EvolDir

May 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

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).

Deadline for abstract submissions is May 30. 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)

Ýsmail Bekar General Secretary

For contact with organising committee: eebst2016@gmail.com

ismailbekar53@gmail.com

Asilomar California LocalAdaptation Jul14-17

EARLYBIRD REGISTRATION CLOSES MAY 1ST

TheAmerican Genetic Association President's Symposium, 'Local adaptation: from phenotype to genotype to fitness', will be held July 14-17, 2016, at beautiful Asilomar, CA (http://www.visitasilomar.com/).

Inthe 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.

TheAGA will provide several travel awards to cover registration for graduate students who would like to attend and present posters. Six abstracts will be selected for oral presentations, and the students will receive $500 awards. DEADLINE TO SUBMIT ABSTRACTS IS APRIL 25TH.

Detailsand registration are available at the AGA website: http://www.theaga.org Invitedspeakers: KeyDistinguished Lecture by Victoria Sork (Dean of Life Sciences, UCLA) SallyAitken University of British Columbia JillAnderson University of Georgia ZachCheviron University of Illinois EmilyDittmar Michigan State University SuzanneEdmands University of Southern California DavidField Inst. Science and Tech, Austria LilaFishman University of Montana JanniceFreidman Syracuse University SteveKeller University of Vermont JohnKelly University of Kansas BrianLangerhans North Carolina State University CurtisLively Indiana University RobertReed Cornell University DouglasSchemske Michigan State University RenaSchweizer UCLA KerryShaw Cornell University PeterTiffin University of Minnesota

Lynda Delph, AGA President

AGAJOH@oregonstate.edu

Asilomar California LocalAdaptation Jul14-17 StudentAwards

***** DEADLINE EXTENDED UNTIL MONDAY, APRIL 25TH *****

Student awards are available for the American Genetic Association 2016 meeting, 'Local adaptation: from phenotype to genotype to fitness', to be held July 14-17, 2016, at beautiful Asilomar, CA.

Several awards are available to cover registration for graduate students who present posters. Six abstracts will be selected for oral presentations, and these students will receive $500 awards. Details and registration are available at the AGA website: http://www.theaga.org APPLY BY Monday, APRIL 25TH

Contact Anjanette Baker at agajoh@oregonstate.edu with any questions.

Invited speakers: Key Distinguished Lecture by Victoria Sork (Dean of Life Sciences, UCLA)

Sally Aitken University of British Columbia Jill Anderson University of Georgia Zach 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

We look forward to seeing you! Lynda Delph, AGA President

AGAJOH@oregonstate.edu

AustinTX UndergradTravelAward Jun17-21

Reminder: Travel Award - Undergraduate Diversity at Evolution 2016

Applications for the undergraduate travel award to bring talented and diverse undergraduates to the Evolution meetings this June 17-21 in Austin, TX (www.evolutionmeetings.org) are due in less than two weeks on April 18th. Application form and more information at http://beacon-center.org/ude/ Details: For the 13th year a cohort of undergraduates from throughout the U.S. and Puerto Rico will be funded to (1) present a poster at the meetings, (2) receive mentoring from graduate students, postdocs and faculty, and (3) participate in a career-oriented 'Undergraduate Futures in Evolutionary Biology' panel and discussion. The program is sponsored by SSE/BEACON and covers the costs of travel, registration, food and accommodation at the meetings. The application deadline is Monday, April 18th, and decisions will be announced by Tuesday, April 26th.

Applications are welcomed from all undergraduates, and the admissions goal is to create a diverse pool of students. An overview of the program and the online application can be found at: http://beacon-center.org/ude/ .Applications consist of a short statement of interest, a letter of recommendation, and the title and abstract of the poster to be presented.

Two events organized by the program on June 20th, the Undergraduate Futures Lecture and Panel Discussion (11:30AM) and Undergraduate Ice Cream Social (8PM), are open to ANY attending undergraduates or postbaccalaureates, regardless of award status/eligibility, as well as their advisors/mentors.

We are also looking for mentors for the program. Please email Dr. Kliman or indicate your interest in being a mentor on the Evolution 2016 conference registration form.

For inquires, please contact one of the organizers: Alexa Warwick awarwick@msu.edu Richard Kliman - rmkliman@cedarcrest.edu Scott Edwards - sedwards@fas.harvard.edu

"awarwick@msu.edu" <awarwick@msu.edu>

ColoradoStateU GenomicsOfAdaptation Jul30

We are pleased to announce a symposium on Genomics of Adaptation to Human Contexts will be held at Colorado State University on July 30, 2016. This symposium will highlight exemplar research that uses large genomic datasets to investigate ecology and evolution in the Anthropocene, featuring keynote talks by Regina Baucom (UMichigan) and Robert Wayne (UCLA). The symposium will be paired with a Software Carpentry workshop (July 28-29, 2016) to train early career researchers in the essential programmatic tools needed to analyze such datasets. The symposium and accompanying workshop are jointly funded by the American Genetic Association and the Genetics Society of America. Please see our website (https://adapt2humans.wordpress.com/) for information on how to register and more!

Registration is required but free for both the workshop and symposium. Space in the workshop is limited, and we will be offering limited travel funds for workshop attendees traveling from outside of the local area. Registration closes on May 15.

See you in July! Brook Moyers (moyers@colostate.edy) Kathryn Turner (kathryn.g.turner@gmail.com) Chris Schell (chris.schell@colostate.edu)

brook.moyers@gmail.com

CornellU EEID EvolutionDisease Jun3-5

Dear Friends and Colleagues,

There is one week left to Register and Submit an Abstract for the Ecology and Evolution of Infectious Disease meeting to be held at Cornell University June 3-5.

Registration and Abstract Submission will close on May 2.

For those of you who may be interested in presenting a poster, we will be working with a professional poster printing service that accept your electronic files and credit card payments and deliver the posters to me the day before the conference. I will the posters printed through this service available on the first day of the conference - no carrying your poster on the plane! Details on this service will be sent with the formal poster assignments shortly after the abstract submission deadline.

Registration fees are $100 for Students and $175 for Faculty/Staff. On-campus lodging is also modestly priced.

Link for Registration: http://blogs.cornell.edu/eeid/-eeid-2016-registration/ Link for Abstract Submission: http://blogs.cornell.edu/eeid/eeid-2016-abstracts/ Link for Travel and Lodging: http://blogs.cornell.edu/eeid/-eeid-2016-travel-and-lodging/ There are four primary themes for the meeting, with both theoretical and empirical work in plant and animal systems to be included under all themes:

1) Polymicrobial Infection and Disease 2) Pathogen Dynamics within the Host 3) Pathogen Genomics, Evolution, and Selective Constraints 4) Disease Outbreaks on the Landscape Scale

We have an excellent lineup of invited speakers and will draw additional oral presentations from the submitted abstracts.

Invited Speakers: Samuel Alizon (CNRS) Raul Andino (UC San Francisco) Greg Dwyer (University of Chicago) Nicole Gerardo (Emory University) Eric Harvill (University of Georgia) Eileen Hofmann (Old Dominion University) Britt Koskella (UC Berkeley) Kevin Lafferty (UC Santa Barbara) Alex Perkins (Notre Dame)

On behalf of the organizing committee, we look forward to welcoming you to Cornell for EEID 2016.

Brian P. Lazzaro, Ph.D. Professor, Department of Entomology Cornell University Ithaca, NY 14853 USA

tel: 607-255-3254 fax: 607-255-0939 http://-/www.lazzaro.entomology.cornell.edu bplazzaro@gmail.com

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DurhamNC EvolutionaryMedicineSociety Jun22-25

The 2016 annual meeting of the International Society for Evolution, Medicine and Public Health (ISEMPH) will take place from June 22-25, 2016 in Durham, North Carolina.

All interested scientists, scholars, students and clinicians are welcome.

The program features 6 plenary talks, 100 oral presentations and 43 poster presentations, and plenty of time to talk with others who share interests in using evolutionary biology to better understand, prevent and treat disease...and those who study disease to advance basic evolutionary biology.

The program for the June 22-25th meeting of the International Society for Evolution, Medicine & Public Health is now available at http://easychair.org/smart-program/-ISEMPH2016/ REGISTRATION FEES INCREASE ON MAY 1ST.

For full information see: https://-evolutionarymedicine.org/isemph2016/ To go directly to registration go to: https://www.regonline.com/-register/checkin.aspx?EventId62428&MethodId=-0&EventSessionId=&startnewreg=1 Plenary speakers include:

-Andrea Graham (Princeton University),

-Carl Zimmer (New York Times),

-Helen Ball (Durham University, UK),

-Joshua Schiffman (University of Utah),

-Marion Koopmans (Erasmus University) and

-Martin Blaser (New York University).

–Wednesday Sessions–

EvMed Director's Meeting

EvMed Student's Meeting

–Thursday Plenaries–

Joshua Schiffman

Topic: Evolution and Cancer

Helen Ball

Changing UK guidance and practice around maternal-infant sleep'did an evolutionary perspective help?

–Thursday Sessions–

Cancer

Human evolution and paleopathology

Selection, stress and homeostasis

Behavior and vulnerability

Sleep

Somatic cell mutation, selection and evolution in health and disease

Immune response

Reproductive ecology of human health

–Friday Plenaries–

Carl Zimmer

Evolutionary Medicine and the Media: Engaging Stories and Tricky Concepts

Martin Blaser

Human Evolution 201: Our early life microbial metagenome guides developmental phenotypes

–Friday Sessions–

Genetics, vulnerability and selection

Lessons from our primate cousins: Evolutionary medicine in nonhuman primate studies

General evolution and medicine

Human evolution, adaptation and disease in Africa

Selection, stress and homeostasis

Microbiome and evolutionary medicine

Translating evolutionary medicine to the clinic–practical lessons for patient care

Life history

–Saturday Plenaries–

Andrea Graham

Why do immune systems harm their bearers? The evolutionary biology of "friendly fire"

Marion Koopmans

Topic: Evolution and infectious disease

–Saturday Sessions–

Evolutionary medicine: A comparative cross species perspective

Metabolism and mismatch

Early nutrition

Human Evolution

Omenn Prize Award Winner

Williams Prize Award Winner

Frontiers of evolutionary medicine

Pathogen evolution

–Sunday Excursions–

Duke Lemur Center

Museum of Natural Sciences

Randolph Nesse <nesse@asu.edu>

Edinburgh TelomereDynamics 31Oct

We are pleased to announce an international conference on "Understanding diversity in telomere dynamics" in Edinburgh, 31st Oct - 3rd November.

In recent years, there has been a burgeoning of interest in how telomere dynamics vary across species and in whether this variation has its roots in, or constrains, the evolution of life histories. The aim of this meeting is to bring together biologists from different backgrounds, and at different career stages, with research interests in the causes and consequences of variation in telomere length. The meeting forms part of a workshop series conducted as part of an international network on telomere dynamics, funded by the Leverhulme Trust. The organisers are Pat Monaghan (University of Glasgow) and Dan Nussey (University of Edinburgh). Topics to be covered will include:

How best to measure variation in telomere length across species and individuals Environmental and genetic sources of variation in telomere length Telomeres and the ageing process How variation in telomere loss and restoration relates to life history variation

Plenary speakers: Vera Gorbunova (University of Rochester, USA) Pat Monaghan (University of Glasgow, UK) Jerry Shay (University of Texas Southwestern Medical Centre, USA) Abraham Aviv (Rutgers New Jersey Medical School, USA)

Timing and Location of the Meeting: The conference will take place at the Best Western Kings Manor Hotel, on the outskirts of Edinburgh. The conference will be residential, with costs including full bed and board over the two days of the meeting. We will start with dinner, followed by talks/discussion on the evening of Monday 31st October 2016, followed by two full days of talks and discussion, ending with breakfast and departure on the morning of Thursday 3rd November.

Costs: The cost of attending the meeting (which will include all registration costs, overnight accommodation for 3 nights (Mon, Tues & Wed) plus breakfast, lunch and dinner for the duration of the meeting) is 375 per person. Some assistance with travel costs may be available, particularly for PhD students - contact the organisers for more information.

Presenting at the Meeting: Slots will be available for short talks (15 min + 5 mins questions) and highlight presentations (5 mins, maximum 2 slides). Abstracts can be submitted via the registration site below.

Registration: Spaces at the conference are limited to 80 and the registration deadline is 30th June. Please note that we will allocate space on a first come - first served basis and registration will close early if all spaces are filled. You can register via our EventBrite webpage:

http://telomerediversity.eventbrite.co.uk For more information, please contact Mary Ryan: mary.ryan@glasgow.ac.uk

We look forward to seeing many of you there!

Best Wishes,

Dan Nussey & Pat Monaghan.

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

"dnussey@staffmail.ed.ac.uk"
<dnussey@staffmail.ed.ac.uk>

FloridaStateU EcolEvolutionEthologyFish Jun14-16

Florida State University (FSU) in Tallahassee, Florida, is pleased to host the 20th Biennial Ecological and Evolutionary Ethology of Fishes (EEEF) Meeting. The meeting will be held on the Florida State campus, with hotel accommodations nearby. Please see https://marinelab.fsu.edu/eeef/ for more information.

Early Registration deadline is 29 April 2016. Graduate student travel grants are available.

The meeting is organized around four primary themes: Population genomics of fishes (Organizer: Joe Travis); Sensory ecology, movement patterns, and behavior (Organizer: Nathan Putman); Species Interactions (Organizer:Chip Cotton); Biodiversity: Discovery, Variation & Conservation (Organizer: Colette St. Mary). While you're here, you'll experience Florida's local seafood and microbreweries. Social events include a welcome reception, a Cocktail & Posters Session, and a closing reception at a local watering hole. We hope that you will also consider hanging around for a while either before or after the meeting to take advantage of some of the wonderful natural areas of this region. E. O Wilson describes the Florida panhandle as one of the richest biodiversity hotspots in North America. It absolutely is like nowhere else in the state, with incredible National Natural Landmarks that include the Florida Caverns, Wakulla Springs, and Torreya State Park along the Apalachicola River. For those seeking more rigorous activities, you can hike the Florida Trail, paddle the pristine Wacissa River, or bike the Tallahassee-St. Marks Historic Railroad State Trail. There are countless outdoor adventures in the region. Beach goers might want to visit St. George Island State Park and visit historic Apalachicola.

Kimberly A. Hughes Professor Department of Biological Science Florida State University 319 Stadium Drive Tallahassee, Florida 32306-4295

Ph: 850-645-8553 FAX: 850-645-8447 Office: 4062 King Life Sciences Building http://www.bio.fsu.edu/faculty-hughes.php "kahughes@bio.fsu.edu" <kahughes@bio.fsu.edu>

Girona EvolutionMarineMicrobes Jun18-24

Announcing the 2016 Gordon Research Conference and Seminar on Marine Microbes:

Marine Microbes GRC The Evolution, Nature and Function of Microbial Interactions

The theme of this Conference is "Evolution, nature and function of microbial interactions". Marine/aquatic microbes live in diverse environments and individual cells and communities face strong ecological and evolutionary pressures on different spatial and temporal scales. In such a complex world, microbial interactions critically drive the evolution of diverse life styles, genome structure, and cellular response that shape their ecology and impact on biogeochemical cycles. The Conference will present and rigorously discuss concepts and ideas at the forefront of molecular microbial ecology and evolution in order to elucidate the nature and role of diverse interactions among microbes in all three domains of life (Archaea, Bacteria and Eukarya) and how it shapes the functioning of complex biological systems in diverse marine (oceans, seas) and aquatic (lakes, rivers, ice) environments. The Conference also aims to include cutting-edge research from diverse fields (biomedical, mathematics, modeling) relevant to the broad diversity of marine microbes (bacteria, archaea, phytoplankton, protists, and viruses). The Conference will feature presentations of unpublished work by investigators at the forefront of the field in and will provide opportunities for junior scientists, postdocs, and graduate students to present their work in poster format and exchange ideas with leaders in the field. A collegial atmosphere will be fostered through extensive discussion sessions and daily opportunities for informal gatherings in the afternoons and evenings, providing an ideal setting for scientists from different disciplines to exchange ideas, brainstorm and discuss cross-disciplinary collaborations.

June 19-24, 2016 PGA Catalunya Business and Convention Centre Girona, Spain

Chair: Catherine Legrand

Web site: http://www.grc.org/programs.aspx?id=13275 Online application: http://www.grc.org/application.aspx?id=13275 —

Additionally, a Gordon Research Seminar will be held in conjunction with the above GRC. What is a GRS? Gordon Research Seminars (GRS) are a series of unique 2-day meetings held in conjunction with an associated GRC that enable graduate students, post-docs, and other scientists with comparable levels of experience to come together in a highly-stimulating and non-intimidating environment to discuss their current research and build informal networks with their peers. The seminars are organized by young investigators with the support of leading scientists from the associated GRC.The Marine Microbes GRS is scheduled to take place from June 18-19, 2016 at PGA Catalunya Business and Convention Centre, Girona, Spain.

Marine Microbes GRS Microbe Coexistence and Coevolution in a Changing Ocean

The Gordon Research Seminar on Marine Microbes is a unique forum for graduate students, post-docs, and other scientists with comparable levels of experience and education to present and exchange new data and cutting edge ideas.

Marine microorganisms interact constantly among themselves and with other members of the trophic network. These interactions define their evolutionary fate and underlie the biogeochemical fluxes that will drive ecological processes in current and future oceans. The seminar will bring together microbial ecologists and evolutionary biologists to discuss and debate about where, when and why marine microbes interact, who are the main players mediating these processes, and what will be the resulting evolutionary and ecological outputs.

Chairs: Javier del Campo & Bryndan Durham

Web site: http://www.grc.org/programs.aspx?id=15346 Online application: http://www.grc.org/application.aspx?id=15346 —

Applications for this meeting must be submitted by May 21, 2016. Please apply early, as some meetings become oversubscribed (full) before this deadline. Note: Applications for oversubscribed meetings will only be considered by the Conference Chair if more seats become available due to cancellations.

Javier del Campo <javier.delcampo@botany.ubc.ca>

GoldCoast Australia SMBE AncientDNA and HumanInnovation Jul3-7

SMBE2016: Ancient DNA and the effects of human innovation on genomes - Gold Coast, Australia, July 3rd-7th 2016

Dear colleagues ,

We would like to invite you to join a symposium on ancient DNA and the effects of human innovation to be held at Annual Meeting of the Society for Molecular Biology and Evolution (SMBE) in Gold Coast, Australia this July. PLEASE NOTE that the abstract submission deadline and the early bird registration deadline have been extended to April 29^th midnight (Eastern Australian time).

Invited speakers of the symposium are Christina Warinner (University of Oklahoma) and Wolfgang Haak (MPI-SHH Jena/University of Adelaide).

Symposium description:

Human innovation - such as the invention of the wheel, the use of boats and the Neolithic revolution - led to major migrations as well as changes in lifestyle throughout history. Humans encountered new ecosystems, domesticated plants and animals, and were faced with new pathogens. These changes did not just affect the genome of our species, but also the genomes of a number of the species around us. Examples of such effects include the development of domesticated species, the extinction of wild fauna, the strong selective sweep causing lactase persistence, and human population growth as well as admixture among populations during secondary contact. Inferring past events from modern populations has its limitations, but the technological revolution in the field of ancient genomics offers the unique opportunity to study populations before, during and after these events. Using the temporal data provided by ancient DNA, a population's demographic history, the general development of genetic diversity as well as allele frequencies at particular candidate loci can be studied. This symposium will gather researchers working on the population history of humans, animals, plants and other organisms as well as their interactions using ancient DNA. Bringing these people together will start fruitful discussions among researchers who study the same processes but who approach them from different angles. Particularly abstracts addressing the following questions will be selected:

(i) What migration routes were taken and how did these population movements shape the modern day population diversity?

(ii) Were domesticated animals and plants accompanying the movements?

(iii) Has human innovation caused specific changes in the genomes of the species involved?

(iv) What impact did the migrants have on wild flora and fauna?

(v) How did pathogens shape the genetic setup of human and animal populations?

Looking forward to see you in Australia,

Cristina Valdiosera (La Trobe University, Australia)

Emma Svensson (Uppsala University, Sweden)

Helena Malmström (Uppsala University, Sweden)

Torsten Günther (Uppsala University, Sweden)

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tguenther@zoho.com

Gold Coast Australia SMBE StructuralVariation Jul3-7

Dear colleagues,

We are pleased to announce the symposium "Structural variation in the light of new sequencing technologies" as part of the July 2016 SMBE meeting in Gold Coast, Australia. We encourage you to submit your abstracts for oral presentations before April 22 (http://smbe2016.org/).

INVITED SPEAKERS: Esther Betrán (The University of Texas at Arlington) Tomas Marques-Bonet (Institut Biologia Evolutiva, Universitat Pompeu Fabra/CSIC, Barcelona)

ORGANIZERS: Arcadi Navarro, Diego Hartasanchez, Marina Brasó-Vives and Josephine Daub (Institut Biologia Evolutiva, Universitat Pompeu Fabra/CSIC, Barcelona, Spain) Hideki Innan (The Graduate University for Advanced Studies, Hayama, Japan)

SUMMARY: Structural variation, including segmental duplications, copy-number variation and inversions, constitute a substantial part of variation in the genomes of humans and other species. Structural variation plays a significant role in evolution, since it can lead to large-scale functional innovation. A better knowledge of the way structural variants arise and evolve, is helping us to understand how they relate to phenotypes that are relevant for both human health and the evolution of our lineage. For this reason, mapping the position of structural variants, obtaining their sequences, annotating their functional contents and understanding their dynamics has gained much interest in the scientific community. Until recently, questions regarding structural variation have been difficult to answer given the limitations of short-read technologies and the relative scarcity of theoretical and numerical tools. New sequencing methods, such as single molecule real time sequencing (SMRT), allow us to gain more insight into the molecular evolution of structural variation. Novel approaches to exploit long-read technologies and data sets have already produced various results on intra and inter-specific copy-number variation and on differences within structural variants themselves. Additionally, recent methodological advances allow novel insights into data. With this symposium we aim to address how the latest sequencing methods, analytical approaches and data sets can further improve our understanding of the role of structural variation in evolution.

We look forward to seeing you in Australia!

Josephine Daub Postdoctoral Researcher

Evolutionary Genomics Lab Institut de Biologia Evolutiva (UPF- CSIC) c/ Dr Aiguader 88 08003 Barcelona email: josephine.daub@upf.edu

"josephine.daub@upf.edu" <josephine.daub@upf.edu>

Gotland PhDStudentsEvolBiol Sep11-15

The 22nd Meeting for PhD Students in Evolutionary Biology, organized by Uppsala University Location: Gotland, Sweden Date: September 11-15th, 2016 Website: http://empseb22.org/ EMPSEB provides a platform for PhD students studying Evolutionary Biology to present their work and to meet their peers from across Europe. Joining the participants are 8 senior scientists who are invited to give plenary talks, run discussion groups, and to provide guidance about starting your scientific career. All of this will be conducted on the beautiful Baltic island of Gotland. The meeting provides the unique opportunity for students to hear the latest research being conducted in Europe, meet future international collaborators, and to present their own work to peers. Registration and abstract submission: Is now open and will close on the 15th of May. Plenary Speakers: Hanna Kokko, University of Zurich; Katerina Guschanski, Uppsala University, plus more speakers to be announced in the coming days on our website, Facebook and Twitter. Follow us on Facebook! https://www.facebook.com/empseb22/?fref=ts and on Twitter! @EMPSEB22 For further information or questions, please visit the conference website: http://-empseb22.org/ If you have any questions, please feel free to email the EMPSEB22 committee president, William Jones at empseb22@gmail.com. We are looking forward to welcoming you to the wonderful island of Gotland in September 2016!

“william.jones@ebc.uu.se” <william.jones@ebc.uu.se>

Hinxton UK VirusGenomicsEvolution Jun8-10

AdvancedCourses and Scientific Conferences

VirusGenomics and Evolution

8-10June 2016

WellcomeGenome Campus, Hinxton, Cambridge, UK

LastCall for Abstracts: Deadline 26 April http://-dmtrk.net/t/2SUU-7OBK-SPQ6L-2T844-0/c.aspx Finalabstracts are invited for this new conference. This meeting will provide a multidisciplinary forum for scientists interested in the genomics and evolutionary analysis of viruses and will address the fundamental questions of viral origins, transmission and pathogenesis.

Theprogramme will cover the genomics of epidemic and non-epidemic viruses, emerging viral infections and pathogen discovery. A draft programme is now available: http://dmtrk.net/t/2SUU-7OBK-SPQ6L-2T845-0/c.aspx Scientificsessions

âViral genome sequencing: diagnostics and public health

âVirus discovery

âEpidemics

âEvolution of pathogenesis

âRe-emerging viral infections

Wewelcome abstracts from all areas relevant to the main themes of the meeting. Several oral presentations will be chosen from the abstracts submitted.

Allabstracts must be received by 26 April. The registration deadline is 10 May.

Forfurther information, please visit the website: http:/-/dmtrk.net/t/2SUU-7OBK-SPQ6L-2T846-0/c.aspx Scientificprogramme committee

JudithBreuer (University College London, UK)

AndrewRambaut (University of Edinburgh, UK)

EmmaThompson (University of Glasgow, UK)

Keynotespeakers

IanGoodfellow (University of Cambridge, UK)

IanLipkin (Columbia University, USA)

Confirmedspeakers

KristianAndersen (Scripps Research Institute, USA)

EllieBarnes (University of Oxford, UK)

SarahCobey (University of Chicago, USA)

JanFelix Drexler (University of Bonn Medical Centre, Germany)

JenniferGardy (University of British Columbia, Canada)

EddieHolmes (University of Sydney, Australia)

PaulKellam (Wellcome Trust Sanger Institute, UK)

PhilippeLemey (Rega Institute, Belgium)

MarionKoopmans (Erasmus Medical Center, The Netherlands)

NickLoman (University of Birmingham, UK)

OliverPybus (University of Oxford, UK)

Anne-MiekeVandamme (Rega Institute, Belgium)

MarcoVignuzzi (Institut Pasteur, France)

Datesfor your diary

Abstractdeadline: 26 April

Registrationdeadline: 10 May

ViewFull Details:

http://dmtrk.net/t/2SUU-7OBK-SPQ6L-2T846-0/-c.aspx Pleasefeel free to forward this information to your colleagues.

Ourupcoming events poster is also available for download: http://dmtrk.net/t/2SUU-7OBK-SPQ6L-2T847-0/c.aspx Updatescan be followed on Twitter: http://dmtrk.net/t/2SUU-7OBK-SPQ6L-2T848-0/c.aspx and Facebook: http://dmtrk.net/t/2SUU-7OBK-SPQ6L-2T849-0/c.aspx Pleasedo not reply to this email. For further information, please contact coursesandconfs@wellcomegenomecampus.org (use "unsubscribe" in the subject line if you no longer wish to receive updates on courses and conferences).

Usethe following link to unsubscribe from all Wellcome Trust Communications: http://dmtrk.net/t/2SUU-7OBK-58SPQ6L97/uns.aspx TheWellcome Genome Campus is operated by Genome Research Limited (GRL), a subsidiary of The Wellcome Trust. GRL is a charity registered in England with the number 1021457.

Treasa Creavin <treasa.creavin@wellcomegenomecampus.org>

Ilhabela Brazil AmoebaeSystematics Sep12-15

Dear colleague,

It is with great pleasure that we invite you to the 8th International Symposium on Testate Amoebae, during the days of September 12-15th, in Ilhabela, São Paulo, Brazil.

The Symposium is promoted every two years by the International Society for Testate Amoebae Research (ISTAR). It typically gathers participants from more than 20 countries, presenting projects on all aspects of research in Testate Amoebae - taxonomy, systematics, ecology, paleontology among others. This year, it is the first time in history that ISTA will be held in the Americas, this was made possible by the logistical and structural help of the Brazilian Society of Protozoology (SBPz).

A very special feature of this symposium is the first-ever, ISOP (International Society of Protistologists) sponsored Young Testate Amoebae Investigator Award (ISOP/YoTAR). Six young scientists will be awarded with this prize and have the opportunity to present in a special session during the conference. A financial reimbursement will be provided to help these young scientists to attend the conference. More details are available at the symposium website.

Keynote presentations will be made by:

Dr. Laura Katz Smith College, MA, USA Dr. Mariusz Lametowiczs Adam Mickiewicz University, Poznan, Poland Dr. Anush Kosakyan University of São Paulo, SP, Brazil Dr. Susannah Porter Department of Earth Science, University of California at Santa Barbara

Registration is open until May 20th. More details are available at the website:

www.ista8.com.br With kind regards,

The ISTA8 organizing committee.

daniel.lahr@gmail.com

Kew UK PlantEvolution May11-12

Last chance to submit an abstract and register for the inaugural State of the World's Plants Symposium: 11-12 May, Royal Botanic Gardens, Kew.

Dr Mimi Tanimoto MRSB

Senior Science Officer - Education and Communication Office of the Science Directorate Royal Botanic Gardens, Kew Richmond, Surrey TW9 3AE

020 8332 5102

m.tanimoto@kew.org

www.kew.org State of the World's Plants Symposium

11-12 May 2016, Kew Gardens

SOTWP_landscape banner 1005x405

Mimi Tanimoto <M.Tanimoto@kew.org>

London EvolutionaryConflict Jun8

Dear colleagues,

Registration for 2016 CEE (Centre for Ecology & Evolution) Summer symposium 2016 entitled: "War and peace: the dynamics of evolutionary conflict" is now live.

We are delighted to welcome 9 speakers (info on website) from leading UK research institutions (UCL, Edinburgh, Exeter, Liverpool, Oxford, Sheffield and Sussex) who will cover four main research themes:

- Intralocus and interlocus sexual conflicts

- Intragenomic conflicts
- Genomics of sexual dimorphism

This one-day conference will be held in the Sir Alexander Fleming Building at Imperial College London, South Kensington, on June 8th.

As well as these 9 invited talks we also invite applications from PhD students to give 3 short talks during the conference, and present posters as well. This symposium is an excellent opportunity for younger researchers to network and present their current work.

To attend and/or submit a talk or if you have any further enquiries please visit the event website, linked below.

Deadline for registration and abstract submission is May 20^th.

We look forward to seeing you on the 8^th June!

On behalf of the CEE Summer Symposium organisation committee.

(Brian Hollis, Kevin Fowler, Mark Hill, Filip Ruzicka)

Event website: http://ceesymposium2016.weebly.com [7356472.jpg?1458915307] CEE Summer Symposium 2016 ceesymposium2016.weebly.com The 2016 CEE (Centre for Ecology & Evolution) Summer Symposium will be held in the Sir Alexander Fleming Building at Imperial College London, South Kensington, on June 8th. The topic of...

Twitter updates: #ceess2016

"Hill, Mark" <mark.hill.13@ucl.ac.uk>

Manchester MolGenomeEvolution Jun20

Registration and abstract submission are now open for Manchester's Molecular and Genome Evolution Symposium (#MaGE2016) on Monday 20th June!

The remit of the symposium is broad, including all aspects of molecular and genome evolution, ranging from genomic analyses or computational algorithm development, to molecular ecology, population genetics, and experimental evolution (see https://manchestermage.wordpress.com/)

MaGE 2016 will be a day-long event in Manchester's Michael Smith Building including two plenary lectures, a series of contributed talks, and a poster session. Plenary lectures will be given by Mary O'Connell (who has recently set up a Computational & Molecular Evolutionary Biology Group at the University of Leeds: http://mol-evol.org) and Jonas Warringer (known for his work on genotype-phenotype relationships at the University of Gothenberg).

MaGE is free to attend, but places are limited so please register at https://goo.gl/aAKlq9 and submit a title if you would like to present a talk or poster. We are particularly keen to give PhD students and post-docs a chance to present their work. All contributed talks and posters will also be considered for a prize, presented at the drinks reception following the symposium.

Hope to see you in June!

MaGE 2016 Organisers

dannagifford@gmail.com

MNHN Paris HumanDNApolymorphism Dec7-10

CONFERENCE ANNOUNCEMENT

The 6th international conference of the series DNA POLYMORPHISMS IN HUMAN POPULATIONS will be held in Paris (France), 7-10 December 2016 at the Musee de l'Homme.

The conference has a general topic: (Cross-Disciplinary) Human Population Genetics. The conference will be hybrid, allying plenary sessions and four specialized workshops.

A *call for abstracts* is now open until the *27^th of May, 2016*. Registrations will start in September.

You can submit abstracts concerning posters, talks in plenary sessions or talks in the frame of the workshops. Multiple abstracts are accepted. To submit, just send an abstract through the conference website. There is room for one more workshop. If you want to organize it (scientifically), please send a proposal.

