAL ANALYSIS OF MULTIVARIATE ECOLOGICAL DATA (July) 2. INTRODUCTION TO BIOINFORMATICS USING LINUX (August) 3. GENETIC DATA ANALYSIS / EXPLORATION USING R (August) 4. INTRODUCTION TO BAYESIAN HIERARCHICAL MODELLING (August) 5. INTRODUCTION TO PYTHON FOR BIOLOGISTS (October) 6. LANDSCAPE (POPULATION) GENETIC DATA ANALYSIS USING R (October) 7. APPLIED BAYESIAN MODELLING FOR ECOLOGISTS AND EPIDEMIOLOGISTS (October) 8. SPATIAL ANALYSIS OF ECOLOGIC AL DATA USING R (November) 9. ADVANCING IN STATISTICAL MODELLING USING R (December) 10. MODEL BASED MULTIVARIATE ANALYSIS OF ECOLOGICAL DATA USING R (January) 11. ADVANCED PYTHON FOR BIOLOGISTS (February) 12. NETWORK ANALYSIS FOR ECOLOGISTS (March) 13. INTRODUCTION TO GEOMETRIC MORPHOMETRICS USING R (June)

Dates still to be confirmed - email for details oliverhooker@prstatistics.com - STABLE ISOTOPE MIXING MODELS USING SIAR, SIBER AND MIXSIAR USING R - INTRODUCTION TO R AND STATISTICS FOR BIOLOGISTS - BIOINFORMATICS FOR GENETICISTS AND BIOLOGISTS

Oliver Hooker PR statistics

3/1 128 Brunswick Street Glasgow G1 1TF

+44 (0) 7966500340

www.prstatistics.com www.prstatistics.com/organiser/oliver-hooker/ Oliver Hooker <oliverhooker@prstatistics.com>

SwissAlps Social Decisions Jul19-22

In this workshop we are very much interested in the evolutionary mechanisms behind social behavior and we will specifically concentrate on sensory constrains. Consequently, we would greatly appreciate the participation of evolutionary biologists.

THE ROLE OF SENSORY ECOLOGY AND COGNITION IN SOCIAL DECISIONS When? 19-22 July 2016 Where? Arolla (Swiss Alps), Switzerland This workshop is organized by Prof. MichaÃ«l Taborsky and Dr. Karin Schneeberger from the University of Bern (CH).

Invited speakers: Prof. Lars Chittka, University of London (UK) Prof. Rui Oliveira, Universidade de Lisboa (PT) Prof. Kevin Laland, University of St. Andrews (UK) Prof. Douglas Chivers, University of Saskatchewan (CA) Prof. Maud Ferrari, Prof. University of Saskatchewan (CA) Prof. Tecumseh Fitch, University of Vienna (AT) Prof. David Stephens, University of Minnesota (US)

DESCRIPTION: The program of the workshop will consist of a combination of plenary talks by invited speakers and work performed in small groups, in which the participants will discuss a particular theme together with one of the invited speakers. The results of these small-group sessions willl be presented to the plenum by student participants, followed by a general discussion.

Social interactions are often assumed to require advanced cognitive abilities, as social behaviour typically happens among a large network of individuals, across different contexts, and over extended time periods. This is at variance with the observation that complex social behaviour can be observed in a wide range of animals, both in the laboratory and field. We think that rather simple cognitive mechanisms can generate complex social responses.

The aim of this workshop is to discuss sensory and cognitive abilities and limitations of animals in the context of the evolution of social behaviour. Topics discussed in the workshop will include, for instance: - how social cues and signals are perceived by individuals - how they are used for decision making - the role of memory for behavioural responses in repeated social interactions - the significance of different sensory modalities for communication in the contexts of conflict and cooperation.

These topics are of great interest to students and scientists from different disciplines, such as evolutionary and behavioural ecology, neurobiology, cognitive sciences, and psychology. Interaction between different fields will identify open questions and directions for future interdisciplinary research

For more info and registration: http://www.cuso.ch/-activity/?p=1128&uid=3033 Queries: ecologie-evolution@cuso.ch

Caroline Betto-Colliard <Caroline.Betto-Colliard@unil.ch>

Instructions

Instructions: To be added to the EvolDir mailing list please send an email message to Golding@McMaster.CA. At this time provide a binary six letter code that determines which messages will be mailed to you. These are listed in the same order as presented here — Conferences; Graduate Student Positions; Jobs; Other; Post-doctoral positions; WorkshopsCourses. For example to receive the listings that concern conferences and post-doctoral positions this would be 100010. Messages are categorized on the basis of their subject headings. If this subject heading is not successfully parsed, the message will be sent to me at Golding@McMaster.CA. In addition, if it originates from 'blackballed' addresses it will be sent to me at Golding@McMaster.CA. These messages will only be read and dealt with when I have time. The code 000000 has all channels turned off and hence gets only a once monthly notifcation of the availability of a monthly review pdf file.

To be removed from the EvolDir mailing list please send an email message to Golding@McMaster.CA. Note that 'on vacation', etc, style messages are automatically filtered and should not be transmitted to the list (I hope), but should you wish to avoid the e-mail's your code can be temporarily changed to 000000.

To send messages to the EvolDir direct them to the email evoldir@evol.biology.McMaster.CA. Do not include encoded attachments and do not send it as Word files, as HTML files, as LaTeX files, Excel files, etc. . . . plain old ASCII will work great and can be read by everyone. Add a subject header that contains the correct category "Conference:, Graduate position:, Job:, Other:, Postdoc:, Workshop:" and then the message stands a better chance of being correctly parsed. Note that the colon is mandatory.

The message will be stored until the middle of the night (local time). At a predetermined time, the collected messages will be captured and then processed by programs and filters. If the message is caught by one of the filters (e.g. a subject header is not correctly formated) the message will be send to me at Golding@McMaster.CA and processed later. In either case, please do not expect an instant response.

Afterword

This program is an attempt to automatically process a broad variety of e-mail messages. Most preformating is collapsed to save space. At the current time, many features may be incorrectly handled and some email messages may be positively mauled. Although this is being produced by LaTeX do not try to embed LaTeX or TeX in your message (or other formats) since my program will strip these from the message.