Conference website:

http://ecoanthropologie.mnhn.fr/DPHP2016/DPHP2016.htm Contact:

dnaparis2016@gmail.com

Franz MANNI <fmanni@mnhn.fr>

Montpellier EcolEvolutionModels Jun6-7

Hi everyone,

We are pleased to invite you to the seventh edition of the seminar for students “Models in Ecology and Evolution” (MEE). The seminar will be held in Montpellier on Monday, June 6 and Tuesday, June 7 at the Institut de botanique.

This seminar, organized by PhD students, is intended for masters, PhD students and post-doctoral researchers with interests in theoretical and modeling approaches in ecology and evolution. The aim is threefold: - Give an overview of the current modeling techniques used in ecology and evolution: which tools for which questions? - Highlight the similarities and complementarities between the different approaches through stimulating debates. - Discuss how models contribute to scientific knowledge and how their outcome is of use to society.

This seminar consists of a series of talks by both invited researchers and students, and aims at promoting exchanges between the participants. Everyone will be invited on Monday evening to chat over a beer in downtown Montpellier.

Registration is free and lunches will be provided by the organization. We encourage participants to register as quickly as possible and to submit talks (15 minutes + 10 minutes for discussion). The deadline for registration is the 2nd of May, 2016.

Link for registration and submission of abstracts: http://www.mee.univ-montp2.fr/registration-3/ The invited speakers are: Calcagno Vincent (INRA, Nice) Casenave Céline (INRA, Montpellier) Dutreuil Sébastien (U Sorbonne, Paris) Fraïsse Christelle (IST, Vienne, Autriche) Gidoin Cindy (CREEC, Montpellier) Llaurens Violaine (MNHN, Paris)

We look forward to seeing many of you in June in Montpellier!

The organization team, Yoann Anciaux, Thomas Aubier, Alain Danet, Marion Jourdan, Thomas Koffel, Marjolaine Rousselle http://www.mee.univ-montp2.fr/ Yoann ANCIAUX PhD (2nd Year) at ISEM (Institut des Sciences de l'Evolution de Montpellier).

+ 33 (0)6 19 86 58 90 anciaux.yoann@gmail.com

Anciaux Yoann <anciaux.yoann@gmail.com>

Montreal RECOMB ComparativeGenomics Oct11-14

RECOMB COMPARATIVE GENOMICS 2016, CALL FOR PAPERS

SCOPE The annual RECOMB Comparative Genomics Satellite Conference (RECOMB-CG) brings together leading researchers in the mathematical, computational and life sciences to discuss cutting edge research in comparative genomics, with an emphasis on computational approaches and the analysis of novel experimental results. The program will include keynote talks, contributed talks, and a poster session.

The 14th RECOMB-CG conference will be held in MontrÃÂ©al, Canada, October 11-14 2016. With this Call for Papers we invite high-quality original full papers on topics related to the conference theme. The conference will also have a poster session. A detailed call for posters will be published later on the conference web page.

TOPICS Papers are solicited on, but not limited to, the following topics: - genome evolution - genome rearrangements - genome variation, diversity and dynamics - phylogenomics - comparative tools for genome assembly - population genomics - comparison of functional networks - comparative epigenomics - paleogenomics - cancer evolution genomics - epidemiology - gene identification and/or annotation

IMPORTANT DATES Paper Submission Deadline: June 6, 2016 Author Notification: July 8, 2016 Final Version Due: July 22, 2016 Conference: October 11-14, 2016

DETAILS ON SUBMITTING MANUSCRIPTS Submitted papers must have not been published or be currently under consideration for publication in any other journal or conference with formal proceedings. All accepted papers will have to be presented by one of the authors at the conference.

Accepted papers will be published in one of three journals: - a special issue of BMC Genomics, edited by a RECOMB-CG PC chair, - a special issue of BMC Bioinformatics, edited by a RECOMB-CG PC chair, - a special section of a regular issue of Bioinformatics (Oxford University Press), edited by a RECOMB-CG PC chair and a Bioinformatics Associate Editor.

As BMC Genomics and BMC Bioinformatics are Open Access journals, there will be an author fee of Ã922 (922 Pounds Sterling) for publication in the event that an article is accepted in one of these two journals.

Papers accepted for presentation at the conference and considered for publication in Bioinformatics will be subject to an extra round of reviewing to ensure they meet the usual standards of the journal. Papers appearing in Bioinformatics will be subject to the regular fees of Bioinformatics for extra pages and colour figures for example.

Authors will need to indicate upon submission their preferred publication option (BMC Genomics, BMC Bioinformatics, Bioinformatics). This preference should be stated in the Abstract section of the Easychair submission page. However, the final decision about the journal for each paper will be taken by the RECOMB-CG PC chairs and communicated to the authors upon acceptance.

Papers must be submitted in PDF format according to the guidelines for authors of the respective journal: https://bmcbioinformatics.biomedcentral.com/submission-guidelines/preparing-your-manuscript http://www.oxfordjournals.org/our_journals/bioinformatics/for_authors/general.html Papers submitted in BMC format must be within 10 pages, while papers submitted in Bioinformatics format must be limited to 7 pages. In both cases a clearly marked appendix can be added to the submission that contains supplementary material made available to the reviewers.

All submissions must be made online, through the EasyChair submission system, at the following address: https://easychair.org/conferences/?conf=recombcg2016 Authors need to register on that web site before submitting. A standard PDF file must be received by midnight on June 6, 2016 (any time zone) in order for a submission to be considered. Re-submission of already submitted papers will be possible until midnight June 8, 2016 (any time zone).

KEYNOTE SPEAKERS Guillaume Bourque (McGill University and Genome Quebec) JosÃÂ©e Dostie (McGill University) Edward Marcotte (University of Texas at Austin) Rebekah Rogers (University of California at Berkeley) Sohrab Shah (University of British Columbia and BC Cancer Agency)

PROGRAM COMMITTEE Max Alekseyev (George Washington University) Lars Arvestad (Stockholm University) Anne Bergeron (UQAM) Marilia Braga (Bielefeld University) Cedric Chauve (Simon Fraser University, co-chair) Leonid Chindelevitch (Simon Fraser University) MiklÃÂ³s CsÃÂ±rÃÂ(University of MontrÃÂ©al) Ingo Ebersberger (Goethe University Frankfurt) Nadia El-Mabrouk (University of MontrÃÂ©al, co-chair)

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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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Novosibirsk BioinformaticsGeneRegul Aug29-Sep2

Download the information letter in PDF format (Eng): http://conf.bionet.nsc.ru/bgrssb2016/wp-content/uploads/sites/2/ 2016/03/2016_03_30_Infoletter_2.pdf

Download the information letter in PDF format (Rus): http://conf.bionet.nsc.ru/bgrssb2016/wp-content/uploads/sites/2/ 2016/03/2016_03_30_Infoletter-2_rus.pdf

Second information letter

BGRS\SB-2016

10th anniversary International Multiconference

Bioinformatics of Genome Regulation and Structure Systems Biology

Novosibirsk, Russia, 29 August - 2 September, 2016

http://conf.bionet.nsc.ru/bgrssb2016 Dear colleagues!

Registration to 10th anniversary International Multiconference “Bioinformatics of Genome Regulation and Structure\Systems Biology” - BGRS\SB-2016 continues!

The Institute of Cytology and Genetics of the Siberian Branch of the Russian Academy of Sciences (ICG SB RAS) will organize this meeting 29 August - 2 September 2016 in Novosibirsk, Russia.

Since 1998 the conference of BGRSSB series are held every two years. In 2014, Multiconference BGRS\SB-2014 was attended by 483 researchers and students from 27 countries. More than 300 reports were presented (materials are available at: http://conf.bionet.nsc.ru/bgrssb2016/archive/)

Multiconference BGRS\SB-2016 will include the following research sections and meetings:

- Section “Genomics, transcriptomics and bioinformatics”

- Symposium “Proteomics”

- Section “Systems biology”

- Section “Evolutionary bioinformatics”

- Section “Computational pharmacology”

- Section “Bioinformatics and systems biology of cell death”

- Symposium “Neuroinformatics”

- Section “Bioinformatics and molecular biology synergism in DNA damage response studies”

- Section “Paleogenetics”

- Section “Systems biology of aging”

- Symposium “Human genetics”

- Section “Animal genetics”

- Section “Bioinformatics and systems biology of plants”

- Symposium “Mathematical modeling and high performance computing in bioinformatics, biomedicine and biotechnology”

Series of collateral events in the frames of the multiconference:

- Open Russian-German workshop on bioinformatics network “Systems computational biology”.

- Young Scientists School “Systems Biology and Bioinformatics”, SBB-2016: 22-25 August 2016. http://conf.bionet.nsc.ru/bgrssb2016/young-scientists-school-3/?lang=en - Sino-Russian Symposium on systems and computational biology with Chinese universities (BRICS countries).

- The seminar “Systems biology programmed cell death”.

- Pre-conference tour to Altai mountains: August 25-28, 2016: http://conf.bionet.nsc.ru/bgrssb2016/tour-altai/
- Social Events (Novosibirsk sightseeing tour).

The conference participants have opportunity to publish full-text papers in special issues of international science journals (BioMed Central series, see details at conference website)

The conference language is English

Registration details: http://conf.bionet.nsc.ru/bgrssb2016/?lang=en Important dates:

- Registration and abstracts submission for BGRS\SB-2016 and Young Scientists School SBB-2016 - May 20, 2016

- Notification of inclusion of the reports to the conference program and to the School program - June 10, 2016

- Young Scientists School: 22-25 August, 2016

- Tour to Altai mountains: 25-28 August, 2016

- The multiconference: 29 August - 2 September, 2016

Sincerely yours BGRS\SB-2016 Program Committee

Our contacts: bgrs2016@icg.sbras.ru,

BGRS\SB-2016 website: http://conf.bionet.nsc.ru/bgrssb2016/?lang=en ICG SB RAS website: www.bionet.nsc.ru BGRS2016 Organizing Committee <bgrs2016@icg.sbras.ru>

Perugia 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 landcape 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)

Invited speakers: *Dr Olivier François*, Laboratory TIMC-IMAG, CNRS, UniversityJoseph Fourier, Grenoble France *Dr Thibaut Jombart*, Department of Infectious Disease Epidemiology, Imperial College, London *Dr Ezechiel Nicolazzi*, Parco Tecnologico Padano

§Statistical Genomics and Bioinformatics group

The call for short papers (1000-1500 words) is now open until *June 15, 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): June 15, 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

UBraunschweig Adaptation

Adaptation in nature “from ecology to genomes Environmental conditions change constantly and individuals have to adapt in order to persist. Adaptation therefore plays a central role in evolutionary processes. However, there are considerable gaps between ecological and genetic perspectives on adaptive evolution. Despite revolutionary changes in data acquisition in molecular biology, our current knowledge about trait evolution in natural systems is scarce. A holistic view on evolutionary processes is typically hampered by a lack of knowledge about the threads connecting molecular genetic traits with higher-level phenotypes. Filling these gaps has been considered a key challenge for biologists of the 21st century.

Research towards these goals must be highly integrative and cover results from organismal biology as well as molecular biology. The summer school ”Adaptation in nature“ from ecology to genomes” from September 27th - 28th 2016, held at the Technische Universität Braunschweig, brings together scientists and students studying adaption in natural systems. It is a joint meeting of the Society of Genetics together with the DIP research unit (Gene expression underlying parallel habitat adaptation in salamanders) funded by the German Research Foundation (DFG) organized by Sebastian Steinfartz (Braunschweig) and Arne Nolte (Oldenburg). The meeting covers a broad range of topics in the context of adaptation, such as convergent and parallel evolution, phenotypic plasticity, ancient adaptation, the ecological context of evolutionary processes and adaptive radiations. It is the goal of the meeting to highlight studies that reveal the interplay between molecular evolution, organismal biology and ecological conditions.

Format and registration: Selected invited speakers will present their results, but abstracts for additional oral or poster contributions can be submitted by email to Sebastian Steinfartz (s.steinfartz@tu-bs.de). An extended poster session will be organized such that the presentation of posters takes a prominent spot in the conference schedule. If you are interested in joining the meeting, please send an email to Sebastian Steinfartz (s.steinfartz@tu-bs.de) before May 31st 2016. Further details on the conference and registration will be sent upon registration.

Awards: The GfG will award the Elisabeth-Gateff-Preis and Anders-Preis to outstanding young researchers during the conference.

When: 2 days, Sept. 27th 9:00 am Sept. 28th 16:00 pm.

Where: Technische Universität Braunschweig (Hauptgebäude).

Fee: Admission fee of 40 euro for members of the GfG otherwise 80 euro. Admission for students is free. Payment details will be communicated upon official registration.

Conference Dinner: Location tba. Conference dinner can be attended for a fee of 25 euro. Payment details will be communicated upon registration.

Accomodation: Attendees are requested to book their own accommodation. We can provide information on the conference venue, traveling and accommodation in and around Braunschweig to those who registered.

Confirmed speakers:

Key Notes: Leif Andersson (Uppsala) Functional genomics Michael Hofreiter (Potsdam) Evolutionary adaptive genomics Axel Meyer (Konstanz) Parallel adaptation in cichlid fishes

Invited Speakers Lutz Becks (Plön) Eco - evolutionary dynamics Kathryn Elmer (Glasgow) Colour variation in salamanders Thomas Flatt (Lausanne) Genomics of adaptation in Drosophila Florian Leese (Essen) Signatures of selection in aquatic invertebrates Juliette de Meaux (Cologne) Arabidopsis ecological genomics Markus Pfenniger (Frankfurt) Fish adaptation to toxic hydrogen-sulphide Karl Schmid (Hohenheim) Adaptation and drift in Arabidopsis relatives Kai Stölting (Fribourg) Hybridisation and evolution of Populus

"nolte@evolbio.mpg.de" <nolte@evolbio.mpg.de>

UGoettingen Germany ConservationGenetics Oct5-7 Reminder

REMINDER: May 1st is the deadline for submission of abstracts for the '2nd Annual Meeting in Conservation Genetics - From Research to Applications'

See

www.landscapegenetics.info/consgen16 for details.

The conference will take place October 5th to 7th, 2016 in Goettingen, Germany.

We look forward to seeing you at the meeting!

The organizing committee Niko Balkenhol (University of Göttingen, Germany) Rolf Holderegger (WSL Birmensdorf and ETH Zürich, Switzerland) Gernot Segelbacher (University of Freiburg, Germany) Janine Bolliger (WSL Birmensdorf, Switzerland) Axel Hochkirch (Trier University, Germany) Felix Gugerli (WSL Birmensdorf, Swizerland) Frank Zachos (Natural History Museum Vienna, Austria) Jan Engler (University of Göttingen, Germany)

"niko.balkenhol@forst.uni-goettingen.de"

GradStudentPositions

Bordeaux GenomicsLocalAdaptation

Dear all,

We have opened a PhD position at the University of Bordeaux doctoral school to work on 'Ecological genomics of local adaptation in maritime pine' at INRA-BIOGECO (see www.bordeaux-aquitaine.inra.fr/biogeco). The PhD topic is associated with two well-funded projects, one from the Initiative of Excellence of Univ. Bordeaux and another one, GenTree, a H2020 European project that will give an international dimension to the student research.

This is a very nice setting for a young researcher to do its PhD and we are searching for enthusiastic candidates that would like to join our team at Bordeaux.

A full description of the PhD project can be found at https://ed-environnements.u-bordeaux.fr/-content/download/11451/99751/version/1/file/-BIOGECO_%202016_Gonzalez.pdf Deadline to deposit candidatures is very short (May 9th) and we would appreciate maximum diffusion of this offer.

Thank you and have a good w-e,

Santiago

– Santiago C. Gonzalez-Martinez Research Director INRA, UMR1202 BIOGECO: Biodiversity, Genes & Communities 69, route d'Arcachon F-33610 Cestas, France Tlf: ++33(0)557122757

email: santiago.gonzalez-martinez@pierroton.inra.fr skype/gmail: santiago.c.gonzalez.martinez web: www.bordeaux-aquitaine.inra.fr/biogeco personal web: sites.google.com/site/santiagocgonzalezmartinez ***updated October 2015***

santiago.c.gonzalez.martinez@gmail.com

BrandonU EvolutionSoybeanPathogens

Funded MSc Position in Soybean Diseases

We are seeking a highly motivated MSc student to work on projects related to the evolution of pathogen diversity in soybean. Projects include examining natural co-infection rates and sequence divergence among strains. The research is highly integrative; combining field work, bioinformatics and cutting-edge molecular biology tools.

Interested students are encouraged to contact Dr. Bryan Cassone (cassoneb@brandonu.ca). Please include a brief description of your interest and a CV in your email.

Closing Date: Open until filled

Start Date: Summer 2016 preferred

Founded in 1899, Brandon University is a small but thriving institution located in southwestern Manitoba. Students have access to fully renovated labs, greenhouses and growth chambers, as well as state-of-the-art molecular and computational equipment.

Bryan Cassone <CassoneB@BrandonU.CA>

CardiffU SheepGenomics

PhD studentship (Cardiff University, United Kingdom) - Genome-wide analysisof maternal ability in the Lleyn sheep

Project Description: This project will be carried out at CardiffUniversity (CU) using cutting edge genomics tools to identify the genetic basisof key valuable production characteristics of the Lleyn breed, especiallymaternal ability and prolificacy. The Lleyn is a very successful and productivebreed that has grown rapidly for the last 15 years throughout the UK. Lleyn breedimprovement has been possible through keeping detailed performance recordingusing powerful statistical tools, but characterising the breed's genome-widegenetic variation will speed up this process).

This project will assess allelic variation across ˜700,000markers spread across the sheep genome and a Genome-Wide Association Study(GWAS) will be carried out to identify genes associated with maternal abilityand prolificacy and to estimate Genomic Breeding Values (GEBVs) forimprovement. The GWAS statistical approaches will take into considerationenvironmental, phenotypic and production variables accounting for relevantfactors and their interactions. Further gene-based analyses will be carried outon the basis of regions identified in the GWAS analysis to develop a test forthe Society to be able to screen animals of interest for breed improvement.

This project will provide excellent training in modernagricultural technology, including genomics, statistical analysis andexperimental design. It will be carried out in close collaboration betweenCardiff University, the Lleyn Breed Society (LBS) and Signet FBC performancerecorders, and will include substantial on-farm research.

Supervisory Team: Professor Michael Bruford (CU supervisor)& Dr Pablo Orozco-terWengel (CU supervisor), Dr John Adams (collaborator LBS) & Signet FBC (collaborator)

Eligibility: Eligible students must have a home of work addressin the West Wales and the Valleys Convergence area of Wales* at the time oftheir application to Cardiff University, and at the time they enrol for studies.

As for minimum academic entry conditions for postgraduate research studyat Cardiff University

Â Applicants for research PhDs at Cardiff University will be expected to have one or both of the following:

- a first degree, normallywith class 2:1 or higher, or equivalent in a relevant subject;
- a relevant Master'squalification or equivalent

Â Start Date: 1st October 2016

Funding: the PhD project is funded by theEuropean Social Fun (ESF Convergence West Wales and the Valleys) by externalpartners from the private and third sectors, and by Cardiff University. ESF funding has not been formally awarded atthe time of advertising this studentship - Cardiff University will meet anyshortfall in funding if the ESF award is not secured.Â

Â The Convergence area covers West Wales and the Valleys, and is made upof the following 15 local authorities: Isle of Anglesey, Gwynedd, Conwy,Denbighshire, Ceredigion, Pembrokeshire, Carmarthenshire, Swansea, Neath PortTalbot, Bridgend, Rhondda Cynon Taf, Merthyr Tydfil, Caerphilly, Blaenau Gwentand Torfaen.

If you are selected for a scholarship, original documentary evidence ofyour eligibility, qualifications and income will be requested prior toconfirming our offer of funding.

Application: Applicants shouldapply following the usual PGR Online application process, specifying theirinterest in this studentship.

Â The selected candidate will be asked to complete a 'Participant Proposal'form, provided by University supervisors when appropriate, to confirm theirapplication and eligibility for this studentship.

Â

Pablo Orozco-terWengel <orozco_terwengel@yahoo.com> Pablo Orozco-terWengel <orozco_terwengel@yahoo.com>

CharlesU Prague EvolutionOfVisionCichlidFishes

Last call: Ph.D. position at Department of Zoology, Charles University in Prague, Czech Republic.

Topic: Evolution of vision in West African cichlid fishes We are seeking a highly motivated Ph.D. student to join a project on adaptive molecular evolution of functional genes in freshwater fishes.

The selected Ph.D. candidate will be focused on adaptation of photoreceptor genes in endemic cichlid fishes distributed in deep crater lakes and rivers in Africa (mainly Cameroon). Evolution of visual sensory system will be approached by genomics and transcriptomics. The selected Ph.D. student will process already collected material, as well as has an option to actively participate in the field sampling in Cameroon.

Start: October 2016. Duration: 4 years.

Salary is composed of the full-time project position (192'000 CZK annually) + standard university scholarship (will start at 75'600 annually and raise up to 115'000 CZK together with the progress of the study duties), which in total corresponds to the average national salary and sufficiently covers living costs in the Czech Republic.

Required: enthusiasm in biology, nature and science; fluency in English; a M.Sc. degree in biology or related fields (or expected to be finished until September 2016).

Desirable (but not necessary): previous experience with laboratory work, especially molecular genetic methods; experience with research projects evidenced by a (co)authorship of research papers or conference contributions.

Deadline: already 20th April 2016 (last call).

All questions and applications (CV + half-page motivation letter) should be sent directly to Zuzana Musilova (zuzmus@gmail.com - preferred , zuzana.musilova@natur.cuni.cz).

More info about the Biodiversity Research Group and the Department of Zoology: http://web.natur.cuni.cz/zoologie/biodiversity/index.php?page=3Dmusilova zuzmus <zuzmus@gmail.com>

CharlesU Prague HomologyOfSexChromsomes

CharlesU_Prague.HomologyofSexChromosomes

PhD position in Transcriptome analysis and homology of sex chromosome in reptiles

A position for a PhD candidate is currently open in the laboratory of Assoc. Prof. Lukas Kratochvil, Department of Ecology, Charles Universityin Prague, Czech Republic. The successful PhD candidate will join our current projects on the study of the evolution of sex chromosomes in reptiles with molecular and cytogenetic methods.

Project description: Recently, we revealed the gene content of the lacertid lizard Takydromus sexlineatus through a novel approach combining transcriptomics and quantitative PCR methodology, and further tested the homology of the sex chromosomes across other lacertid species. Our results demonstrated thatthe gene content of the Z chromosome of the lacertids is not homologous to any reptile including birds, but instead homologous to the X-conserved region of viviparous mammals. It is possible that this part of the vertebrate genome was independently co-opted for the function of sex chromosomes in viviparous mammals and lacertids because of its content of genes involved in gonad differentiation. Therefore, we seek for a motivated PhD student to further analyze the lacertid sex chromosome gene content in a comparative framework and to use this unique system to test hypothesis on the evolution and co-option of sex chromosomes, using a variety of molecular genetics and genomic methods.

More information please check ourrecent publications: http://www.ncbi.nlm.nih.gov/pubmed/26980341 http://www.ncbi.nlm.nih.gov/pubmed/27037610 Qualifications: The applicant should possess Master degree (or equivalent title) and proven expertise in a related field of biology: evolutionary biology, cytogenetics, phylogenetics, genomics and/or bioinformatics. Previous experience in herpetology is not necessary. Good knowledge of the English language is required.

Application: The applicant should send a letter explaining his/herprevious research experience, a full CV and contact information for two references to both lukas.kratochvil@natur.cuni.cz; michail.rovatsos@natur.cuni.cz.

The PhD position will be financially supported with stipend for maximum time of 4 years, starting from October 2016.

The deadline for submission of applications is April 24, 2016.

Lukas Kratochvil

Associate Professor Department of Ecology Charles University in Prague Faculty of Science Vinicna 7, 128 43 Praha 2 www.natur.cuni.cz/en Tel.: +420 221 95 1745 e-mail: lukas.kratochvil@natur.cuni.cz

Rovatsos Michail

Biologist, PhD Department of Ecology Faculty of Science Charles University in Prague Vinicna 7, 12843 Praha 2

“Michail Rovatsos, Ph.D.” <michail.rovatsos@natur.cuni.cz>

ClarkU PlasticityLedEvolution

Two PhD positions are available in the laboratory of Susan Foster and John Baker at Clark University in Worcester MA USA beginning late August 2016 as follows:

The idea that novel trait expression induced by environmental change (phenotypic plasticity) could influence the course of evolution, has re-emerged as a core issue in evolutionary biology in recent years. A central question associated with this issue is whether environmental influences on plastic phenotypes accelerate evolutionary rates by exposing previously cryptic genetic variation to selection, or instead buffer populations from evolutionary change by producing phenotypes that are adaptive under the novel conditions. Assessment of these alternatives has proven exceptionally difficult.

Research in the Foster-Baker laboratory, involving the unusual adaptive radiation of the threespine stickleback fish, Gasterosteus aculeatus, will evaluate these alternatives on both phenotypic and genomic levels by examining patterns of gene expression in relation to salinity challenge in oceanic (ancestral) and derived (freshwater), post-glacial populations in the Pacific northwest of North America. Our primary, general goals are to understand whether high levels of ancestral plasticity are associated with accelerated evolutionary rates both at the levels of individual candidate loci and in genomic regions of divergence.

This research is funded by, and is part of, a > $8 million multinational grant from the John Templeton Foundation involving 49 investigators and 8 leading academic institutions. The research is designed to examine the role of plasticity in evolution. The project is led by Kevin Laland and Tobias Uller (http://synergy.st-andrews.ac.uk/ees/the-project/). Collaborators on the Clark component of the research are William Cresko (University of Oregon), John Gibbons (Clark University), Kevin Laland (St. Andrews University), Juha Merilä (University of Helsinki), and Matthew Wund (The College of New Jersey).

Successful applicants will be engaged in this research project, and so should have an interest in evolution, genomics and bioinformatics, but also will have the opportunity to conduct field research and to design their own research related to that ongoing in our laboratory. We are looking for creative, engaged applicants who are interested in becoming accomplished scholar-mentors, and who would enjoy the collaborative environment of our laboratory and also that of our small but active and highly-respected research university (http://-wordpress.clarku.edu/foster-baker-lab/). Students will have the opportunity to participate in workshops associated with the research at Clark University (http://www.clarku.edu/articles/clark-university-biologist-co-lead-87-million-grant-evolutionary-biology), and also in the larger workshops associated with Templeton Grant.

Interested students should apply to the Biology Graduate program through official channels at Clark University, and submit a single PDF with relevant application information to Susan Foster sfoster@clarku.edu. The positions will remain open until filled.

John John A. Baker Research Associate Professor Department of Biology & Environmental Science Program Clark University 950 Main Street Worcester, Massachusetts, USA 01610 Voice: (508) 793.7609 Fax: (508) 793-7174 Web: http://wordpress.clarku.edu/-foster-baker-lab/ John Baker <JBaker@Clarku.edu>

Copenhagen Computational-PalaeogenomicsMicrobiomics

The Natural History Museum, Faculty of Science at University of Copenhagen is offering a 3 year PhD scholarship as part of the ArchSci2020 European Joint Doctorate Program (www.archsci2020.eu). The broad topic is computational palaeogenomics, and is in the group of Professor Tom Gilbert (http://geogenetics.ku.dk/-research_groups/gilbert_groups/), starting ca. November 1st 2016. The ArchSci2020 network offers the first European Joint Doctorates in Archaeological Sciences, and was created in recognition that there is a need to promote international, intersectoral, and multi/inter-disciplinary collaboration in doctoral-level training. Thus at the large level, ArchSci2020 will train a new cohort of bioarchaeological scientists.

Project description Genetic analysis of historic and ancient samples through second generation sequencing platforms is an increasingly powerful means with which to study the past. In recent years, considerable developments have been made in the laboratory with regards to the generation of genomic and proteomic data from both host organisms and their associated microbes. Associated development in computational tools for the analysis as well as synthesis of such data is lagging. We are searching for skilled bioinformaticians who wish to both contribute to the development of palaeogenomics through the development of new computational tools, as well as analyse bioarchaeological datasets.

For more information on the position, including how to apply, please see: http://jobportal.ku.dk/phd/?show=-3D823007 The closing date for applications is June 1st.

Please direct any questions to

Tom Gilbert Professor of Palaeogenomics Centre for GeoGenetics Section for Evolutionary Genomics Natural History Museum of Denmark University of

Copenhagen Øster Voldgade 5-7 1350 Copenhagen tgilbert@snm.ku.dk

M Thomas P Gilbert <tgilbert@snm.ku.dk>

DeakinU EvolutionPlasticity

The evolution of plasticity during a biological invasion

A PhD scholarship on invasion ecology is available in the Rollins lab in the Centre for Integrative Ecology at Deakin University.

Project: Organisms can deal with novel challenges by changing their phenotype in response to environmental cues (plasticity) and/or by longer-term changes in gene frequencies within a population (adaption). Plasticity itself can be adaptive; so how does it evolve? Invasive species offer a unique opportunity to answer that question, because a founding population (with typically modest genetic variation) must deal with novel challenges in its new environment. Using the cane toad invasion in Australia as our model system, this project will examining the roles of plasticity and evolution in invasion using an experimental framework to study phenotypic traits important to invasion (dispersal ability, immune function and personality). Further, we aim to determine whether epigenetic changes drive plasticity in this system. This project is part of a larger research program investigating the molecular mechanisms (genetic and epigenetic) that underlie invasion. The larger project is well-resourced and multi-disciplinary, combining the efforts of molecular ecologists at Deakin University with invasion ecologists (Professor Rick Shine and his team) from the University of Sydney.

Selection criteria: This PhD project will be primarily based at our collaborator's field station in the Northern Territory but will also include time at the Deakin University Geelong campus. We seek an ecologist who will work closely with team members who are conducting genetic/epigenetic analyses. There will be flexibility to tailor the PhD project to your specific interests and the project can be framed as purely ecological or can incorporate a molecular component.

We seek a hard-working and enthusiastic student with some field experience, a demonstrated ability to work independently and well-developed organisational skills. Preference will be given to applicants with at least one first-authored publication.

Scholarship/application details: The successful candidate will be awarded a PhD stipend of AUD$26,288 per annum (tax-free) over three years. Applicants should send an email to Dr. Lee Ann Rollins (lee.rollins@deakin.edu.au) including: 1) a CV; 2) academic record (subjects and marks); 3) a one-page summary of your research interests and career goals; and 4) details of 3 referees (including any previous research supervisors). Closing date for applications is 1st May 2016.

lee.rollins@deakin.edu.au

ETHZurich HostParasiteCoevolution

http://www.ae.ethz.ch/jobs.html Thegroupof Aquatic Ecology at ETH Zürich / Eawag hasan open Ph.D. Position

tostudyepidemiological, ecological and molecular drivers of co-evolutionarydynamics between hosts and parasites. The study system isthe New Zealand freshwater snail Potamopyrgus antipodarum and its trematodeparasite Microphallus sp. The goal of the project is to understandhow spatial variation in host infection risk ("hot" and "cold"spots of infection) contributes to parasite adaptation and hostresponse. The work includes field work in New Zealand and laboratory infectionexperiments. Subsequent SNP genotyping of the parasite and host individualsallows for population genetic studies on parasite genetic structureand tracking of evolutionary change in the host population.

Workingindependentlyas well as part of our team are necessary qualificationsfor an ideal candidate. You would need to work under sometimesharsh field conditions, cope with longâmaintenance ofexperiments and lab cultures and ideally you have some molecular geneticslab experience. You also need excellent communication (writing, presentating)and data analysis skills. Working language is English.

Generalinformationabout the research group can be found at http://www.ae.ethz.ch/ . Candidatesmustqualify for admission to the Ph.D. programme of ETH (https://www.ethz.ch/en/doctorate.html).The duration of the position isthree years, starting not earlier than September 2016. Salary is accordingto ETH-scale starting from 47 kchf/year. Suitablequalified personsare invited to apply by email. Please attach a single PDF file includinga letter of motivation, C.V. and names plus addresses of two references.Subject line should read “PHD-Position 2016”. Email addressto use is jukka.jokela@env.ethz.ch.

Evaluationofapplications starts May 2016, and continues until the positionis filled.

JukkaJokela professorofaquatic ecology ETHZurich www.ae.ethz.ch Jukka.Jokela@eawag.ch

France 15 EnvironmentalGenomics

Sorry for the short notice, the deadline to apply is this Friday.

15 PHD/RESEARCH POSITIONS ON PROMOTING SINGLE CELL GENOMICS TO EXPLORE THE ECOLOGY AND EVOLUTION OF HIDDEN MICROEUKARYOTES http://www.singek.eu/call-for-positions/ Extended application deadline: 17:00 GMT on the 29th April 2016

*Microbial eukaryotes*cover the widest phylogenetic diversity in the eukaryotic tree of life and are essential components of all Earth’s ecosystems. Paradoxically, they remain largely unknown, hiding a wealth of genes and genomes that are key to understand the ecology and evolution of microbial ecosystems.*SINGEK*is a*H2020 Marie-SkÅodowska-Curie Innovative Training Network (MSCA-ITN)*project aimed at providing a unique and structured*training programme*to*15 Early Stage Researchers (ESRs)*to study*microeukaryotes at the single-cell level*. ESRs will be trained in the use of an array of laboratory methods (cell sorting and molecular tools for nucleic acid amplification and high throughput sequencing), bioinformatic techniques (genome and transcriptome assembly and functional gene annotations), and will work on scientific questions in the fields of microbial ecology and evolution in order to investigate microeukaryotes in unparalleled detail. The*training structure*is a central part of SINGEK project and will include:*local and network-wide activities, secondments to other network.*

All positions are for*3-years *contracts starting in*October 1st, 2016,* most of them leading to a PhD degree. Specific conditions may apply to individual positions depending on local regulations.

Top-level graduates (master degree or equivalent) in biology, bioinformatics, microbial ecology, molecular biology, evolutionary biology, biodiversity, biotechnology, physics, nanoscience, engineering or computer science are encouraged to apply. No discrimination will be made on the basis of nationality, gender, race, religion or disability.

H2020 EU funding imposes*strict eligibility criteria*: At the time of recruitment the researcher must not have resided or carried out his/her main activity (work, studies, etcâ€) in the country of the host institute for more than 12 months in the 3 years immediately prior to his/her recruitment under the project.The researcher should also be in the first four years of their research careers at the time of recruitment by the host organisation and have not been awarded a doctoral degree.

The successful candidate will be employed for 3 years and receive a financial package plus an additional mobility and family allowance according to the rules for Early Stage Researchers (ESRs) in an EU Marie SkÅodowska-Curie Actions Innovative Training Networks (ITN): - Living allowance* - 3110â¬$(permonth) - Mobilityallowance - 600$â¬$(permonth) - Familyallowance * * - 500$â¬$(permonth - ifapplicable)$

The living allowance is a gross EU contribution to the salary costs of the researcher. The net salary will result from deducting all compulsory (employer/employee) social security contributions as well as direct taxes from the gross amounts, according to the law applicable to the agreement concluded with the ESR. Additional information about the funding provided by the ITN projects can be foundhere < http://ec.europa.eu/research/participants/data/ref/h2020/wp/2014_2015/main/h2020-wp1415-msca_en.pdf >.

Candidates may apply through the*SINGEK applications system (http://www.singek.eu/registration-form/) , which will request the following information:

*1.*An application form, including a CV overview, ESRs’ positions of interest (up to 3), and a statement of their motivation for applying.

*2.*A full CV.

*3.*An academic record, with a scan of the degree qualifications.

*4.*Two recommendation letters.

Each project supervisor will revise the candidates’ documentation and, on the basis of the completeness and adequacy of the requested material and quick eligibility check, will score candidates based on: (1) academic profile; (2) personal motivation; (3) scientific skills and relevant experience; and (4) English proficiency. Shortlisted candidates will be invited to teleconference interviews with the relevant project supervisor(s).

*Extended application deadline: 17:00 GMT on the 29th

April 2016 *

Candidates are invited to contact the supervisors to get more details.

Olivier Jaillon <ojaillon@genoscope.cns.fr>

France DeepSeaGenomics

PhD title: *Reevaluating marine biodiversity in deep-sea ecosystems and the drivers of its distribution through metagenomics approaches*

Dead-line for application: 30th of June 2016

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) et Laboratoire Environnement Profond/Etude des Ecosystèmes Profonds, IFREMER Brest Plouzané (Daniela Zeppili), in the context of the project "Pourquoi Pas les Abysses" (Ifremer, France). The candidate will be based in Sète and register at Montpellier University.

To apply, the form to be filled and returned before June 30th to the scientific contacts for application 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

Supervisor* : Sophie Arnaud-Haond (Dr, HDR, spécialité: génétique des populations; Sophie.Arnaud@ifremer.fr) *Co-supervisor *: Daniela Zeppilli (Dr, spécialité : taxonomie et écologie, méïofaune; Daniela.Zeppilli@ifremer.fr))

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. Species inventories obtained in contrasted environments will be analyzed in terms of richness and distribution across distinct biogeographical areas and ecosystems, and the existence of biotic assemblages tested through cooccurence network analysis. Finally, 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 two main taxa, vesicomiids bivalves and shrimp of the genus Alvinocaris present across distinct and distant ecosystems.

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).

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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

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Sophie ARNAUD-HAOND <s-arnaud@univ-montp2.fr>

Grenoble Oxford 2 BacterialGenomics

The New Diagnostics for Infectious Disease (ND4ID) consortium is advertising two PhD studentships to be held at the bioMrieux Innovation Unit in Grenoble, France, with secondment to the University of Oxford, UK.

The projects are titled

Bioinformatics tools for sequencing-based characterization of the resistome and virulence profiles of P. aeruginosa: http://www.nd4id.eu/esr15/ and

Laboratory approaches for sequencing-based characterization of the resistome and virulence profiles of P. aeruginosa: http://www.nd4id.eu/esr14/ Infectious diseases are a major burden to public health and the global economy, not in the least due to antimicrobial resistance. Rapid point of care (POC) in vitro diagnostics (IVD) are key tools in the effective clinical management of patients with infectious diseases.

Yet there is still a large unmet clinical need for more rapid POC IVDs generating more clinically relevant, actionable information. Effectively addressing this need requires a change in the current approach in training researchers on IVDs, generating a new breed of IVD researchers capable of closing the gap between the clinical and technological perspective.

ND4ID takes up this challenge by offering ESRs a world-class first of its kind training programme where they will be exposed to the full breadth of disciplines spanning clinical, technological and market-oriented viewpoints, from both the academic and non-academic sector. Through a set of synergistic research projects on novel POC assays, targeting the most important and urgent clinical needs at world leading academic or private sector research groups, the ESRs are offered a holistic training program, preparing them to be lead players in the future IVD field. This training through research is augmented by a unique comprehensive network-wide training programme covering clinical, technical and translational knowledge and skills of relevance to IVD research, development and exploitation. As such, ND4ID will deliver ESRs that will be in high demand serving as an example for other academic and non-academic actors active in training IVD researchers and further strengthening Europes position in the internally competitive arena of IVD technology.

Interested candidates should contact Sonia Chatellier (sonia.chatellier@biomerieux.com) or Pierre Mahe (pierre.mahe@biomerieux.com) in the first instance.

– Dr Daniel Wilson Wellcome Trust/Royal Society Sir Henry Dale Fellow Associate Professor Nuffield Department of Medicine University of Oxford www.danielwilson.me.uk Daniel Wilson <daniel.wilson@ndm.ox.ac.uk>

London InsectFungalInteractions

PhD studentship available: London, UK The role of bark beetles in the dispersal of tree-pathogenic fungi

Project description: Bark beetles (Scolytinae) form associations with pathogenic fungi that are poorly understood, but are of great concern to forest health. This project aims to clarify the role of wood-boring beetles in the dispersal of tree-pathogenic fungi in the UK. High-throughput sequencing of entire fungal communities can be performed directly on the DNA extracted from individual beetles, which gives unprecedented resolution of fungal species diversity and association with particular beetle species, host trees, climatic conditions or biogeography. Beetles are easily caught in traps and can be used as sentinels for detection of pathogens. This is an exciting opportunity to work at the interface of ecology, taxonomy and genomics.

This full-time studentship is funded by the John Spedan Lewis Foundation. The student will be supervised by Drs Alfried Vogler (Imperial College London / NHM), Daegan Inward (Forest Research), Martin Bidartondo (Imperial College London / Kew Gardens) and Max Barclay (NHM). This studentship is open to UK and EU nationals only. A Master's degree in ecology or evolutionary biology is required. For informal inquiries please contact A. Vogler at a.vogler@imperial.ac.uk<mailto:a.vogler@imperial.ac.uk>. Closing date for applications is April 30, 2016. Online applications can be made via http://www.nhm.ac.uk/our-science/courses-and-students.html . "A.Vogler@nhm.ac.uk" <A.Vogler@nhm.ac.uk>

LundU MaternalEffectsEvolution

A 4-year PhD position is available in the laboratory of Tobias Uller at Lund University, beginning September 2016.

The aim of the project is to test the theoretical prediction that parental effects can facilitate adaptation to novel environments, and that natural selection can convert stress-induced parental effects to adaptive mechanisms of information transfer in variable environments.

The research project will study the mechanisms and adaptive functions of non-genetic inheritance of tolerance to biotic or abiotic stressors in water fleas, Daphnia, using a combination of field- and lab-based experiments. These involve field sampling, large experimental set-ups and a suite of molecular methods, including analyses of gene expression and its epigenetic regulation. It is expected that the PhD student will actively drive the direction of her/his research and there is thus intentional flexibility within the project to encourage theory-driven research. To this end, we offer excellent training in evolutionary theory and in the generation and analyses of molecular and phenotypic data at Lund University and through our international project partners.

This research is funded by, and is part of, a > $8 million multinational grant from the John Templeton Foundation involving 49 investigators and 8 leading academic institutions. The research is designed to examine the role of development in evolution. The project is led by Kevin Laland and Tobias Uller (http://synergy.st-andrews.ac.uk/ees/the-project/).

Successful applicants will be engaged in this research project, and so should have a very strong interest in evolutionary biology - in particular the relationships between development, ecology, and evolution. The candidate should also have good knowledge and practical experience of experimental research on invertebrate laboratory model organisms. An understanding of aquatic ecosystems and zooplankton biology are desired qualifications, and experience of work with algal or Daphnia cultures, DNA sequence analysis and programming (within bioinformatics) are an additional merit. We are looking for someone who is enthusiastic, creative, good at problem-solving, a team-worker, independent, and demonstrate excellent personal organisation skills and a strong work ethic.

More information about the group and our research can be found at http://ullergroup.se/. Further information on the position and how to apply can be found at https://lu.mynetworkglobal.com/en/what:job/jobID:97878/ . Dr Tobias Uller Senior Lecturer & Wallenberg Academy Fellow Department of Biology Lund University

Tobias Uller <tobias.uller@biol.lu.se>

Lyon France Evolutionary genomics

The Bioinformatics and Evolutionary Genomics group (University of Lyon, France) invites applications for a PhD position. The position is funded by the ANR and available from September 2016 or later (application deadline: May 15 2016). We are looking for highly qualified students with a strong interest in evolutionary biology and genomics. Applicants should ideally have a background in evolutionary genomics and/or population genetics and practical skills in bioinformatics/statistics. We offer a PhD position for three years within a highly competitive multidisciplinary and international research environment. The position is open to both French and international candidates.

— PhD Project:

Exploring the dark side of recombination: mutation, conversion and evolution of metazoan genomes

Meiotic recombination is a key aspect of our biology. By ensuring proper chromosome segregation during meiosis and maintaining genome integrity, it plays a crucial role in our fecundity. Recombination also has an essential long-term evolutionary function, facilitating adaptation through linkage dissipation. However, recent progress in our understanding of the underlying molecular mechanisms suggests that recombination also has a dark side. Intra-genomic conflicts, mediated by a particular forms of meiotic drive called GC-biased gene conversion (gBGC), causing transmission biases at the level of the population, are now suspected to stand at the core of the dynamics of recombination. Such intra-genomic conflicts have a strong impact on the proper functioning of recombination and meiosis, as well as on genome-wide fitness landscapes, potentially contributing a substantial genetic load.

We have previously shown that gBGC has a major impact on the evolution of mammalian genomes [1] and that it affects many other eukaryotes [2]. It appears however that the intensity of gBGC varies widely across species. For instance, gBGC is very strong in honey bees [3], but weak (or null) in drosophila [4]; similarly, gBGC appears to be much stronger in mammals and birds than in other vertebrates [5]. Why is gBGC effective in some taxa but not in others? What is the 'raison d'être' of this process?

To try to answer these questions, we propose to quantify the intensity of gBGC, and of several other key genomic parameters (recombination rate, mutation rate, mutation pattern) in a large set of animal species. We will thus explore the relationships between these different parameters, and their co-variations with life history traits (longevity, body mass, mating system, â€) to try to understand the constraints driving the evolution of gBGC.

The project relies on bioinformatics and statistical analysis of large-scale sequencing datasets. The student will have to get acquainted with concepts of population genetics and evolutionary genomics, to quantify gBGC and mutational patterns from allele frequency spectra.

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Interested students should send a CV with a letter of interest and two letters of recommendation to Laurent.Duret@univ-lyon1.fr. The position will remain open until filled.

Supervisor: Laurent Duret (LBBE, Villeurbanne). Contact: Laurent.Duret@univ-lyon1.fr Host laboratory: Laboratoire Biométrie et Biologie Evolutive, UMR CNRS 5558, Université Lyon 1, 43 Bld du 11 Novembre 1918, 69622 Villeurbanne cedex. http://lbbe.univ-lyon1.fr/ References: [1] Duret & Galtier (2009). Ann. Rev. Genom. Hum. Genet. 10:285311. [2] Pessia et al. (2012). Genome Biol. Evol, 4:67582. [3] Kent et al. (2012). Proc. Natl. Acad. Sci. U S A 109, 1801218017. [4] Robinson et al. (2014). Mol. Biol. Evol. 31, 42533. [5] Escobar et al. (2011). Mol. Biol. Evol. 28, 25612575. [6] Mancera et al. (2008). Nature, 454:47985. [7] Williams et al. (2015). eLife 4, 1-21.

_____ Laurent Duret Laboratoire Biométrie et Biologie Evolutive UMR CNRS 5558, Université Lyon 1 43 Bld du 11 Novembre 1918 69622 Villeurbanne cedex France

Phone : +33 (0) 4 72 44 62 97 e-mail : Laurent.Duret@univ-lyon1.fr Web page: http://lbbe.univ-lyon1.fr/-Duret-Laurent-.html?lang=3Den

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MasseyU PolyploidGenomics

A Ph.D. position is available in the Tate lab (http://www.massey.ac.nz/ ˜ jtate/index.htm) at Massey University (Palmerston North, New Zealand) to investigate the genomic basis of cytonuclear compatibility in Tragopogon (Asteraceae) allopolyploids. The project will involve both computational and wet lab work to reconstruct and evaluate plastid genomes and their interacting nuclear gene components. This position will be funded by a Massey University Doctoral Scholarship (http://www.massey.ac.nz/massey/admission/scholarships-bursaries-awards/other-scholarships/search-results/search-results_home.cfm?page=award_display&scholarship_id=1191) for which the successful applicant will need to have an outstanding academic record. An MSc in Plant Biology, Genetics, or a similar field is required. This project is in collaboration with Prof. Murray Cox at Massey University, Dr. Dan Sloan at Colorado State University, and the Soltis lab at the University of Florida.

To apply, please send a letter of interest, CV, academic transcript (unofficial is ok) and the names and contact details for three references to j.tate@massey.ac.nz with 'PhD scholarship' in the subject line. International applicants are welcomed. For full consideration, materials must be received by May 15th. The starting date is flexible but must be no later than 1 November 2016. Please feel free to email Jen with any questions about the scholarship or the project.

This position offers an opportunity to experience New Zealand's unique natural and cultural environment. Located in Palmerston North, a university town with a large international community which offers a range of social and cultural amenities, the city is located close to mountains, rivers and the sea, and presents regular opportunities for hiking, skiing, surfing, and adventure sports.

Jennifer A. Tate, Ph.D. Senior Lecturer in Plant Systematics and Evolution Curator, Dame Ella Campbell Herbarium (MPN) < http://www.massey.ac.nz/herbarium > Plant Science major leader Massey University Institute of Fundamental Sciences Private Bag 11222 Palmerston North New Zealand

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

Homepage < http://www.massey.ac.nz/ ˜ jtate/index.htm >

j.tate@massey.ac.nz

"Tate, Jennifer" <J.Tate@massey.ac.nz>

MaxPlanck Tuebingen 5 BioinformaticsEvolutionaryGenomics

5 PhD positions available in Bioinformatics and Evolutionary Genomics

The Jones and Chan labs at the Friedrich Miescher Laboratory at the Max Planck Campus, Tübingen, Germany, are offering *up to five* PhD projects for talented students aspiring to become skilled bioinformaticians/computer scientists/evolutionary genomicists to work on cutting edge genomics projects. Full funding is provided for the duration of the projects.

We work at the cross-section between functional genomics and evolutionary genetics with the aim of understanding the molecular basis of phenotypic variation in mice and stickleback fish. Both labs are funded by the Max Planck Society (MPG) and hold prestigious European Research Council Grants.

We are looking to recruit talented and motivated team members to analyse existing datasets (including DNA-, RNA-, ChIP-, ATAC-Seq). You will work closely with other wet-lab members with a focus on development of pipelines and analysis of exciting genomic datasets for the projects outlined below (please visit our websites for more details). Where applicable you may also participate actively in wet-lab data generation using our established high-throughput robotics platforms.

1. Recombination Hot- and Coldspots and Adaptive Evolution (JONES - ERC)

By shuffling parental alleles to produce novel haplotypes, recombination impacts the strength of selection on nearby polymorphisms and can influence the rate of adaptation in natural populations. We are using pedigree & population genetic methods to quantify variation in recombination hot- and coldspots across the genome, among individuals, sexes & divergent species and intersect these maps with adaptive loci to investigate how recombination shapes adaptive evolution.

2. Population Genomics: Rapid Adaptation from Standing Genetic Variation (JONES - MPG & DFG)

The type, source and availability of genetic variation can promote or constrain the speed of adaptation, and influence the future evolutionary trajectory a population. We are combining empirical population genomic analyses with theoretical population genetic models of selection-migration balance and selective sweeps from standing genetic variation in order to identify and quantify key factors that influence rapid adaptation in natural stickleback populations.

3. Comparative Functional Genomics and Genome Evolution (JONES - MPG) We are identifying and comparing functional genomic elements contributing to adaptive divergence and speciation by creating de novo assemblies and functional annotations from ChIP-seq, captureC, RNAseq, mapping panels and signatures of selection from hundreds of whole genome datasets from sequenced families and wild-caught individuals.

4. Systems biology of evolution in mice (CHAN - MPG & ERC) We have a number of mapping panels and resources, ranging from large Faroese wild mice, including whole-body morphometrics measurements, to innovative “in vitro” crosses derived from mouse interspecific hybrid stem cells. Using these resources we aim to understand the genetic architecture for adaptive traits and the evolution of gene regulatory networks.

5. Genomics of selection response in Longshanks mice (CHAN - MPG) Dr. Campbell ROLIAN at the Univ. of Calgary has performed 21 generations of artificial selection for increased tibia length in mice (2 “Longshanks” selection lines & 1 control line, >6000 individuals). We will study the selection response from multiple angles, ranging from trait mapping, population genomics, theory (in collaboration with Nick BARTON, IST Austria) to developmental genetics. With this dataset we aim to establish the dynamics of the genotype-phenotype map under strong selection.

Requirements: We invite applications for the above positions at the PhD level. You will have, or are about to complete your MSc or 4-year BSc or equivalent degree. You will have training in genomics, bioinformatics or statistical genetics and hands-on research experience in these fields. You should demonstrate expertise and proficiency in one or more of the following areas:

â handling and analysis of NGS datasets (whole genome, single-cell/molecule sequencing, RNASeq, ChIP-seq, 3C/4C)

â advanced skills in statistical genomics (e.g. QTL or GWAS approaches, genotype imputation, Hidden Markov Models, and haplotype phasing of whole genome data

â de novo genome assemblies and comparative genomics.

â empirical and theoretical population genetics

â familiarity with parallel computing, visualisation of genomic datasets and associated toolkits (e.g. UCSC/Ensembl genome browsers, proficiency with web-based programming and SQL relational databases desirable)

Experience with UNIX and fluency in statistical and/or programming languages is essential (R, Python or Perl, required; C++, SQL, java knowledge desirable). Wetlab skills and experience in other types of data

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MelbourneU GenomeDynamics

Genome dynamics following chloroplast endosymbiosis

The Verbruggen lab at Melbourne University, Australia, is looking for a motivated PhD candidate to work on a project investigating genome dynamics following chloroplast endosymbiosis.

You will study two algal groups, chlorarachniophytes and the green dinoflagellates, both of which have undergone eukaryote-eukaryote (secondary) chloroplast endosymbiosis. Comparative analyses will be carried out to characterise and quantify the changes that occur in the host and endosymbiont genomes during and following secondary endosymbiosis. The project involves generation of genome and transcriptome data, as well as bioinformatic analyses such as genome assembly/annotation, molecular phylogenetics, and modelling of genome evolution.

To be successful you will:

- satisfy the requirements for a PhD degree at the University of Melbourne (http://science-courses.unimelb.edu.au/study/degrees/doctor-of-philosophy-science/overview#overview) - have experience in generating and managing DNA sequences - have a strong interest in evolutionary biology and mathematical modeling - have strong oral and written communication skills

You will be living and working in Melbourne, named as the world's most liveable city for the fifth year running in 2015. The Verbruggen lab is located within Melbourne University's School of Biosciences (http://biosciences.unimelb.edu.au/), providing a vibrant and supportive working environment. To find out more about the lab, go to http://www.phycoweb.net . To apply, please send your CV, a representative piece of English writing (e.g. MSc thesis), and the names and contact information of two or more references (at least one previous supervisor) to jackson.c@unimelb.edu.au. Informal enquiries are welcome. Cut-off date is 30th April 2016.

cjackson1245@gmail.com

MNHN Paris EvolutionWings OrthopteraInsects

MNHN_Paris_EvolutionWingsOrthopteraInsects

Funded PhD project :**Wings for what? Evolution of forms and functions of the orthopteran wings

The Ecole Doctorale of the MNHN supports a three-year PhD project on the evolution of the form and the function of the wings in Orthoptera insects. This project will be located in the MusÂÂum national d'ÂHistoire naturelle, Paris (France), in the CNRS team ISYEB (Institut de SystÂÂmatique, Evolution et BiodiversitÂÂ). It will be supervised by AndrÂÂ Nel (MNHN Professor) and Laure Desutter (MNHN Professor). We are looking for a highly motivated and inquisitive student, who will explore the diversity of the wings in both modern species and fossils taxa of Orthoptera, using 3D imaging. The student will collaborate to molecular projects about Orthoptera phylogeny to test hypotheses of wing evolution.

**

Scientific context :

The relation form - function is crucial in evolutionary biology. It allows understanding the adaptation of the organisms thanks to the modification of the structures or their maintaining with acquisition of different functions. The structure of the orthopteran wings is a remarkable model because they are the most diversified ones among fossil and recent insects, and because they are implied in key functions (flight, communication, reproduction). After recent hypotheses, their evolutionary history seems to be complicate, implying structural and functional convergencies and parallelisms. But none of these hypotheses is well-funded on refutable homologies of wing characters, either for modern species, or for fossil taxa, which are numerous and well-preserved among Orthoptera. Six models of venation is currently used, rendering unstable the systematic of the clade and making problems for the reconstruction of its evolutionary history.

Because they are long and very thin structures, the wings have always been studied in two dimensions, by simplification. Microtomography X-rays allowed us to restore the diversity of wings in three dimensions despite their low thickness and to fill these gaps: established for some taxa, these results provide the tools needed to review the orthopteran wing venation. As for the relation between the venation and the function, it can be explored by multivariate analyzes of forms (ongoing study on a Permian leaf-like wing of katydid). In parallel, recent phylogenetic developments provide the necessary basis of the phylogeny of modern Orthoptera (Muggleston et al 2013, Song et al 2015, Chintauan-Marquier et al 2016): An extensive molecular phylogeny of Orthoptera is underway, with Recent developments in NGS (Chintauan-Marquier et al, in progress).

The aim of the PhD is to test hypotheses on the evolution of wings (venation) and functions (forms) in Orthoptera, reviewing the venations of living and fossil taxa. The phylogenetic framework of reference established by the molecular tool, will be complemented with wing characters for modern and fossil species: the student will be in charge of the morphological part and will participate in molecular developments without work at the bench. The influence of environmental changes, in particular the emergence of the modern flora, on patterns of diversification will be tested.

Our team is ideally located for the realization of the subject: we have established a new method of study of the wing pattern; we propose a new pattern of venation, established on some taxa, but tested on fossils; and we have an extensive knowledge of the modern and fossil diversity of the clade. Finally, we participate in developments on the molecular phylogeny of the Orthoptera, for our own work and through collaborations already well underway.

Profile :

The student will work with both fossils and modern species of Orthoptera. He will be or agree to train to become independent for the reconstruction of 3D segmentation cuts. He must also have a thorough knowledge of the concepts of phylogenetic analysis, in order to complete molecular data set with morphology, and to test patterns of diversification.

Schedule :

The PhD will start in october 2016. Application file should contain a CV, a cover letter, Master score sheets, and two recommendation letters. Complete application files must be sent to anel@mnhn.fr and desutter@mnhn.fr before May 10th. Selected candidates will be interwiewed around May 20th.

Laure Desutter-Grandcolas

Institut de SystÂÂmatique, Evolution et BiodiversitÂÂ

(UMR 7205 CNRS/MNHN/UPMC/EPHE)

MusÂÂum nationald'ÂHistoire naturelle, Sorbonne UniversitÂÂ

45 rue Buffon

75005 Paris

desutter@mnhn.fr

+33 1 40 79 34 02

Laure DESUTTER <desutter@mnhn.fr>

MonashU EvolutionaryTheory

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

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

Successful candidates will be fully funded for the duration of the PhD, and with no teaching requirements. The annual stipend is $26,288 per year (tax free). Additional expenses for research, coursework, and conference attendance will also be covered. Both Australian/NZ domestic and international students are eligible to apply.

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

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

tim.connallon@monash.edu

MonashU EvolutionSexDifferences

PhD on the evolution of sex differences

A fully-funded position (salary and research costs) is available in the research group of Dr Damian Dowling, to pursue a project pertaining to the evolutionary basis of sex differences in life histories. The project will involve experiments that unravel the genetic and environmental factors that facilitate (or constrain) the evolution sex differences in traits such as fertility and longevity. Experiments will use natural populations of the fruit fly (*Drosophila melanogaster*).

The project will integrate techniques of experimental design drawn from evolutionary biology, ecology, genomics and physiology. There will be full flexibility for the successful applicant to pursue their own academic ideas and interests within the scope of the project.

The successful applicant will be highly motivated, and passionate about evolutionary biology; familiar with basic evolutionary concepts, understand the core tenets of experimental design, and have strong quantitative skills. Some expertise or interest in evolutionary genomics is desirable, but not essential.

The applicant will join a vibrant research group comprised of PhD students and postdoctoral researchers, perfect for the pursuit of academic excellence and professional development, with access to state-of-the-art technology platforms for the study of evolutionary ecology and genomics.

The position includes funding for international and national conference visits, and for all research costs. The successful applicant will be awarded a scholarship that covers salary (current rate is $26,288 tax-free per year), and full waiver of fees, and can choose to supplement their salary through teaching assistance during undergraduate lab courses run by Dowling and colleagues.

Monash University is a member of Australia's Group of Eight a coalition of research-intensive universities, and is internationally recognized for excellence in research and teaching. The School of Biological Sciences (http://monash.edu/science/about/schools/biological-sciences/) is home to a collegial and world class research environment, with key strengths in evolutionary ecology and genomics.

Monash is located in Melbourne, a vibrant cultural and recreational centre, and is consistently rated one of the world's most liveable cities (http://en.wikipedia.org/wiki/World's_most_livable_cities).

Application process

Interested candidates should send their CV, academic transcript, and a cover letter outlining their research interests to damian.dowling@monash.edu

Your initial applications need to be received before 1st May 2016

For further information on these scholarships and Monash application procedures, please visit http://monash.edu/science/about/schools/biological-sciences/postgrad/ For further information on the research group of Damian Dowling, visit http://damiandowlinglab.com Review of applications will commence immediately, with applications closing on 1st May 2016

Damian Dowling

Email: damian.dowling@monash.edu

Website: damiandowlinglab.com

Google scholar: http://scholar.google.com.au/citations?user=QwJLmTgAAAAJ&hl=en Twitter: @DK_Dowling

"damian.dowling@monash.edu"
<damian.dowling@monash.edu>

MonashU EvolutionSexualDimorphism

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

Successful candidates will be fully funded for the duration of the PhD, and with no teaching requirements. The annual stipend is $26,288 per year (tax free). Additional expenses for research, coursework, and conference attendance will also be covered. Both Australian/NZ domestic and international students are eligible to apply.

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

To apply, please send a CV, academic transcript, and a brief outline of research interests to tim.connallon@monash.edu. Informal inquiries are welcome. Applicants must hold a Bachelors degree with first-class honours, or a masters degree. Review of applications will begin immediately, and short-listed candidates will be contacted to set up phone/Skype interviews.

tim.connallon@monash.edu

MonashU MitoNuclearEcol

PhD in mito-nuclear ecology

A fully-funded position (salary and research costs) is available in the research group of Dr Damian Dowling, to investigate the evolutionary coevolution between mitochondrial and nuclear genomes, and the ramifications for ageing, speciation, and sexual conflict.

"Mito-nuclear ecology" is a rapidly emerging field, which has grown from the realization that the genes inside of our energy-producing mitochondria, may make surprisingly large contributions to the evolutionary dynamics of populations.

The project will integrate techniques of experimental design drawn from evolutionary biology, ecology, genomics and physiology. There will be full flexibility for the successful applicant to pursue their own academic ideas and interests within the scope of the project.

Successful applicants will be highly motivated, and passionate about evolutionary biology; familiar with basic evolutionary concepts, understand the core tenets of experimental design, and have strong quantitative skills. Some expertise or interest in evolutionary genomics is desirable, but not essential.

The applicant will join a vibrant research group comprised of PhD students and postdoctoral researchers, perfect for the pursuit of academic excellence and professional development, with access to state-of-the-art technology platforms for the study of evolutionary ecology and genomics.

The positions include funding for international and national conference visits, and for all research costs. The successful applicant will be awarded a scholarship that cover s salary (current rate is $26,288 tax-free per year), and full waiver of fees, and can choose to supplement their salary through teaching assistance during undergraduate lab courses run by Dowling and colleagues.

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

Monash is located in Melbourne, a vibrant cultural and recreational centre, and is consistently rated one of the world's most liveable cities (http://en.wikipedia.org/-wiki/World's_most_livable_cities).

Interested candidates should send their CV, academic transcript, and a cover letter outlining their research interests to damian.dowling@monash.edu

Your initial applications need to be received before *1st May 2016*

For further information on these scholarships and Monash application procedures, please visit http://monash.edu/science/about/schools/biological-sciences/postgrad/ For further information on the research group of Damian Dowling, visit http://-damiandowlinglab.com Review of applications will commence immediately, with applications closing on 1st May 2016

Damian Dowling

Email: damian.dowling@monash.edu

Website: damiandowlinglab.com

Google scholar: http://scholar.google.com.au/-citations?user=QwJLmTgAAAAJ&hl=en Twitter: @DK_Dowling

"damian.dowling@monash.edu"
<damian.dowling@monash.edu>

NordU Norway EvolutionaryGenomics

PhD fellowship (3 years) in Evolutionary Genomics

A three-year PhD fellowship in Evolutionary Genomics is available at the Faculty of Biosciences and Aquaculture, Nord University (BodÃ, Norway) from 1 September 2016.

About the PhD fellowship —– FBA invites applications from outstanding candidates for a three-year PhD fellowship within the project "Genomics of speciation, what can we learn from an algae".

The macroalgal genus Fucus (Phaeophyceae, Heterokonta) is an ideal taxonomic group in which to study mechanisms of speciation. Three hybrid zones involving Fucus serratus and F. distichus have been identified in the Central/East Atlantic. The zones consisted of a natural zone in Northern Norway (ca. 10,000 yrs of sympatry), and two others resulting from the introduction of either species. A recent study of the F. serratus / F. distichus contact zones has found strong evidence for reinforcement of prezygotic isolation. The central aim of this project is to understand how reinforcement and the underlying mechanisms of selection promote speciation at the molecular level in Fucus using Next Generation Sequencing technologies to identify 'speciation genes' within allopatric and sympatric distributions of populations and species for which the ages of contact are known to vary in spans of 100s to 10,000 years

Qualifications and requirements —– The candidate should have an MSc degree (or equivalent) in Biology in one of the following fields: ÂGenomicsÂEvolutionary BiologyÂMolecular Ecology

The grades at the qualifying MS examination needs to be C or better (ECTS scale from A-E) with exam date preferable no later than 15 July 2016.

Hands-on experience with genomics, next-generation sequencing and bioinformatics are required. Proficiency in oral and written English is essential and must be documented either by the Norwegian Higher Education Entrance Qualification or internationally recognized certificates, such as TOEFL, IELTS, APIEL or similar. Knowledge of a Scandinavian language will be beneficial for the position.

The successful candidate will join the PhD programme in Aquatic Biosciences at Nord University and is expected to complete a doctorate within the three-year project period. The candidate should fulfill the admission requirements of this PhD programme at FBA and participate in the training components stipulated in regulations of the PhD programme. Application for admission to the programme must be submitted within three months after taking up the position. For admission requirements and regulations, see our web page. We are looking for highly motivated, creative and ambitious applicants with an excellent academic record and the ability to collaborate with other members of a multidisciplinary team whilst developing their own research project.

Salary and Working Conditions —– The salary for PhD candidates is set at wage level 50 in the Norwegian State Salary Scale (approximately NOK 430 500 per year).

As an employee at the Nord University you become a member of the Norwegian Public Service Pension Fund and you will also get access to other social benefits. A statutory amount to the Norwegian Public Service Pension Fund will automatically be deducted from the salary.

The successful person must abide by the laws, agreements and directives that apply to the position at any time. According to the employment policy of the institution, our staff should reflect the population in general. We encourage candidates with minority background to apply for the position. The University practices moderate allocation according to sex quotas in accordance with the Basic Agreement for the Civil Service.

Contact Information ——————- For further information about the position, please contact professor Galice Hoarau e-mail: Galice.g.hoarau@nord.no). Questions related to the application process should be addressed to the office manager Irene Stork Wisth (e-mail: irene.s.wisth@nord.no; telephone +47 75 51 74 42).

The Faculty has as policy to evaluate relevant enclosed documentation. The evaluation will be done by the Norwegian Agency for Quality Assurance in Education - NOKUT. The evaluation will be used in connection with admission to a PhD program. Applicants with foreign education have to fill in and sign a consent form from NOKUT.

Application —— Applications must be submitted electronically by Monday, 9 May 2016. Applicants for this position are requested to include the following information:

Cover letter outlining the candidate's suitability for this position, relevant experience and how she/ he will contribute to the successful implementation of the project (maximum 1 page)

Curriculum vitae, including a list of publications (maximum 3 pages)Certified copies of academic degree transcripts and any other relevant qualificationsContact details for at least two refereesSigned consent form

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NordU Norway NonModelNGS May31-Jun10

PhD course: High throughput sequencing of non-model organisms

Faculty of Biosciences and Aquaculture, Nord University, Norway. May 31 - June 10, 2016

High throughput sequencing (HTS) technologies are being applied to a wide range of important topics in biology. However, the analyses of non-model organisms, for which little previous sequence information is available, pose specific problems. This course will address the specific strengths and weaknesses of alternative HTS technologies, the computational resources needed for HTS, and how to analyze non-model species using HTS. The course consists of practical training in preparing and running fragment libraries, HTS bioinformatics training, and lecturing/seminars of HTS approaches specifically targeting non-model organisms.

Please find a course description and application form here: http://www.nord.no/en/news-events/calender/Pages/PhD-course-High-throughput-sequencing-of-non-model-organisms.aspx We will accept a maximum of 10 students. The closing date for applications is April 29.

If you have questions regarding the course, please contact Prof. Truls Moum at truls.b.moum@nord.no

Jeanett Kreutzmann <jeanett.kreutzmann@nord.no>

SouthernIllinoisU PoisonFrogEvolution

Evolutionary Ecology of South American Poison frogs (genus Ameerega) Zoology Department, Southern Illinois University Carbondale, Carbondale, IL.

A graduate position (either Masters or PhD) is available to study the evolutionary ecology of S. American poison dart frogs (genus Ameerega). Neotropical poison frogs are a species-rich family (Dendrobatidae) that exhibit a diversity of mating systems, parental care strategies and phenotypes. The Brown lab is looking for a student to develop a research program studying ANY core aspect of the lab's research. Topics could include color/pattern evolution, breeding ecology, phylogeography/ biogeography, systematics and speciation (to name a few). The ideal student will be prepared to conduct field-based research, have some experience in molecular ecology/population genetics and/or geospatial analyses.

For more information on the Brown Lab please visit the lab website at: http://www.jasonleebrown.org and the Zoology Department at SIUC http://www.zoology.siu.edu. Students will find all the brains of a nationally ranked research university and all the heart of a small college at SIUC.

Carbondale is located in Southern Illinois and provides a close link to many forested areas and lakes. The regional landscapes varies from bottomlands to uplands with rolling hills, bluffs, and rugged topography. This makes it perfect home for outdoor lovers (when they are not in the rainforest's of S. America). For more info on the city of Carbondale go to http://explorecarbondale.com Interested students are encouraged to contact Dr. Brown (jason.brown@siu.edu). Please include a brief description of your research interests, a CV, and names of two references (with contact info). Competitive funding options are available for both US students as well as international students. Start date of position is August 2016 (or earlier).

Jason Brown <jason.brown@siu.edu>

StockholmNHM Conservation Palaeogenomics

PhD student position in Conservation Palaeogenomics

Swedish Museum of Natural History & Stockholm University

PROJECT DESCRIPTION Species that today are threatened by extinction have typically gone through severe declines in population size during the last 100 years. These demographic declines have likely been accompanied by losses of genetic variation, increases in inbreeding levels, as well as increases in the frequency of deleterious alleles. Yet, there is no strong relationship between these genetic parameters and current population sizes in endangered species. This is because levels of genome-wide diversity in species appear to be more strongly affected by their life histories and ancient demographic events compared to recent changes in population size. The aim of this PhD project is to circumvent this issue by using a palaeogenomic approach to directly quantify the rate of change in genome-wide diversity in declining populations. This will be done through comparisons of complete genome sequences from modern-day samples and from museum samples that are hundreds of years old, which thus predate the demographic declines. The studies will comprise critically endangered carnivores, primates, birds and rhinos and will involve the use of state-of-the-art ancient DNA technology, advanced computational genomics, as well as an opportunity to take an active part in influencing current policies and guidelines in conservation biology. For this project, good knowledge in population genetics, bioinformatics as well as experience of laborative DNA analysis are important qualifications. The PhD project will be supervised by Professor Love Dalén at the Department of Bioinformatics and Genetics, Swedish Museum of Natural History. For more information about the research group, please visit www.palaeogenetics.com/adna ENVIRONMENT The PhD student will be employed by Stockholm University (Department of Zoology), but will be based at the Department of Bioinformatics and Genetics at the Swedish Museum of Natural History (SMNH). The museum is located in Stockholm, which by many is regarded as one of the most beautiful capitals in the world and is home to a vibrant scientific community with several leading research institutes, including the Science for Life Laboratory. The SMNH has a strong mission in natural history research, and its research division has more than 170 employees. The department of Bioinformatics and Genetics hosts three research groups, focused on ancient DNA and population genetics (PI: Prof. Love Dalén), avian systematics and biogeography (PI: Dr. Martin Irestedt), and phylogenomics (PI: Prof. Fredrik Ronquist).

QUALIFICATIONS To be qualified for this PhD studentship, the applicant must have completed a research degree (e.g. Master's), or have passed at least 120 hp (2 years) of biological studies, including an approved independent project of at least 30 hp at advanced level within systematics and evolution, ecology, population genetics, bioinformatics or a similar subject. Applicants who have in principle acquired the corresponding competence in Sweden, or abroad, are also qualified. Only a person who will be or has already been admitted to a third-cycle programme may be appointed to a doctoral studentship. The primary assessment criteria in appointing a doctoral student should be the capacity to benefit from the training. In order to meet the general entry requirements, the applicant must have completed a second-cycle degree, completed courses equivalent to at least 240 higher education credits, of which 60 credits must be in the second cycle, or have otherwise acquired equivalent knowledge in Sweden or elsewhere.

SELECTION Among qualified applicants, selection is made according to the ability to profit from the studies. The criteria to be used are properly documented competence within the described research area, capabilities with regards to speaking and writing in English, analytical thinking, creativity, initiative, independence, and team work performance. The applicant's earlier experience within the field of research can be of relevance especially when further documented by university courses, independent research works, personal references, interview and an application indicating the applicant's motivations in written form.

TERMS OF EMPLOYMENT The four year PhD program includes three years of research and one year of course work. Salary follows the agreement for PhD positions at Stockholm University.

CONTACT For questions about the position and further information about the project, contact Prof. Love Dalén, Email: love.dalen@nrm.se

HOW TO APPLY Applications should be done using Stockholm University's online application system. Please follow the link below to obtain further information about how to write your application and how to access the online application system:

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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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StockholmU PlantInteractions

Dear colleagues,

We seek two highly motivated PhD-students to join the long-term research on the pedunculate oak / coffee.

1. The interactions among fungal pathogens, insects and endosymbionts on oak: http://www.su.se/english/about/vacancies/vacancies-new-list?rmpage=job&rmjob=1334&rmlang=UK 2. PhD student in Plant Ecology: Pest and Pathogens on Coffee at the Agro-ecological Interface http://www.su.se/english/about/vacancies/vacancies-new-list?rmpage=job&rmjob=1306&rmlang=UK The positions are in the Department of Ecology, Environment and Plant Sciences at Stockholm University. The closing date for applications is May 2.

Please don't hesitate to contact us directly by email,

My best,

Ayco Tack & Kristoffer Hylander ayco.tack@su.se kristoffer.hylander@su.se

1. PhD student in Plant Ecology: Interactions between Plants, Microbes and Insects The position will be associated with the long-term research on insect and pathogen dynamics on wild plants in the research group of Ayco Tack. The overall aim of the research is to understand the role of plant-microbe-insect interactions in structuring plant-based communities in nature. The core of the PhD project is to investigate the role of insect microbes (endosymbionts) and plant-based microbes (endophytes, pathogens) in understanding the spatial and temporal dynamics of the diverse insect and pathogen community on the oak tree Quercus robur. The main tasks include field work (field sampling and surveys, dataloggers) and laboratory work (molecular identification of the endophytes and insect endosymbionts). The work may also involve experiments where the microbial community on the leaves or roots is manipulated. The exact direction of the project will depend on the skills and interest of the applicant.

2. PhD-position in Plant Ecology at Stockholm University (coffee, pests, Ethiopia) The position will be associated with the project "Managing coffee to increase farmer's livelihood and biodiversity in Ethiopia" with is financed by SIDA. The aim of the project is to increase the knowledge of how to manage coffee systems for positive synergies between biodiversity and farmer's incomes. The core of the project is to investigate plant-fungal interactions of major coffee pathogens along a gradient in management intensity. Along this gradient we will investigate fungal infestation rates, coffee yields, coffee genetic variation and various measures of biodiversity and management. The field work will take place in Ethiopia but the position is placed at Stockholm University.

Ayco Tack Assistant professor Department of Ecology, Environment and Plant Sciences

Stockholm University SE-106 91 Stockholm, Sweden Visiting address: Svante Arrhenius Väg 20A, room N420 Phone: + 46-(0)8-163959 Mobile: + 46-(0)70-4942557 ayco.tack@su.se

www.plantmicrobeinsect.com www.su.se/profiles/atack www.su.se/profiles/atack

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Tahiti MarineGenomics

PhD position in marine genomics

- Project title: Diversity and color variation in the pearl oyster Pinctada margaritifera: characterisation of the phenome, genome and epigenome.

- Location: Ifremer, Centre du Pacifique, Vairao, Tahiti, French Polynesia.

- Project description: The color diversity of marine mollusks'shells has been intriguing both scientists and non-scientists for a long time. Marine mollusks are an important part of the ecosystem and are a major economical resource in many countries. In French Polynesia, the production of cultured pearls through the aquaculture of Pinctada margaritifera represents the second biggest economical resource of the country (the first being tourism). There is a growing interest in optimizing this aquaculture through the improvement of the pearl quality, and the use of color-selected oysters families to control the final color of the pearl.

Previous investigations demonstrated a link between the shell color of the donor oyster and the color of the pearl subsequently harvested from the recipient oyster. The environment (e.g. depth of cultivation) also has an impact on the intensity of the color of the pearl being produced. Despite these recent discoveries, the molecular mechanisms involved in the expression of the color phenotype, as well as the heterogeneity in the distribution of the color phenotypes in wild populations are still not understood.

In this context, we propose to investigate this question using data at the genomic, transcriptomic and epigenetic level, using individuals within cultivated and wild populations. The student will mostly work with NGS generated data, but the project also has an experimental component (epigenetic aspects) and a field component to sample natural populations.

- Research environment: Ifremer (French Research Institute for Exploitation of the Sea) contributes to the knowledge of the ocean and their resources, through the monitoring of marine and coastal environments and the sustainable development of marine activities. Ifremer performs targeted applied research to address the questions posed by society (climate change effects, marine biodiversity, pollution prevention, seafood quality...).

The Ifremer Pacific Center (COP) is based in Vairao in Tahiti, French Polynesia. With 40 agents mobilized onsite, the French Polynesia Marine Resources (RMPF) research team focuses on the sustainable development of marine exploitation in French Polynesia. The largest research project is linked to a partnership with the perliculture professionals in order to improve the quality of cultured pearls, and study the adaptative response of the pearl oyster facing changing environmental conditions (temperature, ocean acidification, pollution).

The successful candidate will be integrated in a dynamic and young joint research unit, the UMR 241 “EIO” (Oceanian Island Ecosystems) gathering researchers from Ifremer, UPF (University of French Polynesia), IRD (French Research Institute for Development), and ILM (Louis Malard?? Institute).

- Candidate’s profile We encourage applications from candidates with solid knowledge in at least two of the following disciplines: population genetics, evolutionary genetics, bioinformatics, biostatistics, genomics, transcriptomics, epigenetics. Knowledge of the R language is strongly advised, and other scripting languages (for NGS pipelines implementation) are a plus.

- Application instructions: To apply, please send a motivation statement describing your interests in applying for the position, a resume, and contact details for at least two references to Celine.Reisser@ifremer.fr before the 1st June 2016. Interviews will be hold mid-June.

Celine REISSER <Celine.Reisser@ifremer.fr>

TrentU WildlifeGenomics

PhD Position in mountain goat evolution and ecology Location: Trent University (Peterborough, Ontario, Canada) We are seeking a motivated PhD student with interests in ecological genomics, wildlife conservation and management. The candidate will be working in a collaborative project between the lab of Dr. Aaron Shafer at Trent University and the Alaska Department of Fish and Game. The project will use cutting-edge genetic and genomic data to better understand population-level processes in mountain goats: see https://en.wikipedia.org/wiki/Mountain_goat. The successful candidate will undertake research in bioinformatics, wildlife genomics, and population genetics, with sampling in remote areas of Alaska likely to occur.

Applicants with experience/interest in different computer languages (UNIX, perl, R) and seeing the study species in the field are desirable.

The student will be enrolled in the Environmental Life Science Graduate Program at Trent University and join the laboratory of Dr. Aaron Shafer (www.aaronshafer.ca). Trent University is located in Peterborough, Ontario, which is also home to the main office of the Ontario Ministry of Natural Resources. Peterborough is nicely situated south of Algonquin Park and east of Toronto, and has a vibrant cultural and emerging food scene (http://www.designsponge.com/2016/04/peterborough-on-city-guide.html).

Application information: Funding is available for Canadian students. International students are welcome to apply, but restrictions may apply. Please consult: http://www.trentu.ca/graduatestudies/ . If you wish to apply, please send a one-paragraph cover letter describing your background and interests to: aaronshafer@trentu.ca. Please attach to the email your Curriculum Vitae, academic transcripts (unofficial is acceptable), and contact information for two references. Review of applications will begin 01 May 2016 and continue until the position is filled. Anticipated start date is Fall 2016. Informal and MSc inquiries are also welcome.

– Aaron Shafer, Assistant Professor Trent University

aaron.shafer@ebc.uu.se aaron.shafer@ebc.uu.se

UArkansas EvolutionaryBiology

Ph.D. positions, Program in Ecology and Evolutionary Biology, Department of Biological Sciences, University of Arkansas

Several Ph.D. positions are available for motivated students interested in the study of genomic variation in Drosophila species, transcriptomes, and inversion polymorphism. In collaboration with colleagues at Stanford University, University of Iowa, and other international scientists, the positions are centered in the lab of William J. Etges (http://comp.uark.edu/˜wetges/EtgesHP/Etges_Lab.html).

Project 1) Diapause genetics of Drosophila robusta and D. americana. The genetic basis and transcriptome profiling of natural populations of these two broadly overlapping North American species will reveal the genomic basis of overwintering in temperate climates, extension of lifespan under diapause conditions, and help to decipher recent genetic responses to climate change. The project includes genome (re)sequencing of these two species, comparative gene mapping, and assessment of linkage disequilibrium patterns to document the consequences of inversion polymorphism, recombination rate variation, and nonrandom associations of gene arrangements on genome evolution.

Project 2) Life history genomics. We will study how life histories and their evolution are shaped by the dynamic interaction of genes and environments over the life cycle. Genomic variation underlying life histories is composed of dynamic genetic networks that change over the course of ontogeny, and often determines correlations between traits across the life cycle. We will identify differences in gene networks that give rise to different life histories and expression of networks that change with stage and age. Assessing multiple, sequenced genomes of diverged populations of D. mojavensis will aid in understanding transcriptional plasticity.

Relevant publications include: Carson, H. L., and H. D. Stalker. 1948. Reproductive diapause in Drosophila robusta. Proceedings of the National Academy of Sciences (USA) 34:124-129.

Etges, W. J., C. de Oliveira, S. Rajpurohit, and A. G. Gibbs. 2016. Preadult life history variation determines adult transcriptome expression. Molecular Ecology 23:741-763.

Etges, W. J., C. C. de Oliveira, M. A. F. Noor, and M. G. Ritchie. 2010. Genetics of incipient speciation in Drosophila mojavensis. III. Life history divergence and reproductive isolation. Evolution 64:3549-3569.

Etges, W. J., M. V. Trotter, C. C. d. Oliveira, S. Rajpurohit, A. G. Gibbs, and S. Tuljapurkar. 2015. Deciphering life history transcriptomes in different environments. Molecular Ecology 24:151-179.

McAllister, B. F., S. L. Sheeley, P. A. Mena, A. L. Evans, and C. Schlötterer. 2008. Clinal distribution of a chromosomal rearrangement: a precursor to chromosomal speciation? Evolution 62:1852-1865.

Reis, M., F. B. Valer, C. P. Vieira, and J. Vieira. 2015. Drosophila americana diapausing females show features typical of young flies. PLoS ONE 10:e0138758.

Students with interests and experience in programming (Linux, Perl), genome assembly, transcriptomics, and a desire to merge natural history, evolutionary biology, and genomics are encouraged to apply. For more details and questions, email wetges (at) uark.edu.

William J. Etges Program in Ecology and Evolutionary Biology Department of Biological Sciences SCEN 632 1 University of Arkansas Fayetteville, AR 72701 USA voice: (479) 575-6358 lab: (479) 575-7437 FAX (479) 575-4010

Lab: http://comp.uark.edu/˜wetges/EtgesHP/Etges_Lab.html ResearchGate: https://www.researchgate.net/profile/William_Etges Google Scholar: http://scholar.google.com/citations?update_op=verify_email&hl=en&user=KXeh3m0AAAAJ&email_for_op=wetges%40uark.edu&citsig=AMstHGQMVYq4dJnVZnYtBLi09mXTijslCw

Program in Ecology and Evolutionary Biology http://comp.uark.edu/˜wetges/EtgesHP/E%26E_Program.html "William J. Etges" <wetges@uark.edu>

UBasel 2 SpeciesRanges

2 PhD positions on species range limits

University of Basel, Switzerland

* Research topic

Why do species have restricted distributions? - A so far overlooked reason is that range edge populations are commonly small or have a history of serial bottlenecks from previous range expansions. Both scenarios are predicted to lead to the accumulation of deleterious mutations. This genetic load may badly position range edge populations to react to climate change because population growth rates are too low.

* Approaches

The research will involve a crossing experiment with plants of the North American Arabidopsis lyrata from populations at the distribution edges and center. We will assess performance in garden experiments at both range edges and core areas. This part of the work will be done at five places in the eastern USA, in collaboration with local Universities and Botanical Gardens.

* Your profile

Candidates should have an enthusiastic interest in plants and their evolution and a strong background in quantitative thinking, experimental design, statistical analysis, and rearing plants. Applicants must have a university degree in the natural sciences that allows entrance to a PhD program (ideally in evolutionary biology or ecology), and very good organizational, analytical, and scientific writing skills.

* We offer

The project is based at the Department of Environmental Sciences, University of Basel, Switzerland. The Department offers a stimulating environment, including a rich spectrum of research activities in life sciences (plant ecology, population genetics, evolutionary biology, plant physiology and molecular and cell biology). PhD students will be enrolled in the PhD program of the Zurich-Basel Plant Science Center. Finally, Basel is a mid-sized Swiss city, well connected and offering a broad range of cultural and recreational activities.

* Further information and application

For more information, contact Yvonne Willi (yvonne.willi@unibas.ch). Motivated applicants should submit (1) a one-page letter that summarizes interests and relevant experience, (2) their CV, (3) copies of undergraduate and masters/diploma transcripts, and (4) contact information of two references (all as a ***single PDF***) to: franziska.grob@unibas.ch. Applications are welcome until the position is filled and will be reviewed starting on May 27, 2016.

Yvonne Willi <yvonne.willi@unibas.ch>

UBasel 2 SticklebackAdaptationGenomics

2 PhD positions in evolutionary genomics at the University of Basel

OVERVIEW The research group of Dr. Daniel Berner at the Zoological Institute of the University of Basel offers two PhD positions focusing on the genomic basis of adaptive diversification in threespine stickleback fish. The three-year positions are fully funded by the Swiss National Science Foundation (SNF) known for generous salaries, and can start as soon as the candidates have been chosen.

FOCUS The successful candidates will investigate molecular signatures of natural selection and the genetic basis of adaptive phenotypic variation in natural populations of threespine stickleback adapted to ecologically different habitats. This work, making use of one of the top model systems in evolutionary genomics, will involve molecular bench work (for RAD and full genome sequencing) and extensive bioinformatic data analysis. In addition, depending on individual interests and skills, the projects might be developed to further include field, lab and in-silico experiments, and functional genetic analysis.

PROFILE OF CANDIDATES Students applying for the positions should hold a master degree in biology, possess excellent verbal and written English expression skills, enjoy theory-driven empirical work, and be highly motivated to acquire programming competence. Experience in molecular bench work and/or programming (e.g., R, Python) is considered an asset but is not required; applications from diverse research backgrounds are encouraged.

APPLICATION Applications and queries should be sent to daniel.berner@unibas.ch. The application should be prepared as a single pdf document including a concise letter of motivation (< 1 page), your CV (including the contact details of 2-3 referees), and a copy of your academic transcripts. The evaluation of applications will start on April 18 and will continue until suitable candidates have been found.

Dr. Daniel Berner Group leader Zoological Institute University of Basel daniel.berner@unibas.ch http://-salzburgerlab.org/team/daniel_berner/ Daniel Berner <daniel.berner@unibas.ch>

UCork 3 EvolutionaryEcolCognition

Up to 3 PhD positions in Animal Evolutionary Ecology: "The evolutionary ecology of cognition across a heterogeneous landscape"

Why do individuals vary in their cognitive abilities? EVOECOCOG, an ERC funded project, takes the disciplines of cognition and evolutionary biology into a natural setting to answer this question. It aims to do this by investigating a variety of proximate causes and population-level consequences of individual cognitive variation using a great tit Parus major population.

Three objectives capture the projects broad scope:

1. To characterise proximate causes of variation in cognitive and other associated traits

2. To examine links between these traits, key functional behaviours and trade-offs

3. To examine the consequences of this variation for life histories, fitness, natural and sexual selection.

State of the art observational (radio tracking and automated self-administration trials of learning in the wild), chemical (stable isotope analysis of diet), physiological (stress, energetics, immunocompetence), molecular (DNA fingerprinting and metabarcoding) and analytical (reaction norm, quantitative genetic) techniques will be used. The chosen study system, the great tit Parus major, is one of the most widely used in Europe, and will consist of 12 subpopulations across deciduous and conifer woodland fragments in Co. Cork, Ireland, and a recently established larger population in Killarney National Park, World Heritage Site. An existing aviary at the School of BEES will be replaced by a new aviary on the same site, funded with a Science Foundation Ireland ERC support grant.

This advert is for up to three 4-year PhD studentships. The successful students will be based in the UCC Ornithology lab at the School of BEES http://ornithology.ucc.ie. They will join a research team led by Prof. John L. Quinn, consisting of five early career biologists working on this project (see http://ornithology.ucc.ie/current-projects/-evolutionary-ecology-of-cognition/), a Research Support Officer, and a range of other students and postdocs working on a variety of different projects in behavioural and applied ecology.

PhD 1: ^{o}Cognitive plasticity: social, environmental and microbial causes of individual variation±. The aim of this studentship will be to characterise proximate causes of variation in cognitive and other associated traits (e.g. personality), among wild birds, all of which can influence ecologically important behaviour. Quantitative genetic, social, parasite-mediated, microbial, and a range of physiological causes are among the factors that may be explored.

PhD 2: ^{o}The functional significance of cognitive variation for individuals in the wild±. The aim here will be to assay cognitive abilities (e.g. spatial and temporal memory) to understand how individual differences in cognition and other closely related traits (e.g. innovativeness/personality) might influence functional behaviour, including foraging routines, anti-predation behaviour, and energetic trade-offs during reproduction.

PhD 3: ^{o}Sexually and naturally selected cognitive traits±. This PhD studentship position will focus on the interplay between cognition, sexual selection and natural selection. The student will investigate links between cognitive traits measured in the wild, physiological traits, and mate attractiveness, including sexually selected signal variation, reproductive success and extra-pair paternity.

The studentships will be cosupervised by Prof. J. Quinn, Dr Michael Reichert, Dr Gabrielle Davidson, and Dr Ipek Kulahci.

Candidates should possess a 2.1 BSc (Hons) degree or higher in a relevant discipline (e.g. Ecology, Zoology, Evolution, Physiology, Psychology). Applicants must be self-motivated with good numerical, communication, organisational, experimental design, and writing skills. Students with an MSc and direct experience working in relevant research areas are likely to have a strong advantage. A full, clean driving license will be essential early in the PhD (own car advantageous), and experience working with birds in captivity or in the wild would also be advantageous. A willingness to spend long periods of time in the field, and to travel and work across different research sites is important. This position covers EU fee rates (æ5,750 p.a.; non-EU members may apply but would need to cover extra international rate fees themselves), plus a tax-free stipend of æ16,000 p.a.

Please direct informal inquiries to Prof. John L. Quinn at j.quinn@ucc.ie

Application: To apply please send by email to Prof. John Quinn, j.quinn@ucc.ie a CV, details of 2 referees, and an accompanying 1 page letter. The letter should state which specific PhD(s) you are applying

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UGuelph EvolutionaryEcol

PhD Opportunity: Evolutionary Ecology of Icelandic Arctic Charr

Hólar University College, Iceland (Dr. Camille Leblanc), and University of Guelph, Canada (Prof. Moira Ferguson), seek a Ph.D. student to study *Microevolutionary processes in small populations of Arctic charr *(*Salvelinus alpinus*).

Numerous ecological and evolutionary processes contribute to the generation of biodiversity, and the complexity of their interactions has presented a challenge to our understanding of nature. Our knowledge of the roles of development, natural selection, genetic drift, and gene flow in shaping biodiversity is complicated by the spatial and temporal variability inherent in natural systems. A powerful approach to better understand such processes involves monitoring wild populations over generations and obtaining data including pedigrees, phenotype, and fitness, so that we can directly infer evolutionary parameters, particularly those describing selection and genetic variation. We are seeking a talented PhD student to apply such an approach to wild populations of Icelandic Arctic charr, in order to further our understanding of the complex interplay among genes, phenotypes, and ecology, in natural environments.

The successful PhD student will test important microevolutionary theories with individual-based phenotypic records, molecular genetic (SNP) data, and ecological data from 20 populations of Arctic charr residing in a spatially replicated system of lava caves in the MÃ½vatn area of northern Iceland. The monitoring of these populations began in 2012 and will now continue until 2018, providing an impressive long-term dataset for novel insights. Advanced analytical techniques will be used to understand spatial and temporal patterns of genetic variation, natural selection, and ecological covariates. The student will be based at the University of Guelph with Prof. Moira Ferguson but will spend considerable time at Hólar University College with Dr. Camille Leblanc (including annual fieldwork). Our ideal candidate will have interests in evolution, ecology, and genetics, and will have strong quantitative skills - necessary for the advanced analytical techniques used in this field. The student will be able to work independently and as part of a larger team, both in the laboratory and in the field. An MSc degree is preferred and the working language is English.

The project is a long term collaboration between the University of Guelph, Canada (Prof. Moira Ferguson), Hólar University College (Prof. Bjarni K. Kristjánsson, Prof. SkÃºli SkÃºlason and Dr. Camille Leblanc), the University of Iceland (Prof. SigurÃ°ur S. Snorrason, and Prof. Ãrni Einarsson), EAWAG, Switzerland (Dr. Katja Räsänen), and the University of St Andrews (Dr. Michael Morrissey). The project is funded by The Icelandic Science Foundation - Rannís. The position will be filled as soon as a good candidate is found (target date 1. June 2016).

Applicants should send an application letter with a max. 1 page statement of research interests and relevant experience, a curriculum vitae with a list of publications (if any), copies of academic qualifications including copies of unofficial transcripts and the names and e-mail addresses of three referees, as a single pdf file to Dr. Camille Leblanc (camille@holar.is) before *April 30th 2016*.

For further information contact Dr. Camille Leblanc, Associate Professor at Hólar University College, Iceland. camille@holar.is

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Camille Leblanc, lektor (Associate Professor) Hólar University College Department of Aquaculture and Fish Biology Háeyri 1, 550, Saudárkrókur Iceland

Tel: +00 354 455 6387/ mobile +00 354 868 3689

Camille Leblanc <camille@mail.holar.is>

UHuddersfield 3 EvolutionaryGenomics

UHuddersfield. EvolutionaryGenomics

THE UNIVERSITY OF HUDDERSFIELD

DEPARTMENT OF BIOLOGICAL SCIENCES in the SCHOOL OF APPLIED SCIENCES

The Leverhulme Trust Doctoral Scholarship Centre in Evolutionary Genomics

Supervisors: Professor Martin Richards, Dr. Maria Pala & Dr. Ceiridwen Edwards

Three PhD Studentships in Evolutionary Genomics

Closing date for applications: April 30th, 2016

Funding availability: Funded PhD projects for UK/EU students

We are seeking three PhD students in archaeogenetics/palaeogenetics as part of the second cohort of PhD scholars in Evolutionary Genetics for the new Leverhulme Trust Centre at Huddersfield, to begin in September 2016. The successful scholars will receive training from leading experts and undertake cutting-edge research in archaeogenetics, palaeogenetics, bioinformatics, genomics, next-generation DNA sequencing, phylogenetics, population genetics and human evolution.

There are openings this year in the following subjects:

1. Archaeogenetics and palaeogenetics in Southeast Asia and the western Pacific

2. Archaeogenetics and palaeogenetics of southern and eastern Europe

3. Archaeogenetics and palaeogenetics of Native Americans

The students will work in the new molecular biology/ancient DNA facilities at Huddersfield, alongside existing students in these areas, a research fellow who will provide day to day guidance, and the academic staff. Applicants should hold a good bachelor's degree (and preferably also an MSc or MA) in Genetics, Molecular Biology, Statistics, Computing, Bioarchaeology, Biological Anthropology, or other relevant subject, and ideally have experience of generic biological lab techniques such as DNA extraction and PCR. Although training and hands-on supervision will be provided, it is essential that the candidates can operate independently and take the initiative to direct their research.

The studentship will cover the full cost of tuition fees for UK/EU students, and will pay an annual tax-free bursary of ????14,057 for three years (RCUK rates). There are additional funds available for laboratory consumables and travel for conferences, visits to collaborating laboratories and sample procurement.

To apply, please go to: http://halo.hud.ac.uk/-pgr_onlineapps/ and complete the on-line application, ensuring you select full-time PhD Biology. Please type ???????Leverhulme Trust' in the ???????Personal Statement' field. Please also email your CV, transcripts and two letters of recommendation in support of your application to Professor Richards (email m.b.richards@hud.ac.uk) and copy to PGR Administrator Fiona Cross (email f.cross@hud.ac.uk). Please indicate in your email which supervisor and kind of project you are interested in, and why you believe you are well-qualified for that project.

For informal enquiries please contact Prof. Richards on +44 (0)1484 471676 (email m.b.richards@hud.ac.uk), Dr. Maria Pala on +44 1484 472273 (m.pala@hud.ac.uk) or Dr. Ceiridwen Edwards (c.j.edwards@hud.ac.uk)

Related web links:

http://www.hud.ac.uk/research/researchcentres/egrg/ http://www.hud.ac.uk/research/biologicalsciences/ http://www.examiner.co.uk/news/west-yorkshire-news/huddersfield-univers ity-secures-1m-funding-8557938

University of Huddersfield inspiring tomorrow's professionals.

Ceiridwen Edwards <C.J.Edwards@hud.ac.uk>

UHuddersfield EukaryoteEvolution

I am seeking a PhD student in eukaryotic evolution for the new Leverhulme Trust Centre at the University of Huddersfield, to begin in September 2016. The successful scholar will join Dr Martin Carr's group (http://www.hud.ac.uk/research/-researchcentres/egrg/eeg/) and receive training and undertake research in bioinformatics, genomics, high-throughput sequencing, phylogenetics, population genetics and transcriptomics.

The project will focus on the evolutionary biology of choanoflagellates, a group of protists that are the closest known relatives of animals (Carr et al., 2008, PNAS 105: 16641-16646). The choanoflagellates are aquatic organisms, found in both marine and freshwater environments. Published phylogenies suggest that the group evolved in the oceans and has invaded freshwater habitats on only a small number of occasions. This project aims to increase the known diversity of freshwater choanoflagellates in order to study marine: freshwater transitions. Transcriptomes will be generated from newly isolated freshwater species, for phylogenetics and comparative genomics studies; this work will identify freshwater clades in the choanoflagellate evolutionary tree and uncover genes that are unique to freshwater species. The proposed research will cover novel species isolation, transcriptomics, environmental DNA sequencing, phylogenetics and population genetics. The successful applicant will also be encouraged to devise their own research projects during the course of the PhD.

The student will work in new molecular biology facilities, alongside existing students in protist research who will provide day-to-day guidance, along with the supervisor. There will be a strong emphasis on data analysis and interpretation, as well cutting-edge laboratory work, and on producing world-class research papers.

Applicants should hold, or be expected to gain, a good bachelorÂs degree (and preferably also an MSc or MA) in Genetics, Molecular Biology, Statistics, Computing, or other relevant subject, and ideally have experience of computer programming, as well as generic biological lab techniques.

The studentship will cover the full cost of tuition fees for UK/EU students, and will pay an annual tax-free bursary of Â£14,057 for three years (RCUK rates). There are additional funds available for laboratory consumables and travel for conferences, visits to collaborating laboratories and sample procurement.

To apply, please go to: http://halo.hud.ac.uk/-pgr_onlineapps/ and complete the on-line application, ensuring you select full-time PhD Biology. Please type ÂLeverhulme TrustÂ in the ÂPersonal StatementÂ field. Please also email your CV, transcripts and two letters of recommendation in support of your application to Leverhulme Centre coordinator Prof Martin Richards (email m.b.richards@hud.ac.uk) and copy to PGR Administrator Fiona Cross (email f.cross@hud.ac.uk).

For informal enquiries please contact Martin Carr (m.carr@hud.ac.uk, +44 (0)1484 471608)

Dr. Martin Carr Senior Lecturer in Molecular Biology http://www.protist.org.uk Telephone: 01484 471608 Email: M.Carr@hud.ac.uk Web Address : www.hud.ac.uk School of Applied Sciences University of Huddersfield | Queensgate | Huddersfield | HD1 3DH

Martin Carr <martcarr74@gmail.com>

UIdaho ConservationGenomics

Graduate Student Position: Genetic Monitoring of Pygmy Rabbits

We are recruiting a graduate student to conduct a conservation genetics/genomics projects on the Columbia Basin pygmy rabbit (Brachylagus idahoensis). This species was extirpated in Washington, and captive breeding, translocation, and reintroduction efforts have been conducted to re-establish a wild population of this federally endangered population. To date, on-site breeding has produced a large number of rabbits for release, however, relatively few have been detected surviving and reproducing in the wild. Our team has worked collaboratively with the USFWS and the Washington Department of Fish & Wildlife to develop and apply genetic tools to inform management decisions during the breeding, translocation, and initial releases. This graduate student project has 3 main objectives that build on these efforts: 1) to conduct non-invasive, genetic monitoring of the captive breeding and released populations, 2) to develop and evaluate an index of rabbit abundance and density using data from winter surveys of active burrows that can be used for long-term monitoring and 3) to develop a single-nucleotide polymorphism (SNP) dataset and methods for monitoring Columbia Basin pygmy rabbits. The graduate student will conduct field work and laboratory work on this species and lead an experiential learning course to involve undergraduate students in the winter burrow monitoring. Our faculty research team includes Lisette Waits and Janet Rachlow (Dept Fish and Wildlife Sciences University of Idaho), Paul Hohenlohe (Dept of Biological Sciences University of Idaho), and Lisa Shipley (Washington State University). This project could be a MS or PhD level project and students can choose to obtain a graduate degree in Natural Resources or Bioinformatics and Computational Biology at the University of Idaho. We would like the student to start between August 2016 and November 2016. If interested, please send the following in a single PDF: 1) Letter of interest, 2) resume, 3) GRE scores and course transcripts (unofficial fine), and 4) names and contact information for 3 references to Lisette Waits lwaits@uidaho.edu by May 10th.

Lisette Lisette Waits, PhD Distinguished Professor

Department Head Dept Fish and Wildlife Sciences University of Idaho 875 Perimeter Drive MS 1136 Moscow ID 83844-1136 Phone: (208) 885 7823 http://www.uidaho.edu/cnr/faculty/waits "Waits, Lisette (lwaits@uidaho.edu)" <lwaits@uidaho.edu>

ULille ClimateAdaptation

PhD position: Dispersal and maternal transfer of immunity in Capitella capitata: assessing trait association syndromes and the effects of climate change

Deadline: Review of applications will begin immediately and continue until the position has been filled.

Location: Unité Evolution, Ecologie & Paléontologie (EEP), CNRS UMR 8198, Université de Lille, BÃtiment SN2, F-59655 Villeneuve d'Ascq cedex, France

Theme: Climate change affects all ecosystems on the planet. The identification of general effects of temperature warming on species traits is of paramount importance in order to anticipate future changes of ecosystems. These effects, based either on genetic variability or phenotypic plasticity, can affect the functioning and stability of ecosystems and thus affect expected ecosystem services. For instance, temperature rise is expected to favor eventually smaller but more rapidly growing poikilotherms over larger slowly growing ones (the so-called temperature-size rule). In marine organisms, this could potentially affect the dispersal of larvae, and hence the genetic homogeneity of populations, as the size of passively dispersing larvae is bound to affect the duration and scale of dispersal. Immune defenses are also expected to be affected by the selective pressures associated with such a shift.

This PhD is an opportunity to study the association of dispersal ability and immune defense capacities in marine poikilotherms with larval dispersal. Through the study of developmental mode polymorphism in Capitella capitata, a littoral polychaete that can display either direct or indirect development, this project will endeavor to understand how developmental mode and maternal investment in immune protection are linked and thus how an increase in sea surface temperature can affect this trait association, especially through changes in encountered microbial communities.

Overall, this PhD project will address three important questions: (i) are there differential immune transfers among offspring within and among clutches, and, if so, are these different investments related to the dispersal ability of future larvae/juveniles? (ii) How do bacterial community shift with increases in water temperature and will these shifts affect the immunological performance of worms currently living on the littoral of the Hauts-de-France region? (iii) What will be the effects of an increase in water temperature on developmental strategy and transgenerational immunity transfer from mother to offspring in the marine annelid Capitella capitata? To answer these questions, the PhD student will develop lab-based evolution and acclimation experiments as well as theoretical models to predict expected effects resulting from changes in temperature.

Key words: climate change; eco-immunology; experimental evolution; larval dispersal; poecilogony; transgenerational immunity transfer

PhD supervisor(s):

* François Massol (francois.massol@univ-lille1.fr), CR CNRS, HDR, Species Interactions and Comparative Immunology group, Evo-Eco-Paleo unit, CNRS UMR 8198, University of Lille, SN2 building, F-59655 Villeneuve d'Ascq cedex, France. * Virginie Cuvillier-Hot (virginie.cuvillier@univ-lille1.fr), MCF Lille 1, Species Interactions and Comparative Immunology group, Evo-Eco-Paleo unit, CNRS UMR 8198, University of Lille, SN2 building, F-59655 Villeneuve d'Ascq cedex, France.

Funding: Â½ region Hauts-de-France fellowship, Â½ Uni. Lille 1 presidency allocation

Doctoral school: ED "Sciences de la Matière, du Rayonnement et de l'Environnement" ("SMRE" ; ED 104), Université de Lille, Sciences et Technologies ; Filière doctorale : Géosciences Ecologie Paléontologie Océanologie

Profile: We are looking for a highly motivated candidate having a strong interest in both evolutionary ecology and eco-immunology. The ideal candidate will have good capacities for experimental evolution, rearing animals in the lab and setting up experimental treatments, as well as experience in molecular biology, immunological assays and/or biochemistry-related techniques. Prior experience with ecological modeling will be appreciated. Finally, the candidate should have obtained good marks and ranking at the master's degree.

Because of the project's interdisciplinary nature, we are open to applicants from all fields of biology.

Interested applicants should have a look at the SPICI group website (http://spici.weebly.com) for information about the project and our research group.

Contact: Please send your application to François Massol (francois.massol@univ-lille1.fr) and Virginie Cuvillier-Hot (virginie.cuvillier@univ-lille1.fr). This should include (1) a detailed CV, (2) a cover letter putting forward relevant training, (3) a copy of grades and rank for the master degree (first and second-year marks), (4) name and

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ULille IFREMER France ExtremophilicNematodes

PhD title: Search for new antibiotics in extremophilic worms and studying their adaptation and functions in extreme habitats

Dead-line for application: 1st of June 2016

A PhD position is proposed under the joint supervision of two teams Unité EvoEcoPaleo/Ecoimmunology group, Université de Lille CNRS, UMR8198, France and Laboratoire Environnement Profond/Etude des Ecosystèmes Profonds, IFREMER Brest Le Plouzané, France, in the context of the PIONEER program funded by Fondation Total (2016-2019).

To apply: Please send a motivation letter together with your CV to Aurélie Tasiemski (aurelie.tasiemski@univ-lille1.fr), associate professor, EEP lab, PhD supervisor and Daniella Zeppilli researcher IFREMER (Daniela.Zeppilli@ifremer.fr), LEP, PhD co-supervisor before the 1st of June 2016

We are looking for a motivated candidate interested in identifying new antibiotics produced by newly found species of extremophilic nematodes and studying the role played by these peptides in the interactions of the nematodes with their surrounding microbial communities. The discovery of abundant and well-adapted nematode communities in several extreme environments has opened new frontiers in the ecology and biology of the species thriving in such ecosystems. Invertebrates adapt to extreme environments through the establishment of chemotrophic and/or detoxifying microbial symbioses. This obligatory interaction is presumably controlled by an efficient immune system based, among other factors, on the production of AntiMicrobial Peptides (AMPs). There is no consensus sequences of AMPs, with a higher AMP diversity in marine than in terrestrial species and peculiar sequences in extremophile species. The objectives of this thesis are to isolate and biochemically characterize novel AMPs produced by new discovered nematode species living in coastal and deep extreme environments and to (ii) understand the AMP based interactions between nematodes and prokaryotes in extrêmophiles habitats by using multiple approaches. This research will accommodate basic, as well as applied, research (patents are envisaged).

Location: The PhD will take place at the EEP lab, Lille, France and at the LEP lab Brest, France. Cruises for sampling can be envisaged.

Doctoral school : ED “Sciences de la Matière, du Rayonnement et de l’Environnement” (“SMRE” ; ED 104), Université de Lille, Sciences et Technologies ; Filière doctorale : Géosciences Ecologie Paléontologie Océanologie

Funding: Co-funding between Total Fondation and the doctoral School of Lille. CV supporting the motivation and the qualification of the candidate are prerequisites for an application at the doctoral school of Lille.

Applicant profile: Application to this program is open for all students, whatever their nationality, with the equivalent of a master’s degree either in microbiology or in immunology or in ecology. An experience of experimental work in the laboratory is strongly required. Interests for biochemistry and interdisciplinary approaches are necessary as well as mobility.

Francois Massol <francois.massol@univ-lille1.fr>

ULondon EvolutionaryEcol

I am seeking an enthusiastic and hard-working PhD student for a funded 3-yr position to work on the predictability of evolution using livebearing fishes (family Poeciliidae) in the School of Biological Sciences at Royal Holloway, University of London. To be eligible, the student should have at least a good 2.1 BSc degree or higher in a relevant subject area (or equivalent thereof), with evidence for interest in Animal Behaviour, Ecology, and/or Evolutionary Ecology. Preference will be given to candidates with a Masters degree and a demonstrated interest in the topic.

The application deadline is 15th April 2016, and the successful student is expected to start in September/October of this year. For project and scholarship details please see https://www.findaphd.com/search/ProjectDetails.aspx?PJID=57014&LID=1359 .That page will also direct you to the online portal for applications.

For questions about this scholarship, the project, or the application, please contact me (Rüdiger Riesch: rudiger.riesch@rhul.ac.uk).

Best wishes, Rüdiger Riesch

Rüdiger Riesch, PhD Lecturer in Evolutionary Biology School of Biological Sciences Royal Holloway, University of London Email: rwriesch.evolutionarybiology@gmail.com homepage: https://sites.google.com/site/ruedigerriesch/-home Book on Extremophile Fishes: http://-www.springer.com/life+sciences/ecology/book/978-3-319-13361-4 "The most exciting phrase to hear in science, the one that heralds the most discoveries, is not "Eureka" but "That's funny..." –Isaac Asimov

Rüdiger Riesch <rwriesch.evolutionarybiology@gmail.com>

UMelbourne Evolution postgrads postdocs exchange

*** Short postdocs, exchange visits, and PhD/Masters projects in the Holman lab, University of Melbourne ***

Later this month (April 2016), the "Endeavour Scholarships and Fellowships program" will begin asking for applications. This program has a number of options for bringing talented early career researchers to Australia, which are summarized here: http://tinyurl.com/-ongqbkp . Firstly, they provide funds that cover tuition fees and living expenses for non-Australians to conduct an entire 2-year Masters degree, or a PhD of up to 4 years, in Australia. Secondly, they fund 4-6 month research visits to Australia by people currently undertaking a Masters or PhD in a different country. Thirdly, these 4-6 month visits can be used to partially fund a short post-doc (typically these are awarded to recent PhD graduates). Thus, the scheme allows PhD students to undertake a funded â' or exchange visit to conduct research at an Australian university, or to fund a short post-doc.

I have recently joined the School of Biosciences at the University of Melbourne, and am keen to recruit additional lab members. I am interested in sexual selection, social evolution, selfish genetic elements, animal behavior, and a variety of other topics united by the common theme of evolution (see my webpage below). I use a mixture of approaches including experiments with insects, bioinformatics, quantitative genetics and theoretical modeling. A lot of the work I am currently planning uses "omics" methods, including RNA-seq studies of gene expression, ddRAD studies of genetic variation in non-model organisms, and bisulphite sequencing to characterize DNA methylation.

I would be very happy to support applicants wishing to join my lab via the Endeavour program, and am prepared to work closely with good candidates on drafting a competitive application and designing an exciting, fundable project. I am interested in recruiting good candidates at all levels covered by the Endeavour program: Masters, PhD, and postdoc. Desirable skills include bioinformatics, manuscript writing, and broad knowledge of evolutionary biology, though I am interested to hear from anyone who learns quickly, can work well unsupervised, and is passionate about research.

If interested, please contact me directly to discuss possibilities, and enclose a short CV and a brief description of your research interests and expertise.

Luke Holman

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Senior lecturer and ARC DECRA Fellow

School of Biosciences, University of Melbourne

website: https://sites.google.com/site/lukeholman/-home email: luke.holman@unimelb.edu.au

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UOslo Mycology

PhD Research Fellowship in Mycology/Microbiology available at the University of Oslo, Norway

Most fungi reside in natural habitats, but some species have expanded their habitats into buildings, causing adverse health effects as well as damages to the constructions. The main aim in this project is to improve the knowledge about indoor fungal communities (i.e. the indoor mycobiome) by implementing state-of-the-art high throughput DNA sequence (HTS) analyses. Using DNA metabarcoding and other DNA based approaches we will analyze the spatiotemporal variation in the indoor mycobiome within single buildings and on broader geographic scales and identify the main determinants of the indoor mycobiome. We also want to improve reference DNA sequence collections for indoor fungi and improve and adapt existing bioinformatics tools for DNA metabarcoding analyses of the indoor mycobiome.

The fellowship will be for a period of 4 years, with 25% compulsory work. Starting date no later than 01.10.2016. For more information and for applying, see http://uio.easycruit.com/vacancy/1618189/-96323?iso=3Dno "havard.kauserud@ibv.uio.no" <havard.kauserud@ibv.uio.no>

UOtago NewZealand ConservationGenomics

Evolution and conservation of the world's rarest wading bird

A PhD position in conservation genomics is available to study the evolution and conservation of New Zealand bird species with Dr Michael Knapp at the University of Otago, Dunedin, New Zealand.

The New Zealand bird fauna is under threat from introduced predators as well as from non-native competitors and interbreeding with closely related introduced species. This project will evaluate the impact of interbreeding between the world's rarest wading bird, the Black Stilt, and its more common, non-native relative, the Pied Stilt. The research will include analyses of modern and ancient DNA and conduct genome wide analyses of both species. Based on the results from these studies, the project will develop conservation strategies for the Black Stilt. The project is part of our new, Royal Society funded research programme, which uses genomic data to address key questions of bird evolution and conservation in New Zealand's unique environment.

The ideal PhD student will have skills in molecular ecology/population genetics and/or bioinformatics and genome data analyses.

The University of Otago is one of the most research-intensive Universities in New Zealand with a world-class reputation in the life sciences. It provides an environment that allows its students to undertake internationally recognised research, in a diverse and vibrant postgraduate environment and has been ranked as one of the 15 most beautiful campuses in the world. The PhD student will be hosted by the Department of Anatomy, a diverse and research-oriented department with expertise ranging from genomics to biomedical sciences.

For details and instructions on how to apply, please visit http://anatomy.otago.ac.nz/phd-opportunities, where you will find all our currently available PhD positions in genomics and biomedical sciences along with application details. The project advertised here is listed under "Evolution and conservation of the world's rarest wading bird'.

Please apply by 17/May/2016.

Dr Michael Knapp Rutherford Discovery Fellow Senior Lecturer in Biological Anthropology Department of Anatomy University of Otago Dunedin New Zealand

Michael Knapp <michael.knapp@otago.ac.nz>

UppsalaU EvolutionHostAdaptedBacteria

A PhD student position is available in my group:

http://www.uu.se/en/about-uu/join-us/details/-?positionId=99188 PhD position in Microbiology

Uppsala University is an international research university focused on the development of science and education. Our most important assets are all the individuals who with their curiosity and their dedication make Uppsala University one of Swedens most exciting work places. Uppsala University has 40,000 students, 7,000 employees and a turnover of SEK 6,5 billion.

The Department of Medical Microbiology is a very strong and international research and teaching environment, hosting a staff of over 250 scientists, among which over 40 PhD students. In 2015, researchers from the department published over 150 articles in peer-reviewed journals. Research focuses on three domains: Biochemistry/Molecular Cell Biology, Genomics, and Microbiology/Immunology.

Project description: The research group where the candidate will be working studies the evolution of host-adapted (intracellular) bacteria. The overall goal is to better understand the precise molecular mechanisms underlying long- and short-term evolution of host adaptation in bacteria and to identify critical genetic innovations that allow free-living bacteria to adapt to, and then profit from, or live in symbiosis with, eukaryotic hosts. To obtain unprecedented precision about the nature and function of the genes involved in host-adaptation, the successful candidate will establish a Long-Term Experimental Evolution (LTEE) experiment with Legionella pneumophila in several hosts. The LTEE will also help understand the molecular nature of fitness trade-offs occurring when switching from a generalist (many hosts) to a specialist (single or a few hosts) strategy.

Duties: The successful candidate will primarily engage in research work and doctoral studies. Other duties at the institution comprised of administration and teaching may be included in the employment at a maximum lever of 20 %. Salary is subject to established local guidelines.

Qualifications: The candidate must hold a M.Sc. degree (or equivalent, corresponding to 240 credits) in Evolutionary Biology, Genetics, Microbiology or a related field. They should have a strong interest in basic research in microbiology and molecular evolution. Previous practical experience in microbiology and molecular biology is desired. Since the project requires interacting with different research groups, an established ability to work independently and to take initiatives is an asset.

To be employed as a PhD student, the applicant must be accepted in the postgraduate programme. Information concerning doctoral education, requirements and rules of admission can be found http://www2.medfarm.uu.se/-utbildning/forskarniva/. The length of the study period for full time employment is a maximum of four years. Terms for graduate studies can be found in Högskoleförordningen 5 kap §§1-7.

For further details: please contact Lionel Guy, lionel.guy@imbim.uu.se, phone +46 18 471 4366 or Dan Andersson, dan.andersson@imbim.uu.se, phone: +46 18 471 4175.

Application: Please submit a CV, a letter describing your research interest and skills, publications or a copy of master thesis or equivalent, contact information of three referees (phone number and e-mail address) and three reference letters.

You are welcome to submit your application online no later than May 27, 2016 at http://www.uu.se/en/about-uu/join-us/details/?positionId=99188 – Lionel Guy, PhD, Assistant Professor Department for Medical Biochemistry and Microbiology, Uppsala University, Uppsala, Sweden

lionel.guy@imbim.uu.se

USouthernMississippi FishPopGenetics

A graduate assistant position (M.S. or Ph.D) is available in our laboratory to work on population genetics/genomics of marine and coastal fishes exploited in the Gulf of Mexico region. Current lab projects include application of genome scans generated by genotyping by sequencing to linkage mapping and population genomics, controlled breeding of marine species and development of experimental approaches to study the genetic basis of phenotypic traits.

The successful applicant will be provided a 12-month full-time Research Assistantship with a tuition waiver. Candidates should possess a Bachelor's degree in a relevant field (e.g. Biology, Ecology & evolutionary biology, Fisheries science, GPA > 3.5) when applying for this position. The position is available starting fall 2015.

Interested individuals should send a CV, GRE scores, and unofficial transcripts to:

Eric Saillant, Ph.D Associate Professor Department of Coastal Sciences The University of Southern Mississippi Gulf Coast Research Laboratory 703 East Beach Drive Ocean Springs, MS, 39564 Tel. (1) 228-818-8007 Fax (1) 228-872-4204 E-mail: eric.saillant@usm.edu

Eric Saillant <eric.saillant@usm.edu>

UTrento InsectNeuroimaging StartingNovDeadlineMay10

The Center of Mind/Brain sciences @ Trento, Italy offers 14 PhD fellowships commencing in November 2016. Among which one within a project on Insect neuroimaging For an overview of our work visit our group's website: http://r.unitn.it/en/cimec/nphys and contact me to discuss possible projects: albrecht.haase@unitn.it For the application: https://webapps.unitn.it/Apply/-en/Web/Home/dott The deadline for applications is Tuesday May 10, 2016 at 4:00 p.m. Some information on the CIMeC PhD program - CIMeC ranked 1st in Italy for Quality of Research 2013 - 2014-2015 University of Trento ranks 1st in Italy in the rankings of THE - Times Higher Education - 3-yr program (Nov. 1, 2016-Oct. 31, 2019) - all courses are given in English

– Dr. Albrecht Haase Assistant Professor Laboratory for Nonlinear Bioimaging, Department of Physics & Neurophysics Group, Center for Mind/Brain Sciences University of Trento

Piazza Manifattura 1, Building 14, 38068 Rovereto (TN), Italy Tel office: +39 0464 808699 http://r.unitn.it/-en/cimec/nphys Albrecht <albrecht.haase@unitn.it> Albrecht <albrecht.haase@unitn.it>

UZurich ComputEvolutionaryBiol

PhD thesis in computational evolutionary biology

A three-year Ph.D. studentship in evolutionary biology is available in the laboratory of Andreas Wagner at the University of Zurich. We are looking for a researcher to study the origins of evolutionary innovations and phenotypic diversity in genetic systems, such as metabolic networks, regulatory circuits, and enzymes. Lab members are a group with very diverse backgrounds and research projects, unified by their interests in evolution and life's fundamental organizational principles. Ongoing work in the lab ranges from the directed evolution of enzymes to laboratory evolution in E.coli and computational analyses of genetic networks (e.g., Hayden et al., Nature 2011; Payne and Wagner, Science 2014). A sample of the laboratory's research can be found at http://www.ieu.uzh.ch/wagner/ . The successful candidate will have a strong background in bioinformatics and computational biology. Fluency in a major scripting language such as perl, and experience in software development is a must. Also desirable is a strong background in biology. Applications without a demonstrated interest and research history in evolutionary biology will not be considered further. We are looking for an individual with a Masters Degree or equivalent, who is highly self-motivated and can work independently.

The working language in the laboratory is English. German skills, although helpful, are not essential. Zurich is a highly attractive city in beautiful surroundings, with a multinational population, and many educational and recreational opportunities.

To be considered, please send a single (!) PDF file merged from the following parts to annette.schmid@ieu.uzh.ch: CV including publication list, academic transcripts, a statement of research interests not exceeding three pages, and three academic references. Please include the word "PEVOLPHD16" in the subject line. Applications will be considered until April 22, 2016, or until the position is filled, whichever comes first. The position is available from the fall of 2016.

Annette Schmid Administrative Assistant of Prof. A. Wagner University of Zurich Institute of Evolutionary Biology and Environmental Studies Wagner lab, Y27-J52 Winterthurerstrasse 190 CH-8057 Zürich Switzerland Mail to: annette.schmid@ieu.uzh.ch Phone +41 (0)44 635 61 42 Fax +41 (0)44 635 61 44 at the office on Monday and Thursday

"annette.schmid@ieu.uzh.ch"
<annette.schmid@ieu.uzh.ch>

VrijeU Brussel AntarcticSeaStars

PhD scholarship (4 years) in molecular ecology at the Vrije Universiteit Brussel (VUB), Department of Biology, Marine Biology Lab, Belgium.

We are searching for a highly motivated PhD student that will work on evolution, population genetics and connectivity in Antarctic sea stars utilising a genomics approach (DNA barcoding, microsatellites and next generation sequencing) in the framework of the interdisciplinary project

Refugia and Ecosystem Tolerance in the Southern Ocean (RECTO).

Because of its long history and geographic isolation, the Southern Ocean (SO) provides a natural laboratory for research on evolution and biodiversity. Confronted with fast-paced environmental changes, biota in Antarctic ecosystems are strongly challenged and face three possible outcomes: adaptation, migration or extinction. Past glaciation periods have already forced marine zoobenthos of the SO into refugia, being either ice-free continental shelf areas, the deep sea or sub- or peri-Antarctic regions, followed by recolonization when the ice retreated. In a multidisciplinary approach and involving all major Belgian research groups studying evolution and diversity of SO faunas, RECTO will strive at understanding how such past events have driven diversification and adaptation in different animal groups and how these can be applied as proxies to understand the contemporary situation and predict future scenarios.

The Marine Biology Lab at the VUB specialises in research on molecular ecology of marine fauna from the poles to the tropics and from invertebrates to fishes. In the new collaborative research project RECTO the evolutionary history of Antarctic sea stars will be studied.

Profile of the PhD student:

- Master in (marine) biology with excellent study results
- Experience in genomics (lab work and bioinformatics)
- Interest in the ecology and evolution of Antarctic sea stars

- Excellent oral and written English skills (for minimum requirements see www.vub.ac.be/en/studying-at-the-vub/language-requirements)

- Willingness to participate in long sampling campaigns under extreme conditions in the Southern Ocean

- Obligation to finalise a doctoral thesis within 4 years

The marine biology lab offers excellent coaching in an inspiring research environment with up-to-date research facilities in the international and multilingual capital of Europe.

Interested candidates are requested to submit their application (motivation letter, address of three referees, summary of master thesis, MSc certificate with grades, proof of proficiency in English and curriculum vitae) with the subject line 'RECTO PhD scholarship application' to the head of the Marine Biology Lab, Prof. Dr. Marc Kochzius (marc.kochzius@vub.ac.be) before 01. May 2016. Expected starting date is 01.06.2016.

Marc Kochzius <vub.marine.biology@gmail.com>

Jobs

AdamMickiewiczU Poland Bioinformatics

Research Group Leader in Bioinformatics

Adam Mickiewicz University in PoznaÅ (AMU) and International Institute of Molecular and Cell Biology in Warsaw (IIMCB) invite applications for Research Group Leader

We seek a talented, motivated and dynamic scientist, preferentially (but not limited to) at the early in his/her career to establish a joint AMU & IIMCB research group located at the Institute of Molecular Biology and Biotechnology, Faculty of Biology, Adam Mickiewicz University (IBMIB-AMU) in PoznaÅ, Poland.

IIMCB (http://iimcb.gov.pl) and Faculty of Biology AMU to which IBMIB-AMU (http://ibmib.amu.edu.pl) belongs are among Poland's top-ranked academic institutions in the field of biology, working together based on a bilateral agreement. Research topics at both institutes cover a wide spectrum of molecular and cellular biology, biotechnology, structural and computational biology. Both institutes are involved in various national and international research projects and provide cutting-edge equipment and facilities for wet-lab work and bioinformatics. IBMIB-AMU, where the group will be located, is situated at a modern academic Morasko campus in PoznaÅ and provides outstanding research opportunities for their scientists in a stimulating environment.

For the Research Group Leader position we will consider candidates with a strong scientific track record in bioinformatics and clear evidence of leadership as well as an ability to attract extramural funding. The successful candidate will be expected to develop an independent research program in bioinformatics to complement research activities in IBMIB-AMU and IIMCB, and will be responsible for teaching a course in bioinformatics and training of young scientists within the framework of MSc and PhD studies at AMU.

The startup package includes the salary of the group leader, two PhD student positions, start-up funding, furnished laboratory and office space at IBMIB-AMU and access to all shared equipment of both institutions. The initial contract will be for 5 years, with a possible extension dependent on the results of periodic evaluation(s). The starting date is negotiable.

Deadline for application is April 30, 2016. Applications should be submitted by email to rekrutacja@iimcb.gov.pl

Applicants should prepare a single pdf file including: â a cover letter explaining reasons for application, â a Curriculum Vitae including a list of publications, â a statement of scientific achievements (up to 1 page), â a summary of the applicant's future research plans (2 pages) including potential for prospective collaboration with particular groups at IBMIB-AMU and IIMCB, â addresses of two academic reference persons, â copies of three most important papers, â one page description of candidate's experience in teaching and a summary of proposed MSc and PhD-level courses in bioinformatics

The application must contain the following statement: "In accordance with the personal data protection act from 29th August 1997, I hereby agree to process and to store my personal data by the Institution for recruitment purposes".

Ciomborowska Joanna <joannac@amu.edu.pl>

Alberta GroundSquirrelHeadTech

Head Field Technician Required ASAP - Columbian ground squirrels Kananaskis, Alberta, Canada

We are looking for a head field technician to assist with, and coordinate, fieldwork on the ecology of a wild population of Columbian ground squirrels. The head technician will supervise 3 volunteers for the period of May 1 to Aug 31, 2016 (preference may be given to applicants who can start up to a week earlier (i.e., ˜ Apr 23-24). Duties will include monitoring the phenology (when animals emerge from hibernation), reproduction and survival of individuals, data entry and data verification. Fieldwork will involve live-trapping and handling of animals, behavioural observation, radio-telemetry (to locate natal burrows) and assistance with the measurement of physiological (metabolism) traits on free-ranging animals. The successful candidate will have previous fieldwork experience, ideally in a field camp/station setting, have experience in data entry and management and show a high level of responsibility. Good organizational, multi-tasking and supervisory abilities are essential. Applicants who have experience working with terrestrial vertebrates will be given priority. Additionally, you should have an interest in a number of the following (the more the better!): ecology, evolutionary biology, wildlife, field biology, and animal behaviour. All work is conducted out of field stations and, as such, successful applicants need to enjoy the outdoors, be up-beat, positive, responsible and work well as a member of a team.

Fieldwork is carried out in the spectacular Rocky Mountains of southwestern Alberta, Canada, home to some of the most majestic wildlife in North America. You will be staying at the University of Calgary's Barrier Lake research station in Peter Lougheed Provincial Park, Alberta (http://bgs.ucalgary.ca/facilities/facilities). You will interact with other researchers working on a diversity of projects in behavioural and population ecology, ranging from insects to large mammals.

Salary is $1800/month. Food and accommodation are provided. The successful candidate will be required to provide for their own travel to Saskatoon, Saskatchewan. Travel between the field station and Saskatoon is provided. If you wish to apply for this position, please send a CV with a cover letter and contact details of three references (with e-mail address), by email to Jeff

Lane (contact info below), ASAP. Applications will be reviewed as they are received and, to receive full consideration, we thus encourage applicants to submit their materials ASAP. Please indicate in your application that you are applying for the head technician position (we are also posting for 1 volunteer). Note that only those eligible to work in Canada (Canadian citizens or landed immigrants, American citizens eligible for TN status or foreign nationals with work permits or working holiday visas) will be considered.

We thank everyone for applying, but only those selected for interview will be contacted. Only applicants available for the entire period will be considered.

Contact: Dr. Jeff Lane Department of Biology University of Saskatchewan jeffrey.lane@usask.ca www.lanelab.ca "Lane, Jeffrey" <jeffrey.lane@usask.ca>

CaryInst US EvolutionZoonoticDiseases

Lab/Data Manager Opportunity at Cary Institute of Ecosystem Studies

We are seeking a full time data and laboratory manager to support research activities in computational ecology of zoonotic diseases. Main duties will include the collection and curation of data from diverse sources including published literature, the web, and existing repositories and online databases. This main task will require some programming proficiency (R preferred). Additional duties include standardizing metadata across curated data files, and managing multiple data streams from distinct collaborative projects. The applicant should possess previous training in the biological sciences, and research experience with infectious diseases and ecology is preferred. In addition to R programming experience, proficiency with ArcGIS (or equivalent open access software) is desirable. The successful candidate will be collaborative with good verbal and written communication skills; detail- oriented; and enjoy a high degree of independence. This position offers the opportunity to engage in ongoing lab research projects, and to develop independent side projects exploring questions related to infectious disease.

This is a fully benefitted position for one year, subject to annual renewal contingent on performance and available funding.

The final candidate will be required to successfully complete a post- offer, pre-employment screening and background check. All candidates must be authorized to work in the U.S.

To apply, visit our website at www.caryinstitute/who we are/jobs and complete our online job application. Interested applicants should send a 1-page cover letter detailing their interest and qualifications for the position, and the contact info for 3 references. Please include job code 16022-I in your correspondence.

The Cary Institute is an Equal Employment Opportunity (EEO) and Affirmative Action (AA) employer. It is the policy of the Company to provide equal employment opportunities to all qualified applicants without regard to race, color, religion, sex, sexual orientation, gender identity, national origin, age, familial status, protected veteran or disabled status, or genetic information.

Patricia Jones <jonesp@caryinstitute.org>

ImperialCollege London EvolutionChytridFungi

Imperial College London

Research Assistant

Reference number: SM095-16KO closing date 22nd May 2016 http://www3.imperial.ac.uk/employment Department of Infectious Disease Epidemiology; Imperial College London, School of Public Health

Salary Range: 29,800 - 31,360 per annum

The Fisher Lab is seeking an experimentalist to join a research group investigating the evolutionary ecology of chytrid fungi causing global amphibian extinctions. Continuously funded since 2003 by UK Research Councils, we are investigating the patterns and processes that are leading to disease-driven amphibian declines by utilising population genomics, experimental ecology and fieldwork. Our work has been key to identifying the fungal lineages and species that are emerging to cause amphibian declines, and the vectors that are leading to the spread of these invasive pathogens. The project will focus on discovering new lineages of amphibian-infecting fungi from around the world, comparative genomics of the different lineages, and will seek to identify the regions from which contemporary infections originate.

Funded by the Leverhulme Trust, the project's primary objective is to investigate the spatial epidemiology and molecular evolution of panzootic amphibian chytridiomycosis by linking patterns of host-specificity, competition and virulence to the spatial origins of infecting lineages. An initial focus of the project will be the amphibian biodiversity hotspot of Madagascar, and the candidate will be expected to spend some time co-ordinating surveys in that country.

Our ultimate goal is to increase our awareness of evolutionary ecology of these pathogens, and the risk that they pose to species worldwide.

Applicants should have a BSc or MSc or equivalent in one of the following areas: biology, genetics, epidemiology or related quantitative disciplines. You will also have strong knowledge of, and interest in, pathogen epidemiology and knowledge of research methods in genetics and genomics and the ability to work with animals. The post may require work in challenging fieldwork settings.

This is a full time post for a fixed-term of one year. The candidate will join a vibrant department of over 130 epidemiologist at Imperial College London, recently ranked joint 2nd in the QS world University rankings.

Our preferred method of application is online via our website http://www3.imperial.ac.uk/employment. Please complete and upload an application form as directed.

For informal enquiries please contact Professor Matthew Fisher: matthew.fisher@imperial.ac.uk

"Fisher, Matthew" <matthew.fisher@imperial.ac.uk>

IthacaCollege NewYork 1yr TeachingEvol

Dear colleagues,

Ithaca College seeks applications for a one-year term position at the assistant professor level, to begin in August. The position emphasizes teaching ecology & evolutionary biology at the introductory undergraduate level. Applications are due April 22nd, which is only two weeks away. The official position description appears below. With my best regards ˜ Brooks Miner Assistant Professor, Department of Biology Ithaca College

ASSISTANT PROFESSOR - 001217

Organization : Biology

Primary Location : United States-New York-Ithaca

Description : The Biology Department at Ithaca College invites applications for a full time, one-year, non-tenure-eligible faculty appointment at the Assistant Professor level to begin August 16, 2016. The primary responsibility is to coordinate and teach the Spring 2017 Fundamentals of Biology II: Ecology and Evolution, a large introductory course and associated labs for allied health students. In Fall 2016, the faculty member will teach a lecture course primarily for non-science majors as well as laboratory sections of Fundamentals of Biology I: Cells and Bodies. Responsibilities will amount to 12 teaching contact hours each semester.

Qualifications : Preference will be given to individuals with prior undergraduate teaching experience, and to individuals who have completed a PhD in an appropriate field by August 2016. Successful candidates will demonstrate the ability to teach in ways that value the varied learning needs and interests of a culturally diverse student population, and that reflect a commitment to encouraging the success of all students. We also seek candidates who have relevant experience and/or a record of professional engagement with groups and communities underrepresented in the academy. Candidates from underrepresented groups whose exclusion from the academy has been longstanding are strongly encouraged to apply.

Department Description: The Biology department is housed within the school of Humanities & Sciences, which consists of approximately 2,500 undergraduates. The department offers both a B.A. and a B.S. in Biology, a B.A in Biology teacher education, and a B.S. in Biochemistry (in collaboration with the Chemistry department). The department teaches a variety of courses for Biology/Biochemistry majors, general education classes for non-science majors, and service courses for other programs in the Health Sciences. With the major focus at Ithaca College on teaching, excellence in teaching is a critical factor in evaluation of faculty.

College Introduction: At Ithaca College, a comprehensive residential campus community of 6,500 students, we strive to be at the forefront of the higher education landscape. Our strategic plan, IC 20/20, positions us to offer a distinct integrative learning experience that makes students ready for the personal, professional, and global challenges of our age. We seek candidates who embrace integrative learning and want to be a part of this exciting time in Ithaca College history. We encourage creative collaboration and innovation in our faculty and staff, providing support and resources for them to grow in their fields and lead students to their own innovative ideas and achievements. We welcome different ways of thinking and look for candidates with unique points of view and life experiences. We are inclusive of individuals with a wide range of cultural, personal, and professional backgrounds, talents, and skills. Our campus is a vibrant and rewarding community where diverse minds can learn, succeed, and excel. When reviewing candidates, we are looking for indicators of a number of core competencies. Prospective candidates must be adaptable, collaborative, inclusive, respectful, responsive, results driven, and sustainable. They must communicate effectively, demonstrate leadership, exhibit professional integrity and ethics, take initiative, value personal and professional development, and show that they will engage in the college. Nestled in the heart of New York State's scenic Finger Lakes region, Ithaca College sits atop South Hill overlooking picturesque Cayuga Lake and is just minutes away from the city center. Combining small town warmth and charm with the vibrancy of a college community, the thriving and culturally diverse city of Ithaca has been rated by Kiplinger's as one of the top 10 places to live in the United States.

To learn more about Ithaca College, visit us at ithaca.edu.

Instructions for submitting your application: Interested applicants must apply online at ithaca.edu/jobs/ and attach a cover letter, curriculum vitae, and a statement of teaching philosophy that includes approaches to teaching large lecture courses. Two letters of recommendation should be emailed directly to Leann Kanda, Chair of Search Committee, at lkanda@ithaca.edu. Questions about the online application may be directed to the Office of Human Resources

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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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LANGEBIO Mexico 4 GenomicsBioinfomatics

?LANGEBIO-Mexico (http://www.langebio.cinvestav.mx/) is opening 3 young researcher and 1 head of services position.

1. Catedras CONACyT (CONACyT Research Fellows). We are seeking 3 young investigators aiming at developing independent research lines in: 1) Paleogenomics, 2) Bioinformatics, or 3) Plant genomics

"Catedras" are research positions intended for Mexicans looking forward to come back to Mexico or foreigners living in Mexico. Competitive salary, modest startup package and benefits provided. Short driving distance from Guanajuato, a UNESCO World Heritage site.

Open call (in Spanish) is here: http://langebio.cinvestav.mx/doctos/c_catedras_langebio_2016.pdf More info about Catedras Conacyt: http://www.conacyt.mx/index.php/el-conacyt/convocatorias-y-resultados-conacyt/convocatoria-catedras/convocatorias-catedras-conacyt-para-jovenes-investigadores-2016 2. Head of Bioinformatics Services. We are seeking a computational scientist to become the Head of Bioinformatics Services at LANGEBIO's Genomics Core Facility. The research component of this position is optional.

More information: http://www.morenolab.org/pdf/Bioinformatics_services_open_call_2016_ENGLISH.pdf Kind regards,

Selene

Selene L. Fernandez-Valverde Ph.D.

CONACYT Research Fellow - LANGEBIO Cinvestav

Irapuato, México

sfernandezv@langebio.cinvestav.mx

slfernandezva@conacyt.mx?

Selene Lizbeth Fernandez Valverde <s.lizbethfernandez@uq.edu.au>

Monsanto CA VegetableGenomics

ï»¿ Vegetable Genomics Scientist Location: Woodland, CA Req# 018Y8 Monsanto is seeking a highly motivated and talented genomics scientist who will perform and guide analyses using biostatistical methods, including population genetics, quantitative genetics, and bioinformatics, to support global discovery genetics research across multiple vegetable crops.Â The role will be positioned within the discovery genetics team and located at our R&D site in Woodland, California, USA.Â The scientist will manage, analyze and interpret phenotypic data and large scale genomic data, as well as develop new scripts and tools to enable routine and non-routine analyses.Â The candidate should be capable of effectively communicating results and providing statistical training and consulting to interdisciplinary teams.

Responsibilities: 1. Leverage world-class genomic datasets to perform statistical genetic analyses and develop scripts that will support Monsanto's vegetable trait discovery pipeline.

2. Implement statistical methods to identify associations between trait phenotypes and genetic markers in structured and unstructured populations (e.g. linear regression, ANOVA, mixed effects models, QTL mapping, genome-wide association mapping, genomic selection).

3. Combine phenotypic and genotypic data to assess diversity and structure in vegetable germplasm.

4. Generate and update consensus genetic linkage maps for various types of mapping populations. Construct reference maps that successfully integrate both genetic and bioinformatics data.

5. Conduct analyses to support evaluation and improvement of genotyping platforms.

6. Communicate results concisely and accurately in written and oral form to stakeholders.

7. Provide statistical training and consulting with scientists and research associates.

8. Direct research associates to meet business goals and identify development opportunities.

9. Pursue intellectual property opportunities around project responsibilities, in collaboration with patent science and legal functions.

Required Skills/Experience: Master's degree or higher in population genetics, statistical genetics, biostatistics, computational biology, bioinformatics, breeding or related field of study.

Broad and extensive knowledge of theoretical and applied statistics, with strong skills in statistical modeling, data quality control and data mining.

Experience constructing genetic linkage maps.

Proficiency with one or more common statistical analysis software environments (e.g. R, SAS).

Experience with at least one scripting language commonly used in genomics research (e.g. Python, Perl) Self-motivation and strong initiative.

Ability to balance workloads from multiple competing tasks, excellent organization and time management skills.

Outstanding written and verbal communication skills.

Desired skills: PhD degree in population genetics, statistical genetics, biostatistics, computational biology, bioinformatics, breeding or related field of study.

Applied knowledge of plant breeding Experience developing interactive interfaces for data analysis and visualizations (e.g. R Shiny, JavaScript) Proficiency querying enterprise level databasesÂ

To apply for this role please visit "http://-www.monsanto.com/careers/Vegetable Genomics Scientist" type in Req #018Y8.

lisa.a.power@monsanto.com
lisa.a.power@monsanto.com

OregonStateU CuratorFisheriesWildlife

Dear Colleagues,

Oregon State Universitys Department of Fisheries and Wildlife (http://fw.oregonstate.edu) invites applications for a full-time Instructor / Curator. We seek an energetic, enthusiastic colleague with a passion for biological collections to help advance our nationally and internationally recognized teaching, research and outreach programs. Our interdisciplinary, collaborative department works throughout the Pacific Northwest and the world in diverse environments, and has long focused on understanding vertebrate biology and biodiversity as a foundation of effective conservation and management. Our Corvallis location affords easy access to Oregons diverse habitats and natural resources, including the Pacific Ocean, the deepest lake in the United States, extensive networks of rivers and streams, progressive urban and agricultural areas, mountains and high deserts.

The successful candidate will teach three to four Ecampus or summer session courses per year on topics related to zoology, taxonomy, systematics, ecology, evolution, natural history, conservation and curation; manage and curate OSUs collections of fishes (http://ichthyology.oregonstate.edu), mammals, birds and aquatic Invertebrates, train and direct undergraduate collections assistants, produce scholarly work related to research, curation or outreach using natural history collections, and provide service to the department, university and profession.

To apply, please submit a cover letter, curriculum vitae, brief statements detailing your interest and experience in teaching, curation, and promoting diversity (one page each), and contact information (email and telephone) for three professional references at http://oregonstate.edu/jobs/ (posting number P00199UF). The position requires a masters degree in vertebrate zoology, ichthyology, mammalogy, ornithology, museum studies, or a related field. A more detailed position description, including other minimum and preferred qualifications, also appears on that site. Applications must be received on or before Sunday, May 8th to be considered.

Questions about the position can be directed to the chair of the search committee, Dr. Brian Sidlauskas, at brian.sidlauskas@oregonstate.edu.

Link to posting: https://jobs.oregonstate.edu/postings/24008 – Brian Sidlauskas Associate Professor and Curator of Fishes Department of Fisheries and Wildlife Oregon State University 104 Nash Hall Corvallis, OR 97331

brian.sidlauskas@oregonstate.edu 541-737-6789 (office) 541-224-3850 (cell) http://ichthyology.oregonstate.edu http://people.oregonstate.edu/ ~ sidlausb/ https://www.facebook.com/brian.sidlauskas https://twitter.com/briansidlauskas "Sidlauskas, Brian" <Brian.Sidlauskas@oregonstate.edu>

StanfordU HopkinsMarineStation ResTech DNAbarcoding

Research Technician- 70505

Description

Research technician at Stanford University's Hopkins Marine Station, in Pacific Grove, CA. Under the direction of the Principal Investigator the technician will assist with research related to genetic characterization of marine communities using DNA barcoding of kelp forest and fish market samples in the context of ongoing research into marine conservation and management. The position will also include grant reports and data analysis.

Research duties include:

*Extracting DNA and documenting genetic variation. This will include processing samples in the lab for DNA extraction and sequencing as well as entering, managing, and analyzing the resulting data. This will require the use (or development) of many research skills using a variety of molecular genetic tools. These include, but are not limited to DNA extraction, PCR, gel electrophoresis, next generation DNA sequencing and bioinformatics. *Laboratory maintenance including maintaining the lab and taking responsibility for ordering some of the general supplies.

There is potential for extension of the technician position to other research projects.

Qualifications

The successful applicant will be highly organized, have attention to detail, be able to work as an independent part of a team, have a basic understanding of and facility with standard computer software programs, and have practical experience with a variety of standard molecular tools (for example, DNA extraction, PCR, gel electrophoresis, DNA sequencing, etc). In addition to these basic requirements, we desire an applicant with an interest in marine ecosystems and their ecological functioning.

Application

Submit applications online at https://stanford.taleo.net/careersection/2/jobdetail.ftl?job=3D150870&src=JB-10064 A cover letter may be included in the additional attachments section.

Review of applications will continue until the position is filled.

Final offers of employment are contingent upon successful completion of national criminal background check, national sex offender registry search and, where applicable, driving record.

Stanford is an equal opportunity employer and all qualified applicants will receive consideration without regard to race, color, religion, sex, sexual orientation, gender identity, national origin, disability, veteran status, or any other characteristic protected by law.

Jenny Giles <jlgiles@stanford.edu>

StockholmU BioinformaticsEvolutionaryGenomics

Position in Bioinformatics / Evolutionary Genomics at Science for Life Laboratory and Stockholm University

* A 2-year position in bioinformatics/evolutionary genomics, with possibility for extension, is available in the research group of Dr. Tanja Slotte, a SciLifeLab Fellow in Ecological Genomics (https://tanjaslottelab.se). * We address fundamental biological and evolutionary questions using advanced combinations of laboratory work and computational analyses - for recent examples of our work, see e.g. Slotte et al. 2013 Nature Genetics, Douglas et al 2015 PNAS, Steige et al 2015 MBE.

The position * For us, bioinformatics is central to staying at the forefront at our field, and you will have a key position in our team, working closely together with group members all the way from planning experiments to final analyses and visualizations of results. * You will be part of a tight interdisciplinary team working with large- scale data analyses based on NGS sequencing and omics data from multiple technology platforms. * You will be part of the vibrant and growing bioinformatics community at SciLifeLab, and for knowledge transfer within SciLifeLab, you will also be affiliated with the National Bioinformatics Infrastructure Sweden (NBIS; www.bils.se, www.nbis.se).

Qualifications * We seek a candidate with a PhD in bioinformatics or a related field who has strong competence in analyses of next-generation sequencing (NGS) data, and who has the ability to drive projects and collaborate productively with team members. * You need to be proficient in one or more scripting languages (e.g. Perl, Python, Ruby) and familiar with Unix environments. * Basic understanding of statistics and probability, or a background in population genomics/comparative genomics is beneficial, as this is a strong component of our work. * Experience of working with PacBio data is a merit. * Excellent organizational skills and communication skills in both written and spoken English are required.

The environment * We are located at Science for Life Laboratories in Stockholm (http://www.scilifelab.se), which harbors world-leading expertise in high-throughput sequencing technology and bioinformatics. * The working atmosphere is international with English as the working language. The city of Stockholm is known for its beauty, its buildings and architecture and its abundant clean and open water.

Application * Please apply online through the Stockholm University application system no later than April 30th: http://www.su.se/english/about/-vacancies/vacancies-new- list?rmpage=job&rmjob89 * For questions about the position, please contact Dr. Tanja Slotte (tanja.slotte@su.se)

Tanja Slotte, SciLifeLab Fellow in Ecological Genomics
Department of Ecology, Environment and Plant Sciences
Stockholm University

Email: Tanja.Slotte@su.se; Tanja.Slotte@scilifelab.se

Visiting Address: SciLifeLab Stockholm Tomtebodav. 23 a 171 65 Solna SWEDEN

"tanja.slotte@su.se" <tanja.slotte@su.se>

StockholmU EvolOrganismalBiology

Associate Professor in Zoological Organism Biology

Ref. No. SU FV-3365-15 Closing date: 16 May 2016.

The Department of Zoology has a long history of basic and applied research on animals ranging from insects to large mammals, at five divisions: Ecology, Ethology, Population genetics, Functional morphology and Systematics and evolution. The Department holds a staff of around 100 employees, of which 16 are permanent Lecturers/Professors and 40 PhD students. The Department keeps a research station (Tovetorp) south of Stockholm with facilities for various field- and laboratory experiments. The advertised position in Zoological organism biology will be affiliated to the Division of Functional morphology that has a long tradition of research in neuroscience, endocrinology, reproductive biology, and also more recently insect sensory physiology and behavior, as well as genomics and evolution of life history traits of insects. At present the organisms under study are insects, including Drosophila, the water flea Daphniaand fish, for all of which rearing facilities are available. Access to state of the art imaging equipment, as well as genomics and bioinformatics resources are provided by affiliated core facilities. Researchers at the division actively collaborate with scientists at several of the other divisions in the Department in projects such as "Insect life cycle genomics and adaptations in the wild" and "Insect - host plant interactions".

Subject description Organism biology encompasses functional morphology and experimental physiology.

Main responsibilities Research, supervision and teaching. The teaching is primarily in animal diversity, comparative anatomy and physiology.

Qualification requirements In order to qualify for employment as associate professor, the applicant must have demonstrated good teaching skills and have a doctoral degree, or equivalent research expertise, of relevance to the subject area and the main responsibilities of the position.

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

Assessment criteria In the appointment process special consideration will be given to scientific and teaching proficiency, which will be weighted equally. Assessment of scientific proficiency will primarily focus on merits within the subject area of the position.

Additional information Female applicants are particularly welcome, as most associate professors at the department are men.

The Faculty's criteria for assessment of research and teaching skills: www.science.su.se The language of instruction for introductory courses and programmes is in Swedish. If the successful candidate does not speak Swedish at the time of appointment, there are many higher level courses that could be taught in English.

Stockholm University strives to be a workplace free from discrimination and with equal opportunities for all.

Contact Further information about the position can be obtained from the Head of the Department, Professor Birgitta Tullberg, telephone: +46 8 16 40 36, Birgitta.Tullberg@zoologi.su.se or Professor Dick Nässel, telephone: +46 8 16 40 77, Dick.Nassel@zoologi.su.se.

For questions regarding the application process, please contact administrator Carina Nymark, telephone: +46 8 16 17 67, Carina.Nymark@su.se.

Union representatives Anqi Lindblom-Ahlm (Saco-S) and Lisbeth Häggberg (Fackförbundet ST), telephone: +46 8 16 20 00 (operator), and Gunnar Stenberg (SEKO), telephone: +46 70 316 43 41.

Application Apply for the position at Stockholm University's recruitment system by clicking the "Apply" button. It is the responsibility of the applicant to ensure that the application is complete in accordance with the instructions in the job advertisement, and that it is submitted before the deadline.

We would appreciate it if your application is written in English. Since it will be examined by international experts, English is the working language.

The University's rules of employment and instructions for applicants are available at:Instructions - Applicants.

You are welcome to apply!

We are one of Europe's leading universities in one of the world's most dynamic capitals. A relationship with Stockholm University delivers quality outcomes whether you are an employee, student, researcher or stakeholder. Our education and research produce results.

Closing date: 16/05/2016 URL to this page http://www.su.se/english/about/vacancies/vacancies-new-list?rmpage=job&rmjob=1125&rmlang=UK Christopher W. Wheat, Ph. D.

Associate Professor, Senior Lecturer Population Genetics Department of Zoology Svante Arrheniusväg 18 B, Room D 551 Stockholm University S-10691 Stockholm Sweden

chris.wheat@zoologi.su.se

Office: +46 816 4020

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TrinityU Texas 9mnth TeachingEvolution

Visiting Faculty in Biology

The Department of Biology at Trinity University invites applications for a temporary, full-time, 9-month Visiting Assistant Professor position in the areas of evolutionary or organismal biology, to begin in August 2016. We seek outstanding candidates that possess a Ph.D. and are enthusiastic to teach in our integrative introductory biology courses and additional courses as needed by the Department. Applicants with the ability to teach advanced undergraduate lecture and lab courses on topics such as evolution or vertebrate/invertebrate biology and who are comfortable teaching in the field will be highly competitive.

Trinity University is a top-ranked, small, private liberal arts and sciences university that values high quality undergraduate teaching and supports high impact undergraduate research. The Department of Biology (https://new.trinity.edu/academics/departments/biology), located in Trinity's state-of-the-art Center for Sciences and Innovation, has 13 highly collaborative faculty and serves majors in Biology, Neuroscience, Biochemistry and Molecular Biology, and Environmental Studies. Trinity is located in San Antonio, a large, vibrant, cosmopolitan city located in south central Texas. San Antonio's cost of living is relatively low for a major metropolitan area. More information on the city of San Antonio can be found athttp://visitsanantonio.com/ . Applicants should electronically submit a cover letter, curriculum vitae, statement of teaching philosophy and contact information for three references to Prof. Jonathan King, Chair of Search Committee, Department of Biology, Trinity University, One Trinity Place, San Antonio, TX 78212. Email applications are welcomed at Biology@trinity.edu. Review of applications will begin immediately and continue to position is filled. Women and minority candidates are strongly encouraged to apply. Trinity University is an Equal Opportunity/Affirmative Action Employer. https://inside.trinity.edu/human-resources/employment-opportunities/fac ulty/7131

Michele A. Johnson, Ph.D. Associate Professor Trinity University Department of Biology One Trinity Place San Antonio, TX 78212 michele.johnson@trinity.edu office phone: 210-999-8918 lab phone: 210-999-8914 www.trinity.edu/mjohnso9/ Michele Johnson <mjohnso9@trinity.edu>

UCyprus ConservationBiol

ANNOUNCEMENT OF ACADEMIC POSITION

The University of Cyprus invites applications for one (1) tenure-track academic position at the rank of Lecturer or Assistant Professor.

DEPARTMENT OF BIOLOGICAL SCIENCES

One position at the rank of Lecturer or Assistant Professor in the field of:

Ecology of terrestrial biota (Includes molecular ecology, population ecology, community ecology, ecosystem ecology, mathematical ecology, ecological modeling, macroecology, biogeography, behavioral ecology, conservation ecology, invasion ecology and global change ecology, as well as any other relevant field).

For all academic ranks, an earned Doctorate from a recognized University is required.

Requirements for appointment depend on academic rank and include: prior academic experience, research record and scientific contributions, involvement in teaching and in the development of high quality undergraduate and graduate curricula.

The minimum requirements for each academic rank can be found at the webpage:

http://www.ucy.ac.cy/hr/el/-recruitmentsupportoffcacadresearch/20-gr-art icles/recruitment-support-offc-acad-research/55-guidesproceduresacadmpe rsn

Applications must be submitted by Friday, 8th of July 2016.

For more information and details concerning the announcement (documents needed, salary levels etc), , candidates may refer to the website of the Department of Biological Sciences: http://www.ucy.ac.cy/biol/en/ Spyros Sfenthourakis

Associate Professor Department of Biological Sciences University of Cyprus P.O. Box 20537 1678 Nicosia Cyprus

tel: +357 22893998 mobile: +357 99055691 home: +357 22335677 fax: +357 22895331

Email: sfendour@ucy.ac.cy

Website: http://biodiversitylab.ucy.ac.cy Spyros Sfendourakis <sfendour@ucy.ac.cy>

UKansas DrosophilaHostPathogen

The Department of Molecular Biosciences, University of Kansas, seeks an assistant researcher with interests and experience in molecular biology and Drosophila husbandry. The successful candidate will work with a research group that addresses the broad themes of host-pathogen interaction and genetic conflict using Drosophila. This position consists of an initial 2-yr appointment beginning in mid-August 2016. The applicant should be extremely organized, work well with others, have a willingness to learn, and be able to participate at many levels in the laboratory. Required qualifications include a B.S. in Biology or closely related field and experience with molecular biological techniques as evidenced by application material.

For a complete announcement and to apply online, go to https://employment.ku.edu/staff/5919BR .A complete online application includes the following materials: CV, Cover letter, contact information for two reference letters. Initial review of applications begins 05/15/2016 and continues as needed to ensure a large, high quality, and diverse applicant pool. For first consideration, please apply before 05/15/2016.

The University of Kansas prohibits discrimination < http://policy.ku.edu/IOA/nondiscrimination > on the basis of race, color, ethnicity, religion, sex, national origin, age, ancestry, disability status as a veteran, sexual orientation, marital status, parental status, gender identity, gender expression, and genetic information in the universitys programs and activities. Retaliation is also prohibited by university policy. The following persons have been designated to handle inquiries regarding the nondiscrimination policies and are the Title IX coordinators for their respective campuses: Executive Director of the Office of Institutional Opportunity & Access, IOA@ku.edu, 1246 West Campus Road, Room 153A, Lawrence, KS 66045, 785-864-6414, 711 TTY (for the Lawrence, Edwards, Parsons, Yoder, and Topeka campuses); Director, Equal Opportunity Office, Mail Stop 7004, 4330 Shawnee Mission Parkway, Fairway, KS 66205, 913-588-8011, 711 TTY (for the Wichita, Salina, and Kansas City, Kansas medical center campuses).

"Unckless, Robert Lewis" <unckless@ku.edu>

UKansas ResAsst EvolGenomics RNASilencing

A research assistant position is immediately available for a highly motivated individual with an interest in genomics and evolutionary genetics in the laboratory of Dr. Justin Blumenstiel, Department of Ecology and Evolutionary Biology, University of Kansas. The focus of the research project is to study the co-evolution between selfish DNA and genome defense by RNA silencing. More information about the lab can be found at http://www.blumenstiellab.org/ . Required qualifications include a Bachelor's degree in Biology or related field and at least 6 months of laboratory experience in molecular biology, as evidenced by application materials. The initial appointment is for one year with the possibility of renewal. The position is contingent upon funding. The position is expected to begin as early as June 1, 2016. Inquiries can be sent to: jblumens@ku.edu.

For a complete announcement and to apply online, go to https://employment.ku.edu/staff/5997BR .A complete online application includes the following materials: CV, Cover Letter with description of most recent research experience and contact information for three references. Initial review of applications begins 05/20/2016 and continues as needed to ensure a large, high quality, and diverse applicant pool. For first consideration, please apply before 05/20/2016.

The University of Kansas prohibits discrimination < http://policy.ku.edu/IOA/nondiscrimination > on the basis of race, color, ethnicity, religion, sex, national origin, age, ancestry, disability status as a veteran, sexual orientation, marital status, parental status, gender identity, gender expression, and genetic information in the universitys programs and activities. Retaliation is also prohibited by university policy. The following persons have been designated to handle inquiries regarding the nondiscrimination policies and are the Title IX coordinators for their respective campuses: Executive Director of the Office of Institutional Opportunity & Access, IOA@ku.edu, 1246 West Campus Road, Room 153A, Lawrence, KS 66045, 785-864-6414, 711 TTY (for the Lawrence, Edwards, Parsons, Yoder, and Topeka campuses); Director, Equal Opportunity Office, Mail Stop 7004, 4330 Shawnee Mission Parkway, Fairway, KS 66205, 913-588-8011, 711 TTY (for the Wichita, Salina, and Kansas City, Kansas medical center campuses).

Justin Blumenstiel Associate Professor

Department of Ecology and Evolutionary Biology University of Kansas 1200 Sunnyside Avenue Haworth Room 7026 Lawrence, KS 66045

jblumens@ku.edu 785-864-3915 http://www2.ku.edu/~eeb/faculty/blumenstiel.shtml "No Drosophila female could conceivably lay two billion eggs in her lifetime." - R.C. Lewontin and J.L. Hubby

"Blumenstiel, Justin P" <jblumens@ku.edu>

UKonstanz 3 EvolutionaryBiol 2

- Please contact me, if you would like to know more about those three full professorships in Konstanz

Axel.Meyer@uni-konstanz.de Tel. + 49 7531 88 4163

Three Full professorships (W3-salary scale) at the University of Konstanz

1. Professorship (Job Add 2016/054)

The University of Konstanz, with its "Institutional Strategy to promote Top-Level Research", has been receiving continuous funding since 2007 within the framework of the Excellence Initiative by the German Federal and State Governments.

The Movement Ecology Cluster is a joint venture of the University of Konstanz and the Max Planck Society to decode the general mechanisms and principles of movement and collective behavior from the cellular to the population level.

For this cluster, the University of Konstanz is filling as soon as possible the following position:

W3-Professor of Organismal Interactions

(Job Add 2016/054)

We seek applicants who are internationally recognized for their research in the field of Organismal Interactions and who address fundamental questions in ecology, behaviour or evolution. We are particularly interested in researchers who have made important conceptual advances and have worked across, or integrated, levels of biological organisation and complexity (e.g. genes and social behaviour, individual interactions and group or population dynamics). This could involve behavioural studies, experimental evolution, microbiomics, co-evolution, plant-insect interactions or the study of mechanisms of interactions among organisms.

All application materials (curriculum vitae, publication list, a list of grants and awards, details of teaching experience, as well as statements of current research topics, future research directions and interests) should be sent as one pdf file and in English to Prof-2016-054@uni-konstanz.deuntil the 15th of April 2016.

Further information is available on our website: http://www.uni-konstanz.de/stellen or by contacting Hanns Fahlbusch, phone +49(0)7531/88-2413, e-mail: hanns.fahlbusch@uni-konstanz.de.

For further information of all Job Offers please visit our website: http://www.uni-konstanz.de/stellen . —–

2. Professorship (Job Add 2016/055)

The University of Konstanz, with its "Institutional Strategy to promote Top-Level Research", has been receiving continuous funding since 2007 within the framework of the Excellence Initiative by the German Federal and State Governments.

The Movement Ecology Cluster is a joint venture of the University of Konstanz and the Max Planck Society to decode the general mechanisms and principles of movement and collective behavior from the cellular to the population level.

For this cluster, the University of Konstanz is filling as soon as possible the following position:

W3-Professor of Limnology/Aquatic Ecology

(Job Add 2016/055)

We seek applicants who are internationally recognized for their research in the field of Organismal Interactions and who address fundamental questions in ecology, behaviour or evolution. We are particularly interested in researchers who have made important conceptual advances and have worked across, or integrated, levels of biological organisation and complexity (e.g. genes and social behaviour, individual interactions and group or population dynamics). This could involve behavioural studies, experimental evolution, microbiomics, co-evolution, plant-insect interactions or the study of mechanisms of interactions among organisms.

All application materials (curriculum vitae, publication list, a list of grants and awards, details of teaching experience, as well as statements of current research topics, future research directions and interests) should be sent as one pdf file and in English toProf-2016-55@uni-konstanz.deuntil the 15th of April 2016.

Further information is available on our website: http://www.uni-konstanz.de/stellen or by contacting Hanns Fahlbusch, phone +49(0)7531/88-2413, e-mail: hanns.fahlbusch@uni-konstanz.de.

For further information of all Job Offers please visit our website: http://www.uni-konstanz.de/stellen . —–

3. Professorship (Job Add 2016/056)

The University of Konstanz, with its "Institutional Strategy to promote Top-Level Research", has been receiving continuous funding since 2007 within the framework of the Excellence Initiative by the German Federal and State Governments.

The Movement Ecology Cluster is a joint venture of the

University of Konstanz and the Max Planck Society to decode the general mechanisms and principles of movement and collective behavior from the cellular to the population level.

For this cluster, the University of Konstanz is filling as soon as possible the following position:

W3-Professor of Genetic Adaptations in Aquatic Systems

(Job Add 2016/056)

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UMunich 2 ResAssoc EvolutionaryGenetics

Research Associate Position in Evolutionary Genetics at Ludwig-Maximilians-Universit????t M????nchen

Two six-year (3+3) research associate positions (Akademischer Rat auf Zeit A13) are available in the Department of Evolutionary Biology at the Ludwig-Maximilians-Universit????t M????nchen (LMU) with a payment scale comparable to a Senior Lecturer/Reader salary in the UK.

The position. We seek a highly motivated, mature researcher with a proven publication record in evolutionary genetics and related fields (comparative genomics, population genetics, experimental evolution, molecular ecology). For candidates actively seeking funding, this position provides a great opportunity to develop one's own research agenda and start an independent research group. Scientific co-operations within and outside the department are explicitly encouraged (http://www.en.biologie.uni-muenchen.de/forschung/topics/index.html).

The position comes with 5 hours of teaching duties during the semester (approx. 145 hours per annum) including lecturing, course administration and student supervision. With both the Graduate School for Evolution, Ecology and Systematics (EES http://ees.bio.lmu.de/) and the European Erasmus Mundus Program in Evolutionary Biology (MEME http://www.evobio.eu/) you will meet an international and highly motivated group of students.

The environment. The successful candidate will be based in the Department of Evolutionary Biology where we take an integrative approach to the study of evolutionary processes (http://www.evol.bio.lmu.de/). We apply a large range of methodology including fieldwork, population genetic modelling, large genomic approaches, to experimental evolution work and functional characterization at the single cell level. With the retirement of Prof.

Wolfgang Stephan and the recent appointment of Prof. Jochen Wolf the Department currently undergoes a transition, which is not reflected on the website yet. Therefore, please consult (http://www.ieg.uu.se/evolutionary-biology/wolf/) for information on Prof. Wolf's research.

Munich University (LMU) and Munich Technical University (TUM) are both recognized among Europe's premier academic and research institutions being consistently ranked among the top Universities worldwide. In particular the life science branch with its newly inaugurated campus offers excellent technical facilities and many interaction possibilities including the Gene Centre, several Max-Planck-Institutes and the Helmholtz Centre (http://www.campusmartinsried.de/en/336-2/).

With the highest concentration of supercomputing in Germany the Leibniz Supercomputing Centre and its local partners provide access to state-of-the art computing facilities (https://www.lrz.de/english/) for genome-scale analyses. Munich is Bavaria's capital, a vibrant, yet relaxed city with many traditions still alive and a high quality of living.

In contrast to the current funding climate in many other European and non-European countries, funding rates are relatively high in Germany, and there are several sources to apply from, see e.g.

http://www.research-in-germany.org/en/research-funding.html or http://www.dfg.de/en/research_funding/programmes/index.jsp. In addition, transnational European funding schemes offer attractive opportunities (https://erc.europa.eu/funding-and-grants).

How to apply. Applicants holding a PhD with a proven publication record are encouraged to apply. Teaching experience is beneficial.

Applications including a statement of motivation including relevant expertise, a CV and the contact details of at least two references should be sent as a single .pdf file to jochen.wolf@ebc.uu.se subject term 'research associate'. The position remains open until filled.

Preferred start date is August 1st 2016 but can be negotiated depending on the applicant's situation.

Jochen B. W. Wolf, PhD, Professor Department of Evolutionary Biology Evolutionary Biology Centre Uppsala University Norbyv????gen 18D SE-752 36 Uppsala Sweden

phone: ++46 18 471 4120 fax: ++46 18 471 6310 http://www.ebc.uu.se/Research/IEG/evbiol/research/Wolf/ Jochen Wolf <jochen.wolf@ebc.uu.se>

UNewMexico GreenhouseManager

Greenhouse Manager

The Department of Biology at the University of New Mexico is searching for a full-time greenhouse manager who will be responsible for maintaining plants and infrastructure in the research, teaching, and public greenhouses on the UNM main campus. The manager will work closely with faculty and students and will be heavily involved in research, undergraduate and graduate education, and public outreach.

For more information, and to apply:

unmjobs.unm.edu/applicants/Central?quickFind025

You may also contact Dr. Ken Whitney, whitneyk@unm.edu, for more information.

Ken Whitney

Associate Professor Department of Biology University of New Mexico Albuquerque, NM 87131

whitneyk@unm.edu

http://biology.unm.edu/whitney/ Kenneth Whitney <whitneyk@unm.edu>

UNorthCarolina Greensboro 3yr Teaching

Please post the following job ad on evoldir. I'm hoping to attract someone with evolutionary biology interests.

Thanks,

Malcolm

—

Position Title: Academic Professional

Department: Biology - 12204

Job Description:

The Department of Biology at UNC-Greensboro is searching for a full time Academic Professional to develop and implement contemporary, evidence-based instructional approaches within our introductory level (General Biology; GB) courses (classrooms and labs), develop a GB teaching assistant training and assessment program, participate in external STEM grants and research, engage in community-based STEM activities, and teach and advise students in our undergraduate program. We are seeking an energetic and well-trained individual with evidence of experience and dedication to improving STEM education at the introductory College/University level and the retention and recruitment of undergraduate students in STEM fields.

This is a 10-month position from August 15, 2016 to June 15, 2017 with an initial contract period of 3 years that is renewable upon review. Starting salary is $57,000 per 10-month appointment. Submit your cover letter, a personal statement on teaching philosophy that addresses the challenges listed above, your curriculum vitae, and three reference letters to UNCG's Job Search website position #950.

You may view the posting as a search committee member by visiting the following link: http://jobsearch.uncg.edu/hr/postings/3641 . You may view documentation and videos on how to use the UNCGjobsearch system at the UNCGjobsearch Support Portal.

Please contact Helen Sedwick in Biology - 12204 at 336-334-4405 if you have any questions.

Malcolm Schug <schugmd@icloud.com>

UOregon ResAsst MicrobialEcol

Announcement and Advertisement Posting 16046 Career Research Assistant Institute of Ecology and Evolution Officer of Research (12-month appointment, funding contingent), 1.0FTE Closing: Application review begins April 15, 2016; position open until filled

The Institute of Ecology and Evolution at the University of Oregon currently has an opening for a full time Research Assistant to work in the area of microbial ecology. The successful candidate will play a key role in the Biology and the Built Environment (BioBE) Center (http://biobe.uoregon.edu/), funded by the Alfred

P. Sloan Foundation. The BioBE Center is engaged in research focused on the built environment microbiome the diversity of microbial life indoors, where humans spend roughly 90 percent of each day. The vision of this national research center is to understand buildings as complex ecosystems and to explore how architectural design mediates urban microbial ecology and evolution. For a description of partner projects see http://www.microbe.net/ . Extensive experience using molecular techniques is required, including some combination of skills in DNA/RNA extraction, PCR, qPCR, library preparation for high-throughput DNA sequencing, bioinformatics, and phylogenetic analysis. Ability to work in a team atmosphere is a must. A Master's degree in biology is desirable, but individuals with a bachelor in biology or a related field from an accredited institution and extensive experience are also encouraged to apply. The successful candidate will be responsible for conducting laboratory research under the direction of BioBE Center Director Jessica Green (pages.uoregon.edu/green). Salary will be commensurate with education and experience. We invite applications from qualified candidates who share our commitment to diversity.

The initial appointment is for one year, with the possibility of renewal dependent on funding and satisfactory performance. The University of Oregon is located in Eugene, Oregon, recently rated in the top "100 Best Places to Live"15 (http://www.livability.com/or/eugene) with plentiful outdoor recreational activities and a vibrant running and bicycling community.

Please e-mail a cover letter and current CV with names and contact information of three references as a single attachment to: ie2jobs@uoregon.edu Subject: Posting 16046

Or mail to: Posting 16046, 5289 University of Oregon, Eugene, OR 97403-5289.

To ensure consideration, please submit applications by April 15, 2016, but the position will remain open until filled. Position subject to criminal background check.

EO/AA/Veterans/Disability Institution committed to cultural diversity.

– INSTITUTE OF ECOLOGY AND EVOLUTION 5289 University of Oregon, Eugene OR 97403-5289 F (541) 346-2364 http://IE2.uoregon.edu EO/AA/ADA institution committed to cultural diversity. The University encourages all qualified individuals to apply, and does not discriminate on the basis of any protected status, including veteran and disability status.

"ie2jobs@uoregon.edu" <ie2jobs@uoregon.edu>

UWestAlabama AquaticBiodiversity

The Laboratory of AQuatic Evolution (LAQE) at the University of West Alabama is a new research group focused on the evolution and conservation of aquatic biodiversity. We are seeking a research associate/lecturer to assist with ongoing projects including, but not limited to: 1) Speciation in ancient lakes (Lake Baikal, Siberia); 2) Adaptation to extreme aquatic environments (blackwater and caves) in the southeastern United States; 3) Functional genomics of mitochondria.

The University of West Alabama is a small, public Master's-granting institution located within commuting distance of Meridian, MS and Tuscaloosa, AL. The University offers an attractive benefits package and competitive salaries. Affordable housing is available in Livingston, Alabama, within walking distance of campus.

Duties and responsibilities: - Maintain a small fish facility. - Assist with lab research projects. - Instruct undergraduate laboratory sections. - Purchase, inventory, and organize lab supplies. - Participate in lab meetings. - Help train new lab members.

Qualifications: - Master of Science degree in biology or a related field. - Experience with phylogenetic systematics and NGS bioinformatics. - Experience with general molecular biology techniques (DNA extraction, PCR, electrophoresis). - Proficiency with Microsoft Excel (required) and R (preferred). - Highly organized and detail-oriented.

Interested candidates should compile an application containing; 1) cover letter 2) curriculum vitae 3) transcripts of all college work 4) contact information for three professional references.

Application Deadline: Review of applications begins immediately and continues until position is filled. Complete applications (pdf) should be attached to an email with the header "Research associate application" and sent to: msandel@uwa.edu

The position is pending federal funding, which is secured through July 2019. Questions can be addressed to:

Michael Sandel Assistant Professor Department of Biological and Environmental Sciences The University of West Alabama 205-652-3475 msandel@uwa.edu

The University of West Alabama does not discriminate on the basis of race, color, national origin, gender, religion, age, disability or sexual orientation in employment, or the provision of services. Applications from members of minority groups are encouraged.

"Sandel, Michael" <msandel@uwa.edu>

UZurich Paleogenetics

Assistant Professorship in Paleogenetics: Zurich, Switzerland The Faculty of Medicine at the University of Zurich invites applications for an Assistant Professorship in Paleogenetics The position is available at the Institute of Evolutionary Medicine (Director: Prof. Dr. Frank Ruhli).

We are looking for a young and dynamic personality at an early stage in his/her career, flexible and willing to contribute significantly to this dynamic research area. Successful candidates will have demonstrated ability to independently conceive novel research projects and bring them to successful completion. We seek individuals with the following qualifications: - Training in the field of biomedicine (MD and/or PhD) - Expertise in molecular biology and DNA sequencing; experience with the analysis of ancient remains - Internationally recognized scientific track record - Interdisciplinary networking with translational research prospects - Excellent social skills; open and integrative personality - Interest for modern teaching methods Knowledge of the German Language is not mandatory, however to acquire some proficiency in German over time is expected.

The University of Zurich is an equal opportunity employer. The Faculty of Medicine implements specific measures in the selection process to increase the proportion of women with a faculty position.

Please hand in your application for this position at https://www.recruiting.med.uzh.ch/position/-5046272 by April 30st 2016.

For additional information, please contact the president of the search committee, Prof. Dr. Anita Rauch: Tel. +41 44 556 33 00, anita.rauch@medgen.uzh.ch."

Dr. Kaspar Staub Institute Manager, Senior Research Assistant Morphology/Imaging Group Institute of Evolutionary Medicine (IEM) University of Zurich Winterthurerstrasse 190 CH-8057 Zurich, Switzerland Office Y42 G88a Phone +41 44 635 05 13, Mobile +41 79 473 83 55, Fax: +41 44 635 57 02 kaspar.staub@iem.uzh.ch http://www.iem.uzh.ch/people/kasparstaub.html Kaspar Staub <kaspar.staub@iem.uzh.ch>

Victoria Australia ResFellow PopGenetics

We are advertising for a Research Fellow (Population Geneticist) to join a research laboratory located in the Parkville Precinct a Biomedical Research Hub in Victoria, Australia. The position involves a large-scale cross-institutional population genomic/genetic research programme that utilises advanced genomic sequencing and bioinformatic technologies to explore the evolution and population biology of parasitic worms of major human health importance, including Schistosoma. The Research Fellow will have a track record in bioinformatics, genomics and/or population genetics to assess genetic variation within and among populations of flatworms on a genome-wide scale, and characterise drug and vaccine targets and essential molecules involved in host-pathogen interactions. As there are no effective vaccines for flatworm parasites, current control relies largely on a handful of drugs, making drug resistance a constant threat. Therefore, this project provides a unique avenue toward developing radically new approaches for the control of flatworms, built on a deep knowledge and understanding of flatworm molecular biology and evolution. Link to the position http://jobs.unimelb.edu.au/caw/-en/listing/ (Use the position number 0040676 under Job Keyword Search).

If you require more information, please contact Neil Young (nyoung@unimelb.edu.au)

All the best,

Neil

Neil David Young <nyoung@unimelb.edu.au>

WestAustralia 5FieldTeam GnaralooTurtleConservation

Gnaraloo Turtle Conservation Program, Australia, 5x Positions available

We are seeking a Program Assistant to be part of the program *from 26 September 2016 to 30 May 2017.*

The Program Assistant manages the GTCP field team and works onsite as part of the team to undertake daily surveys of turtle nesting and feral animal activities in the monitored rookeries, community and school participation with the program, data analysis, scientific reporting and other office work.

The GTCP Program Assistant works in Perth (*September*), Gnaraloo (*October February*) and in regional and metropolitan locations in Western Australia (*March May*).

For details on how to apply, see the GTCP Program Assistant Ad:

https://drive.google.com/file/d/-0B7QHaDm8nv0WSkJjQkhJR1hFN3c/view?usp=-3Dsharing The PA Application Form can be found here:

https://docs.google.com/document/d/-1UIshSN3beSYENsMvk_u8GTuZzg6YYTXcUv25rT8n3js/-edit?usp=sharing *Internship Opportunities 2016/17*

We will appoint interns from Australia and overseas to be part of the program *from 15 October 2016 to 15 April 2017*.

The interns work, under direction and guidance, as part of the GTCP field team to undertake daily surveys of turtle nesting and feral animal activities in the monitored rookeries, community and school participation with the program, data analysis, scientific reporting and other office work. Work is undertaken on Gnaraloo (*October February*) and in regional and metropolitan locations in Western Australia (*March April*).

The GTCP *does not charge a participation fee* and provides interns with accommodation, meals and required travel within Western Australia for program commitments. *The internships are volunteer and not paid positions.*

For details on how to apply, see the GTCP Scientific Intern Ad:

https://drive.google.com/file/d/-0B7QHaDm8nv0WX2FxejM1Vi1YR1k/view?usp=-3Dsharing The Internship Application Form can be found here:

https://docs.google.com/document/d/1juq-k-S39z83KtgQoO1x9anfmtachyFmBKUkY7LGZDU/-edit?usp=sharing *Applications close 5pm (AWST) 30 May. Late applications will not be accepted.*

Gnaraloo Recruitment

Please consider the environment before printing this e-mail or its attachments

Gnaraloo Turtle Conservation Program (Facebook)

Ningaloo Coast World Heritage Area

+ 61 8 9942 5927

www.gnaraloo.com.au PO Box 99 Carnarvon Western Australia 6701

gtcprecruit@gmail.com

Other

AGA award student article

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

The American Genetic Association has granted the 2016 Stephen J. O'Brien Award for best article lead-authored by a student to Genevieve Metzger for the article, 'Genetic Structure across Broad Spatial and Temporal Scales: Rocky Mountain Tailed Frogs (Ascaphus montanus; Anura: Ascaphidae) in the Inland Temperate Rainforest < http://jhered.oxfordjournals.org/content/106/6/700.full > (Metzger et al. 2015. J Hered 106(6):700-710). The award includes a $2,000 prize, up to $1,500 reimbursement to attend the AGA Symposium, and an AGA membership and subscription to Journal of Heredity.

The Award Committee had the following comments:

'This study is an excellent comprehensive analysis of genetic structure of an ancient amphibian species inhabiting a unique ecosystem of North America. It incorporates an impressive dataset (and information from previous mtDNA phylogeography) with thorough and integrative analyses. The article is well-written and clear in examining the roles of climatic factors, landscape ecology, phylogeography, and genetic diversity.'

The article is available with free access at http://jhered.oxfordjournals.org/content/106/6/700.full We congratulate this emerging researcher on her achievement.

Scott Baker Editor, Journal of Heredity

agajoh@oregonstate.edu

ASN RegionalMeetings Awards

DEADLINE April 1st: ASN Awards for Support of Regional Meetings in Ecology, Evolution and Behavior

The American Society of Naturalists solicits proposals from organizers of regional meetings in the fields of ecology, evolution and behavior. The purpose of these small awards is to promote increased participation in regional meetings that fall along the research interests supported by the ASN and to use this support as a way of recruiting new membership to ASN. The awards typically provide subsidized registration for ASN members at these regional meetings. Please note that these awards are not intended to support workshops. Organizers of regional meetings should submit a brief proposal describing the research focus of the meeting for which funds are requested as well as details of the meeting such as anticipated number of participants, meeting venue and dates.

/Instructions:/Proposals should clearly describe (1) overlap of the regional meeting with ASN research interests, (2) extent that the support would reach out to new audiences to grow ASN's membership, (3) potential size of the impact on ASN membership, and (4) a brief budget justifying the amount requested and how the funds will be used. To standardize the applications, there is a strict one-page limit (US Letter size paper, 1-inch margins, standard [e.g., Times] 12-point font, and no more than six lines per inch) for each component (i.e., proposal, budget description). We anticipate funding 4-6 awards, typically valued at $2000-$3000.

Please send proposals to the ASN Regional Society Liaison Committee Chair Renee Duckworth at rad3@email.arizona.edu by April 1st.

Renee Duckworth <rad3@email.arizona.edu>

Australia Cairns VolFieldAssistant FairyWrens

Volunteer field assistants

We are looking for two field assistants to help monitor a colour-banded population of Lovely fairy-wrens in Cairns, Australia, for a research project on female ornamentation from University of Melbourne.

Time period: From early July or mid September to end of November. Assistants are expected to stay for a minimum of 10 weeks, but a period of 5 months is preferred.

Duties: Regular mist-netting, censusing of colour-banded birds, searching for and monitoring nests, recording song, behavioural observations, territory mapping, video analysis, data proofing and assisting in behavioural experiments. Working days are long, with early starts six days a week. Enthusiasm, self-motivation and organisation, and a strong work ethic are a must.

Qualifications: mist-netting, banding, experience monitoring colour-banded birds and nest-searching. Must also be early riser, physically fit, able to work in extreme weather conditions (hot, humid, and occasional tropical rain), maintain a positive attitude and enjoy shared living conditions. Good knowledge of English is a requirement. Having experience in behavioural observations and a driving licence is a plus but not a requirement.

Compensation: Free onsite accommodation is provided, but assistants cover travel to the site and their own food costs. The project will reimburse up to AUD$500/month (5 months= $2500) or week $125/week (10 weeks=$1250) towards receipted food and travel expenses.

Assistants will have the opportunity to enjoy the unique wildlife of North Queensland and leisure time to visit Cairns, the Great Barrier Reef or the world heritage rainforests.

For more information contact: Ana Leitao (anamvleitao@gmail.com). To apply, please email a letter outlining previous relevant field research experience, availability (5 months or 10 weeks and start time) and a CV including names and contact information for 3 referees. Applications received until the 23th of April 2016 will receive full consideration. Later applications may be considered.

anamvleitao@gmail.com

Australia Melbourne VolFieldAssistant FairyWrens

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

Time periods: Four-month minimum, commencing early September, or early January.

Duties include catching birds for personality testing before and after the breeding season (Oct-Jan), and regular censusing of colour-banded birds during the breeding season, searching for and monitoring nests, behavioural observations, video analysis, and data proofing. Working days are long, with early starts six days a week. Enthusiasm, self-motivation, and a strong work ethic are a must.

The study is based at Serendip Sanctuary, a small reserve with abundant birdlife on the outskirts of Melbourne.

Qualifications: experience monitoring colour-banded birds, nest-searching, and mist-netting. Must also be early riser, physically fit, able to work in extreme weather conditions, and enjoy basic shared living conditions.

Onsite accommodation in a house with shared dorm-style room is provided, but assistants cover travel to the site and their own food costs. The project will reimburse up to AU$750/mo towards receipted food and travel expenses.

For more information contact: Timon van Asten (t.van@unimelb.edu.au). To apply, please email a letter outlining previous relevant field research experience, and a resume including names and contact information for 3 referees that are familiar with your mist-netting and/or nest-searching experience.

"timonv@student.unimelb.edu.au"
<timonv@student.unimelb.edu.au>

Cause and Effect

dear and reputable members of the evoldir,

over the last few years i have exchanged several emails with elliott sober about the "nature of selection". During the last bout of exchanges last fall, an issue about relative fitness arose that epistemologically looks terminally damning to current relative-fitnessical modelling of natural selection (NS), but about which i have not been able to find literature.

already in that occasion, elliott found in page 17 of his 1984 masterpiece "the nature of selection" a possibly relevant citation of a passage from a 1974 book by michael t.ghiselin ("the economy of nature and the evolution of sex"), to which i have no access.

i would like to kindly ask you, dear and reputable members, to point out published materials and informal remarks made by anybody that may be relevant to this issue (presented below; excerpts of the emails further below). All replies will be shared back with evoldir unless you request otherwise. I recommend that you focus on the gist of the arguments below and in the emails, rather than on the flawed examples that i use.

the main issue is why NS's relative-fitnessical story telling and modelling are allowed to mention causally non-interacting elements just to satisfy the prurient "who's winning" narrative attractor. To put it more colorfully, i have long wanted to mention the beloved paddington bear in say my papers on molecular evolution, but i have refrained from doing it because the concededly adorable bear does not play any causal role in the issues discussed in my papers.

why then do NS story telling and NS modelling mention by default, e.g. in an asexual case, all "competing clones" of a "species" even though some of them may not be involved in any way in an eventual favoring or disfavoring by NS of some other clone(s), i.e., even though some of the "competing" clones may be causally totally irrelevant to the NS process at stake and may be persisting across generations without any change in numbers and trophic appropriation spectrum?

some interesting aspects of this epistemologically most crass violation of perhaps the most fundamental axiom of scientific narratives are: i) how should a criterion for inclusion of elements in NS narratives look (even if only for the asexual case), one that would make it impossible to include causally irrelevant bystander elements? ii) how can one deal with bystander elements that increase in frequency in reaction to decreases in other element(s) driven by NS (e.g., due to predation on the latter) but are not involved in causing the decreases in any way? iii) which research on NS and evolution has been stymied and which artifactual confusions exist in the literature that may be due to the fact that current NS modelling does not restrict itself strictly to studying only cause and effect?

an example of (iii) is perhaps the lack of progress in overcoming the circularity accusations levied against NS studies, i.e., in fending off such accusations with more than anti-scientific conjurings of the epistemological singularity of NS narratives. Where could NS research go if it respected strictly the principle that all winners and losers in NS stories must show correspondingly altered (even if not globally so) biosynthetic gains and losses (for reproduction and metabolism as well as for clonal and single-cell growth), be these alterations due to "zero-sum" trophic give-and-take or to trophic-niche expansions and contractions? Gene genealogies could be stamped brute-force onto life's cytoplasmic tree whose branches extend forwards in time (reticulated when lineages are sexual) with pulsating thickness reflecting their realized instantaneous biosynthetic footprint, in order to so correlate the strategies of trophic appropriation and trophic persistence of cytoplasmic lineages with the red-queen-like turnover of the gene coalitions that are differentially sucked forward in time inside the branches as they contribute to generate the branches' contractions and dilatations.

similarly, researchers could look at how inter-specific competition sets limits within species to mutant invasions and polymorphism maintenance, and also look at how, e.g., males "winning" in sexual selection mediate how genes and gene coalitions profit from the biosynthesis payoffs brought to the table by the choosing females (literally for the biosynthesis of progeny).

maybe this mountainous epistemological flaw will give birth to no more than a murinely trivial revival of community-matrix antics expanded perhaps to include intra-specific trophic polymorphisms and their microniches, but one thing appears certain: Violating the principle that scientific narratives are only then legitimate when they restrict themselves to shedding light on cause and effect is guaranteed to have pernicious short- and long-term effects in any scientific discipline, unless the violations cease, are studied, and their past consequences are purged.

— / —

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

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

ESEB FundingForEqualOpportunities

PLEASE NOTE THAT THE DEADLINE HAS BEEN EXTENDED UNTIL 30 APRIL 2016!!

The European Society for Evolutionary Biology (ESEB) welcomes applications for the newly introduced Equal Opportunities Fund. Applications are not limited to European countries. This is the first call for proposals for activities that increase awareness of the problem and possible solutions. Such proposals can include, but are not limited to, short workshops (for instance, on unconscious bias) and/or seminars (with invited speakers) at your home organization, data collection, data collection and publication activities and similar events. It must be clear from the proposal how the activity will improve our knowledge and awareness of unequal opportunities, or how the activity will improve equal opportunities directly, in the ESEB specifically, or Evolutionary Biology as a field in general. There are two calls per year, with the next upcoming deadline being the 30th of April 2016.

More information about the Equal Opportunities Initiative is available at http://eseb.org/prizes-funding/equal-opportunities-initiative/ ELIGIBILITY

* Applicants must be ESEB members (for becoming a member of ESEB, please visit http://eseb.org/society/membership/) * Applications can be submitted by scientists at any stage of their professional career (e.g., Masters and PhD students, postdocs, and lecturers). * Applicants must provide proof of support of the host institution where the activity should take place (letter from head of department) * Applicants must explain explicitly how their activity will improve our knowledge, awareness of unequal opportunities, or how the activity will improve equal opportunities directly, in ESEB specifically, or Evolutionary Biology as a field in general. * Applicants must detail which group of people, and how many, will benefit from this activity (for instance, 50 undergraduates, 10 graduate students, 15 faculty members) * Budgets should be reasonable (usually not exceeding 1000,- EUR), and detail costs per person (that benefit from this event).

HOW TO APPLY

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

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

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

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

Kind regards, Ute Friedrich –

ESEB Office Manager Email: office@eseb.org Website: eseb.org

julia.schroeder@gmail.com

EuropeanSocEvolBiol Funding CallApplications NewDeadline Apr30

PLEASE NOTE THAT THE DEADLINE HAS BEEN EXTENDED UNTIL 30 APRIL 2016!! ——

The European Society for Evolutionary Biology (ESEB) welcomes applications for the newly introduced Equal Opportunities Fund. This is the first call for proposals for activities that increase awareness of the problem and possible solutions. Such proposals can include, but are not limited to, short workshops (for instance, on unconscious bias) and/or seminars (with invited speakers) at your home organization, data collection, publication activities and similar events. It must be clear from the proposal how the activity will improve our knowledge and awareness of unequal opportunities, or how the activity will improve equal opportunities directly, in the ESEB specifically, or Evolutionary Biology as a field in general. There are two calls per year, with the next upcoming deadline being the 30th of April 2016.

More information about the Equal Opportunities Initiative is available at http://eseb.org/prizes-funding/-equal-opportunities-initiative/ ELIGIBILITY

* Applicants must be ESEB members (for becoming a member of ESEB, please visit http://eseb.org/society/-membership/) * Applications can be submitted by scientists at any stage of their professional career (e.g., Masters and PhD students, postdocs, and lecturers). * Applicants must provide proof of support of the host institution where the activity should take place (letter from head of department) * Applicants must explain explicitly how their activity will improve our knowledge, awareness of unequal opportunities, or how the activity will improve equal opportunities directly, in ESEB specifically, or Evolutionary Biology as a field in general. * Applicants must detail which group of people, and how many, will benefit from this activity (for instance, 50 undergraduates, 10 graduate students, 15 faculty members) * Budgets should be reasonable (usually not exceeding 1000,- EUR), and detail costs per person (that benefit from this event).

HOW TO APPLY

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

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

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

Kind regards, Ute Friedrich –

ESEB Office Manager Email: office@eseb.org Website: eseb.org

Julia_Schroeder <julia.schroeder@gmail.com>

Evolution2016 FilmVideo Contest

2016 Evolution Film Festival/Video Contest (#evofilmfest) Scientists and science educators of all stripes ???????? students, postdocs, faculty, and full- or part-time science communicators ???????? are invited to enter the Sixth Annual Evolution Video Competition, sponsored by the Duke Initiative for Science & Society, the Howard Hughes Medical Institute (HHMI), the Society for the Study of Evolution (SSE) and the BEACON Center for the Study of Evolution in Action.

To enter, please submit a video that explains a fun fact, key concept, compelling question, or exciting area of evolution research in THREE MINUTES OR LESS.

Entries may be related or unrelated to your own research, and should be suitable for use in a classroom (K-12, undergraduate, graduate???????your choice). Videos should be both informative and entertaining. (In other words, no taped lectures or narrated Powerpoint presentations!) Animations, music videos, and mini documentaries are all fair game.

The finalists will be screened at the 2016 Evolution meeting in Austin, TX. (You do not need to attend the conference in order to enter a video.) First- and second-place winners will receive up to $1,000 and $500, respectively.

The deadline to submit your video(s) is TUESDAY, MAY 31st, 2016 (11:00 PM, EST).

For more information (and to see entries from previous years) please visit evolutionfilmfestival.org, #evofilmfest or contact Jory Weintraub (jory@duke.edu)

Jory Weintraub <jory.weintraub@gmail.com>

FieldMuseum Chicago NSF REU BiodiversityEvolution

NSF Research Experience for Undergraduates (REU) in the Evolution of Biodiversity across the Tree of Life

We are looking for 8 undergraduate students to participate in hands-on research in biodiversity science and receive training in cutting-edge techniques and analysis in evolutionary biology for 10 weeks during the summers of 2016-2018.

Applications close April 22, 2016.

Students will learn research techniques that include DNA sequencing and computational analysis of genetic and genomic data, morphological measurements and phylogenetic analysis, and microbiology and next-generation microbial sequencing. Scientific projects to be conducted by the students include the evolution of morphological variation in extinct therapsids, tropical bird biogeography, population genetics of sharks, influence of disease on bird genetic diversity in urban environments, quantitative analysis of meteorites, the influence of hydrostatic pressure on morphological diversity in octopuses, and co-diversification of ants and their gut bacterial communities. In addition students will receive career mentoring in a diversity of STEM fields, gain experiences in public outreach and science communication, receive training in ethics/responsible conduct of research, and participate in a diversity workshop to help overcome bias in science.

https://www.fieldmuseum.org/reu https://www.fieldmuseum.org/2016-reu-program-offerings Students will be provided a stipend, dormitory housing, and assistance with travel costs.

Participants must be U.S. citizens or permanent residents, and an undergraduate during the entire period. We especially encourage students from groups traditionally underrepresented in science to apply.

To apply, please send complete the online application: https://www.fieldmuseum.org/2016-reu-program-offerings Applications close April 22, 2016.

Please direct any questions to Jonathan Hense (jhense@fieldmuseum.org).

Please share widely.

Thank you, Corrie Moreau

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

ISBE2016 TravelAward

Travel funds have been made available by the National Science Foundation to provide partial travel support for early career investigators to attend the 16th Congress of the International Society for Behavioral Ecology in Exeter, UK (http://www.isbe2016.com). Applicants must be US citizens or permanent residents currently working at US institutions who are graduate students, postdoctoral researchers, or pre-tenure faculty.

To apply for a travel award, please submit the following items as a single PDF document <5 pages in length:

(a) a short curriculum vitae (2 pages or less);

(b) a brief description of up to 3 of your most significant contributions, including research (published or not), teaching, or service (i.e., outreach, departmental committees, society office, etc.);

(c) a brief diversity statement;

(d) a brief description of what you would gain from participating in ISBE 2016;

(e) the oral or poster presentation abstract that you have submitted or will submit to ISBE; and

(f) a travel budget including the actual or estimated costs for airfare and accommodation for the conference and a list of other sources of funding.

The document should be named $B!H(BLastName_TravelAwardApp$B!I(B and submitted via email to travelaward2016@gmail.com by Monday May 23, 2016. We will emphasize diversity in awardees (including, but not limited to, membership in underrepresented groups, gender, and career stage).

We intend to notify all applicants of the outcome of their applications by June 15, 2016. Awardees will be expected to develop and publish a Data Nugget based on their own research or that seen at ISBE 2016 (http://datanuggets.org) and to submit their travel receipts for reimbursement. Eligible expenses include costs for travel and attendance (e.g., flights, lodging, taxi, train, meals) but not registration or conference-provided meals. To be reimbursed, flights must follow these policies (http://www.nsf.gov/pubs/policydocs/-pappguide/nsf16001/aag_6.jsp#VIF). Application materials and travel receipts may be made available to NSF upon request.

Any questions can be directed to the Selection Committee (Drs. Alycia Lackey, Michael Martin, and Robin Tinghitella) at travelaward2016@gmail.com.

Robin M. Tinghitella

Assistant Professor Department of Biological Sciences University of Denver 2050 E Iliff Avenue Denver, CO 80208

Office: Boettcher West 243 Lab: Boettcher West 13 Phone: (303)871-3658 Web: http://-/tinghitellalab.weebly.com Robin Tinghitella <Robin.Tinghitella@du.edu>

Island Conservation

Dear friends,

Already is available another outreach video from our Lab, focused in explain the environmental danger of pets and feral cats on islands: < https://vimeo.com/-140250256 >

In this case we focused on the problem of the introduction of pets in island ecosystems (we have worked this issue in the National Park of the Atlantic Islands of Galicia in Spain). Aware of the problems that we the ecologist have, to make the population aware about this problem, we believe this video could be used to raise public awareness about this complex environmental problem. You are free to share it in your social networks, if you want. PD: By clicking on the button CC (choose captions) it is possible to choose subtitles in several languages

Sincerely yours,

Luis Navarro

Luis Navarro phone 1: (+34) 986 812619 Depto. Biología Vegetal phone 2: (+34) 647 343097 Facultad de Ciencias fax: (+34) 986 812556 As Lagoas-Marcosende email: lnavarro@uvigo.es Universidad de Vigo http://webs.uvigo.es/lnavarro 36200-Vigo http://webs.uvigo.es/plantecology Spain http://-www.divulgare.net Luis Navarro <lnavarro@uvigo.es> Luis Navarro <lnavarro@uvigo.es>

Nominations MolEcolPrize

I am soliciting nominations for the annual Molecular Ecology Prize.

The field of molecular ecology is a young and inherently interdisciplinary research area. As a consequence, research in molecular ecology is not currently represented by a single scientific society. Likewise, there is no body that actively promotes the discipline or recognizes its pioneers. To help fill this void, the editorial board of the journal *Molecular Ecology* created the Molecular Ecology Prize to recognize significant contributions to this area of research.

The prize will go to an outstanding scientist who has made significant contributions to Molecular Ecology. Presumably these contributions would mostly be scientific, but the door is open for other kinds of contributions that were crucial to the development of the field. Previous winners are: Godfrey Hewitt, John Avise, Pierre Taberlet, Harry Smith, Terry Burke, Josephine Pemberton, Deborah Charlesworth, Craig Moritz, Laurent Excoffier, Johanna Schmitt, and Fred Allendorf.

Please send your nominations with a short supporting statement (no more than 150 words) by 15 May 2016 directly to me (fred.allendorf@gmail.com).

Thanks on behalf of the Molecular Ecology Prize Selection Committee. We look forward to hearing from you.

Fred Allendorf

fred.allendorf@gmail.com

Fred Allendorf <fred.allendorf@gmail.com>

Passer Sparrow Blood Samples

Dear list members,

I am a researcher at the University of Oslo, Norway working on reconstructing the phylogeny of Passer sparrows using whole genome sequencing. I would be very interested to hear from anyone that had blood samples or isolated DNA from any of the following species. I would also be interested in hearing from anyone sampling bird species in the regions that these species occur in.

* Grey-headed sparrow - P. griseus - found across Sub-Saharan Africa * Parrot-billed sparrow - P. gongonensis - Eastern Central Africa, particularly Kenya, Ethiopia and Somalia * Golden sparrow - P. luteus - across the southern Sahara, Burkina Faso, Niger, Mali, Sudan, Mauritania, Senegal * Cape sparrow - P. melanurus - Cape of Africa - Namibia, South Africa * Great sparrow - P. motitensis - Cape of Africa - Namibia, South Africa * Desert sparrow - P. simplex - Northern Africa - Algeria, Tunisia, Libya, Niger, Mauritania - also Iran and Turkmenistan (likely two separate lineages) * Dead Sea sparrow - P. moabiticus - Middle East - Israel, Jordan, Turkey, Pakistan (separate lineage?) * Sind sparrow - P. pyrrhonotus - Pakistan, India and Eastern Iran * Cinnamon sparrow - P. rutilans - Eastern Asia - China and Japan in winter * Iago sparrow - P. iagonensis - Cape Verde Islands * Saxual sparrow - P. amodendri - Kazakhstan, Uzbekistan, China, Mongolia * Pegu sparrow - P. flaveolus - Myanmar, Thailand, Cambodia, Vietnam

I am also interested in samples from the following subspecies of the House Sparrow, Passer domesticus

* P. d. indicus - India, Pakistan, Bangladesh, Myanmar, Southern Iran,

* P. d. hufufae - Oman, United Arab Emirates

If you do have samples and are interested in contributing/collaborating, I would be very happy to hear from you.

All the best

Mark

Mark Ravinet Researcher CEES Oslo mark.ravinet@ibv.uio.no

Mark Ravinet <mark.ravinet@ibv.uio.no>

Rick Harrison InMemoriam

Dear Evoldir community:

It is with great sadness that we note the recent unexpected passing of Richard 'Rick' Harrison, professor of ecology and evolutionary biology at Cornell University. Rick was well known for his studies of hybrid zones and speciation in addition to his leadership roles in the evolution community. Rick served as editor-in-chief for the journal Evolution during a period of growth for the journal. He also was a tremendous mentor to undergraduates, graduate students, and postdocs and in collaboration with this group worked on a wide range of systems and questions in evolutionary biology.

Here is a memorial notice published by the Cornell Chronicle:

http://www.news.cornell.edu/stories/2016/04/-evolutionary-biologist-rick-harrison-dies-70 A symposium was held in 2010 to celebrate the contributions of Rick to the field of evolutionary biology and the community that Rick helped to mentor. Here is a link to an article from this symposium that gives a summary of Rick's scientific contributions:

http://www.ncbi.nlm.nih.gov/pmc/articles/-PMC3736974/ Rick will be greatly missed.

Chris Willett (willett4@email.unc.edu)

RoyalSociety EvolBiol PhotographyCompetition

The 2016 Royal Society Publishing photography competition is now underway. This competition is split into 4 categories - behaviour; ecology and environmental science; evolutionary biology; and micro-imaging - and is free to enter. The overall winner will receive a prize of Â£500 (or currency equivalent) and winners of the categories not chosen as the overall winner will receive Â£250 (or currency equivalent). The closing date for entries is 1 June.

Visit https://royalsociety.org/journals/photo-competition for further details and to submit your photograph.

Felicity Davie Royal Society Publishing T +44 20 7451 2647 http://royalsocietypublishing.org The Royal Society 6-9 Carlton House Terrace London SW1Y 5AG Registered Charity No 207043

"Davie, Felicity" <Felicity.Davie@royalsociety.org>

Science Videos Training

Subject line: New class - creating science videos with your smartphone

Dear colleagues, Are you interested in creating videos to connect the public with your research? If so, you're in luck. SciFund Challenge, an outreach-focused nonprofit, is running a video training class for scientists. You are invited!

The class will be running for five weeks, from May 15 to June 18, 2016. The class is intended for scientists that are new to outreach and to video creation, but would like to get started with it. The class is open to scientists at any level, in any discipline. The class will be online, so all countries are welcome.

Video production often requires a lot of additional equipment, but our class doesn't. We focus our class on using the smartphones that we carry in our pockets for shooting great video.

The deadline to apply is May 14th, but our classes usually fill up early. Act soon if you are interested! Here's the link to learn more: http://bit.ly/1V296KS Questions? Comments? Please send them my way!

Cheers, Jai Ranganathan jai@scifund.org

Jai Ranganathan <ranganathan@nceas.ucsb.edu> Jai Ranganathan <ranganathan@nceas.ucsb.edu>

SocialInsect Mating ColongFounding

Hello everyone,

I, along with Nicole Fischer and Jenny Jandt are working on a review comparing the behavior of social insects in lab vs. field conditions. As I am sure many are aware, there are numerous papers that corroborate behavioral patterns in both contexts but also papers that show significant discrepancies. Our hope is to reconcile some of these differences. One aspect that is of particular interest to us is mating behavior and colony founding. Anecdotally, we have heard many researchers describe their efforts to observe or initiate mating or colony founding events with widely varied success. However, these attempts are often unpublished (especially if these attempts were unsuccessful), and therefore difficult to access for people not involved.

Here, we request that if you have any experience with social insect mating behavior or colony founding, please respond to the linked survey. It should take less than 5 minutes and would be incredibly helpful. If you study multiple species or multiple systems, please take the survey as many times as you are willing with one survey focused on a single species/group.

https://www.surveymonkey.com/r/MLR56RQ Additionally, if you have any anecdotal experience regarding methodology, patterns you have observed (e.g. species that have mating swarms are easier to observe than species with male leks), how long it took to successfully observe a mating/founding event, etc., we would appreciate these stories. They can be emailed directly to me at:

sarah.bengston@rochester.edu

We appreciate your time and effort.

Best wishes,

Sarah Bengston, University of Rochester

Nicole Fischer, University of Arizona

Jenny Jandt, University of Otago

Sarah E. Bengston, PhD NSF Postdoctoral Fellow University of Rochester 860-575-4534

sbengsto@gmail.com

Software DAMBE update

Dear All,

I have uploaded a new version of DAMBE with the following improvements:

1. Improved handling of files with multiple data sets: If you have simulated files containing multiple sets of sequences, click 'File|Open file with multiple data sets' where you will have options to align multiple files and analyze them by distance/MP/ML methods. For alignment, you may use the internal aligner or use external programs such as MAFFT or MUSCLE (you should download these programs for windows and save them to a directory), or analysis with ML, you may use the internal ML method or run external PhyML or PHYLIP's DNAML/DNAMLK/PROML/PROMLK (again you should download these programs for windows and save them to a directory). These functions of running external alignment/phylogenetic programs can also be accessed when you read in a file with a single set of sequences, e.g., click 'Alignment|Align by external MAFFT' or 'Alignment|Align by external MUSCLE'

2. I have also added some function to improve running the external programs.

a. PHYLIP: people often wish to run PHYLIP's DNAML/PROML to have the alpha (of gamma distribution) and transition/transversion ratio (R) estimated, but PHYLIP programs require you to input these values. I have added a simplex method to run these programs to estimate alpha and R. If you need to estimate only alpha or only R, then a brent method is used.

b. PhyML: People often wish to root the resulting tree with node support but PhyML does not provide this convenience. After you have run PhyML, either from DAMBE or separately, just copy and paste the tree into DAMBE by click 'Phylogenetics|Paste tree into tree panel' and then click 'Tree|reroot'.

(you should download these programs for windows and save them to a directory. You can access these functions in two ways. One is when you have read in a file with a single set of sequences, e.g., VertCOI.fas included with DAMBE. You can click 'Phylogenetics|Run external programs'. The other is when you have read in a file with multiple sets of sequences. You can read in such a file by click 'File|Open file with multiple data sets'. These functions are available only in the Windows version of DAMBE)

3. Anticodon identification: identify the anticodon and anticodon stem-loop. This function has been improved in accuracy, and I have identified quite a number of misannotation of tRNA in bacterial genomic sequences using the function.

4. Index of translation elongation (I_TE): this is an improvement over CAI by taking into consideration the background mutation bias (Xia, X. 2015. A Major Controversy in Codon-Anticodon Adaptation Resolved by a New Codon Usage Index. Genetics 199:573- 579). DAMBE includes codon tables for highly and lowly expressed genes for a number of species to facilitate computation of I_TE.

5. Protein isoelectric point: this is for measuring what net electric charge a protein will carry. Useful when one is interested in studying coevolution between protein and its substrates (including nucleotide sequences).

6. The function for building phylogenetic tree based on pairwise alignment is substantially improved.

7. Robinson-Foulds distances: 1) all pairwise distances from all input trees or between one tree and all other trees.

8. Some functions are probably too specialized to mention here, such as those identifying Shine-Dalgarno (SD) sequences and anti- SD sequences. If you are curious about some menu items DAMBE, please let me know.

Not all functions have been tested thoroughly. I look forward to your feedback.

Best Xuhua http://dambe.bio.uottawa.ca< http://dambe.bio.uottawa.ca/ > http://science.uottawa.ca/biology/people/xia-xuhua Xuhua Xia <Xuhua.Xia@uottawa.ca>

Software Genesis

Dear Community,

For those of you using the RAxML Evolutionary Placement Algorithm (EPA) or Erick Matsen's pplacer tool there is now a toolkit available at http://genesis-lib.org/ to

-Read, manipulate and write .jplace files -Extract, filter and merge placements -Calculate distance measures (e.g., Earth Movers Distance) -Visualize read abundances on the branches of the tree

Cheers,

Alexis

– Alexandros (Alexis) Stamatakis

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

www.exelixis-lab.org Alexandros Stamatakis <alexandros.stamatakis@gmail.com>

Software LinkageMapping

Dear evol community,

Please note my new free software, Lep-MAP2, for linkage map construction for single and multiple full-sib (and similar) crosses. I can be used for very large numbers of offspring and markers and can be run parallel on typical computer clusters.

For more info, there is an article out on Lep-MAP2: http://gbe.oxfordjournals.org/content/8/1/78.full The software can be obtained from sourceforge, https://sourceforge.net/projects/lepmap2/ Cheers, Pasi Rastas Research Associate Butterfly Genetics Group Department of Zoology University of Cambridge United Kingdom

"pmr47@cam.ac.uk" <pmr47@cam.ac.uk>

Software SLiM2 0 ForwardGeneticSimulation

Hi everyone. We would like to announce the release of SLiM 2.0, a forward genetic simulation package (http://messerlab.org/slim/). Its features include:

- complete scriptability of simulations, allowing immense flexibility and power - interactive development and execution of simulations in a graphical user interface, SLiMgui - support for complex genetic structure, population structure, types of selection, mating systems, etc., etc.

Because of its scriptability, you can do pretty much whatever you can write in a script. The manual weve written for SLiM gives example "recipes" for all kinds of models, such as:

- a model of human evolutionary history (following Gravel et al. 2011) - a model of a CRISPR/Cas9 "gene drive" sweeping through a linear island chain - a model of social learning of a culturally inherited trait that influences fitness - a model of gametophytic self-incompatibility and S-locus evolution in plants - a model of fixation probabilities under Hill-Robertson interference

And on and on; you can really do almost anything, because of the flexibility of its scripting language, and you can see each model's dynamics unfolding graphically as it runs in SLiMgui. SLiM is open source, and runs on Mac OS X and Linux (although the SLiMgui graphical user interface runs only on Mac OS X). For more info, you can:

- Read a blog post about it at http://ecoevoevoeco.blogspot.com/2016/04/announcing-slim-20-flexible-fast.html - Download it from http://messerlab.org/slim/ We hope people find this useful, both in research and in the classroom!

Cheers,

Ben Haller and Philipp Messer Cornell University

bhevoldir@sticksoftware.com

SpeciesAtRisk Fellowships Call

We are pleased to announce that ZSL's EDGE of Existence Programme is now accepting applications for 2017-19 EDGE Fellowships. We would be very grateful if you would forward the details below to anyone that you feel may be interested in submitting an application.

Please note, this year the Fellowship is only accepting applications on EDGE species found on our curated list of mammals, amphibians, birds, reptiles and coral species. We are particularly interested in focussing on African species but are accepting applications on all of the species found on the list. Please find the Fellowship advert and list of eligible species attached.

EDGE Fellowships

The Zoological Society of London's EDGE of Existence programme (www.edgeofexistence.org) is the only global conservation initiative focusing specifically on threatened species that represent a significant amount of unique evolutionary history. One of the most effective ways in which the programme is working to secure the future of EDGE species is by awarding two-year Fellowships to future conservation leaders "EDGE Fellows" working on poorly-known EDGE mammal, amphibian, bird, reptile or coral species. We are now accepting applications for the 2017-19 Fellowship Programme. EDGE Fellows follow a comprehensive two-year training programme comprising:

* A 4-week Conservation Tools training course at the beginning of the programme to provide Fellows with essential training in techniques to plan and implement their project; * A grant of £10,000 to undertake a 2-year project on a top-priority EDGE species; * Ongoing technical support/mentoring (achieved via online modules, web- based tutorials/seminars, and field visits) throughout the Fellowship; * A 2-week Conservation Leadership training course in London on successful completion of Fellowship to help Fellows prepare for the next stage of their career.

The application form, guidelines, and eligibility criteria are available to download on the EDGE of Existence website (http://www.edgeofexistence.org/conservation/fellows.php) or can be requested from the EDGE Fellows Co-ordinator (olivia.couchman@zsl.org). We strongly encourage applicants to discuss their projects with us before applying, and are happy to give feedback on a draft of the application before the deadline. The application deadline is 15th June 2016. All applications will be reviewed by a panel of experts. Successful applicants will be informed by the end of August 2016.

The Zoological Society of London is incorporated by Royal Charter Principal Office England. Company Number RC000749 Registered address: Regent's Park, London, England NW1 4RY Registered Charity in England and Wales no. 208728

Rikki.Gumbs@zsl.org

SSE 2017 SymposiumProposals

Call for Symposia for the 2017 Annual Meeting

The 2017 annual meeting of the Society for the Study of Evolution is planned for June 23-27, 2017 at the Oregon Convention Center in Portland, OR. The SSE Council invites proposals for the two Society-sponsored symposia to be held in conjunction with the meeting. Symposium proposals should include: (1) a synopsis of the symposium theme (about one page); (2) a tentative list of speakers, including institutional affiliations, and topics; (3) a rationale for the symposium explaining why this topic and this group of speakers are particularly appropriate for a Society- sponsored symposium; and (4) a statement that all potential speakers have been contacted and agree to participate in the symposium.

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

The Council will select two proposals for half-day symposia at the annual meeting in June 2016. All applicants will be notified of the Council's decision in August. The Society provides travel support for organizers and participants in sponsored symposia. Details are available on request. To be assured of full consideration, proposals must be received by midnight Eastern Standard Time on June 6, 2016.

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

"Brodie, Edmund Darrell (Butch) (edb9j)" <edb9j@eservices.virginia.edu>

Submit trees to OpenTreeofLife

Open Tree of Life recently released version 5.0 of the synthetic tree of life, a summary of published phylogenetic trees and publicly-available taxonomic hierarchies. You can browse and download the tree at https://tree.opentreeoflife.org This tree is dynamic - we update the tree by incorporating nominated phylogenies submitted to the site. It is also incomplete, lacking much of our current knowledge from published phylogenetic studies. We invite you to improve the tree by contributing your own published phylogenies, uploading phylogenies available elsewhere online, or curating existing phylogenies, at https://tree.opentreeoflife.org/curator We can take trees in newick, NEXUS, or NeXML format, or by direct import from TreeBASE.

Instructions on importing trees and nominating trees for synthesis are available at https://github.com/OpenTreeOfLife/opentree/wiki/Submitting-phylogenies-to-Open-Tree-of-Life
Thank you, The Open Tree of Life team https://tree.opentreeoflife.org/contact Emily Jane McTavish <ejmctavish@gmail.com>

PostDocs

BangorU RisingStarFellowships

'Rising Star' fellowships will be very prestigious and highly competitive positions, designed to attract the very best 'rising stars' of academic research. 'Rising star' packages will be funded at approximately £0.2m per annum and can involve collaboration with relevant commercial or third sector organisations

'Rising Star' applications can be submitted at any time.

http://businesswales.gov.wales/expertisewales/rising-stars https://www.bangor.ac.uk/biology/ Eligibility Criteria

Rising Star Fellowships applicants should meet the eligibility criteria set out below:

Applicants should have over 7 years of experience since completion of PhD (or equivalent degree) and scientific track record showing great promise Applicants should have an excellent research proposal Applicants can be of any nationality Applicants must submit a completed application form and associated documents (supervisor form, ethics form, and CV) Applications must comply with the fundamental ethic principles as detailed in the ethics section Applicants must have the support of their chosen host institution Applications that do not meet the eligibility criteria or do not adhere to the guidelines given here will be rejected by the management team.

Application Process

Applicants will need to propose a suitable project to be carried out in a Welsh host institution in the list. Projects should be described in no more than 18 pages for Rising Star fellowships using the appropriate application form that can be downloaded here

The research project will be created by the applicant but they must discuss this with their potential host institution before submission. A completed 'partner form' is required from a host institution to say that they are willing to host the fellow, should they be successful.

All projects will be subject to ethical scrutiny and applicants will need to provide a completed ethical issues form with their application.

Applicants should also submit a copy of their most recent CV, no more than three pages in length. This should include information about their education, previous employment and other relevant experience, information about any career breaks taken for maternity or caring responsibilities etc, and a list of all their publications and grants awarded. Applicants should also give the names of two referees who know their work and the proposed area of research.

Dr John Mulley School of Biological Sciences Bangor University Deiniol Road Bangor Gwynedd LL57 2UW United Kingdom

Tel: +44 (0)1248 383492 Email: j.mulley@bangor.ac.uk Web: www.johnmulley.com Twitter: @johnmulley < https://twitter.com/JohnMulley >

Rhif Elusen Gofrestredig 1141565 - Registered Charity No. 1141565

John Mulley <j.mulley@bangor.ac.uk>

ColbyCollege InsectWingPolyphenism

Dear friends and colleagues,

My lab at Colby College has an opening for a postdoc, supported by NSF funding through April 2019. The project takes an integrative set of approaches to examine the developmental mechanisms and evolution of wing polyphenism is soapberry bugs. This species has a rich and well described natural history of adaptation to an introduced host plant and is amenable to modern methods of molecular developmental biology. The position will involve functional genetics (via RNAi), gene expression (via in situ hybridization, qPCR and RNAseq), morphometrics, bioinformatics and other tools of developmental biology. I am hoping to find someone with a strong interest in eco/evo-devo and experience with at least some of these methods. Colby College is a selective undergraduate institution located in Waterville, Maine, about one hour from Portland, Acadia National Park and excellent skiing. We are about 3 hours from Boston by car or bus. While this is a research position, I encourage applicants with an interest in teaching and mentoring undergraduates. It will be possible during the postdoc to teach as instructor-of-record in Colby's January term. More background on the project is available at our outreach website, https://www.bugsinourbackyard.org/bug-story/ Please contact me with any questions if you are interested. Applications should be submitted through Colby's HR office http://www.colby.edu/-administration_cs/humanresources/employment/-postdoc_research_4_2016.cfm Thank you, Dave

David R. Angelini Assistant Professor, Department of Biology, Colby College Secretary, Pan-American Society for Evolutionary Developmental Biology Director, Bugs In Our Backyard Project, http://-www.bugsinourbackyard.org/ 5734 Mayflower Hill, Waterville, ME 04901, USA - office phone: 207-859-5734 http://web.colby.edu/aphanotus/ Twitter: @Aphanotus @Jhaematoloma

"drangeli@colby.edu" <drangeli@colby.edu>

CornellU EvolutionGenomicMechanismsBehavior

I anticipate evolutionary biologists will be the best pool of applicants for this position, since they tend to be sophisticated in genomic and bioinformatic techniques and often are interested in natural variation in genes and behavior. The desired candidates will be interested in the evolution of genomic mechanisms of behavior.

Many thanks!

Alex

Postdoctoral opportunity: Genomic mechanisms of animal personality, Cornell University

The Ophir Lab (www.ophirlab.com) at the Cornell University is looking for a postdoctoral candidate with strong bioinformatics skills to investigate the individual variation in behavior and genomic profiles of a non-model system, the African giant pouched rat. The project seeks to identify genetic signatures that correlate with behavioral profiles (or behavioral syndromes) assessed in these wild-caught, laboratory housed rodents of unusual size. Individuals with experience performing genome-wide association studies, RNA-seq, single nucleotide polymorphism identification (e.g., double digest RADseq), and proficiency with standard methods of bioinformatics are particularly desired. The candidate should be familiar with conducting traditional laboratory behavioral tests including open field, elevated plus maze, Barnes maze, defensive burying tests, etc, and comfortable with working with large exotic rodents. The project offers a unique opportunity to begin to understand the genetic architecture that underlies animal personality.

Cornell University offers a vibrant community of researchers working at the interface of brain, behavior and evolution, an outstanding Biotechnology Resource Center that hosts excellent sequencing and bioinformatics facilities, and the University-wide Center for Vertebrate Genomics, among other wonderful resources.

Applications should include a current CV along with a cover letter that provides a short statement of research interests and contact information for three references. Applications should be submitted by email to ago25@cornell.edu, with the subject line: Postdoc.

Applications are being accepted immediately and official review will begin April 30, 2016, and will continue until the position is filled.

The position will be supported for at least one year at NIH postdoc rates (http://grants.nih.gov/grants/-guide/notice-files/NOT-OD-16-047.html), with the option for continued funding contingent on performance and available funds. A start date of June 2016 is ideal, but flexible.

Alexander G. Ophir, PhD 224 Uris Hall Cornell University Department of Psychology Behavioral & Evolutionary Neuroscience Ithaca, NY, 14853, USA

Phone: (607) 255-3714 Fax: (607) 255-8433 http://ophirlab.com “Alexander G. Ophir” <ophir@cornell.edu>

CSIC UPF Barcelona Bioinformatics

The Evolutionary and Functional Genomics Lab led by Josefa Gonzalez is seeking a highly motivated postdoctoral researcher to join our research team at the Institute of Evolutionary Biology (CSIC-UPF). The postdoctoral researcher will work on a project funded by a European Research Council Consolidator Grant that aims at identifying the genetic basis, the molecular mechanisms, and the functional traits relevant for environmental adaptation.

The postdoctoral researcher will be responsible for the in silico characterization of candidate adaptive mutations identified in natural populations of Drosophila melanogaster. Among others, the tasks involved in the postdoctoral research project will be to identify pathways under selection, and to analyze the expression and the epigenetic changes of genes nearby the candidate adaptive insertions.

A PhD in Populations Genetics or a related field, good programming skills, and goodwriting skills are required. Previous postdoctoral experience will be considered. We offer a full-time position for 2 years with the possibility of extension. Salary will depend on the experience of the candidate. Starting date: September 2016 but alternative dates can be discussed. Application: Please send your CV and a brief letter of motivation before the 5th May 2016 to: josefa.gonzalez@ibe.upf-csic.es

Dr Jordi Lanuza Masdeu Communication manager Institut de Biologia Evolutiva (IBE) (CSIC-UPF) Despatx P85, Edifici CMIMA Passeig MarÃtim de la Barceloneta 37-49 08003 Barcelona comunicacio@ibe.upf-csic.es Tel. 932309645 (Ext. 6050) Web: http://www.ibe.upf-csic.es Follow us on Twitter: @IBE_Barcelona Follow us on Facebook: IBEvolutiva Follow us on LinkedIn

Jordi Lanuza Masdeu <comunicacio@ibe.upf-csic.es>

Faro Portugal LandPlantPhylogenetics

– Post-Doctoral Research Fellowship V 1 vacancy (3 years total)

"Determining the causes of inter-genomic conflict in the land plant phylogeny"

*Fellowship Reference: *CCMAR/BPD/0007/2016

The Centre for Marine Sciences (CCMAR) in the Algarve, Portugal, opens a position for a Post-doctoral Researcher (BPD) in the project "Determining the causes of inter-genomic conflict in the land plant phylogeny" financed by the Portuguese Foundation for Science and Technology - FCT/MCTES (PIDDAC) under the following conditions:

Project description: The project will determine the causes of the conflict among the current best phylogenies derived from each of the three genomes of land plants and their algal ancestors. Because the substitution process can vary both among sites (data heterogeneity) and among lineages (time heterogeneity), heterogeneous substitution models will be used in a Bayesian phylogenetic context to test the adequacy of model fit through posterior predictive simulations. The fellowship holder will be expected to use bioinformatic tools to determine phylogenetic relationships.

Scientific orientation: Cymon J. Cox (CCMAR) - Plant Systematics and Bioinformatics Research group.

Work place: Building 7, Campus de Gambelas, Universidade do Algarve, Faro, Portugal.

Requirements:

1. The applicant must be fluent in spoken and written in English (the latter to be assessed from the motivation letter to be submitted with the application);

2. The applicant must have a PhD and publications in an area related to the work plan.

Evaluation criteria:

1. Experience in the analysis of molecular sequences and knowledge of phylogenetic methodologies V 70%

2. Competency in bioinformatic techniques including proficiency with Unix-based systems and programming/scripting languages (in particular Python) V 30%

The selection jury will exercise the right to contact and interview candidates should they require further information or clarification about their application. In the event that no applicant has the necessary profile the jury reserves the right to close the call without any recruitment.

During the fellowship, and in the event that the fellowship holder should resign, the jury reserves the right, upon convenience and opportunity, to assign the fellowship to the next applicant in accordance with the ranking position of the selection jury.

Grant conditions: The grant will have an initial duration of 12 months, starting in 1st August 2016 eventually renewed for 2 additional 12 month periods until the end of the research project. The fellowship must be undertaken exclusively (full time) according to the Portuguese law 40/2004, of 18 of August (Scientific Research Fellowship holder statutes), Fellowship Regulation of the Portuguese Foundation for Science and Technology in force (www.fct.pt/apoios/bolsas/docs/RegulamentoBolsasFCT2015.pdf) and the rules of CCMAR research grants http://www.ccmar.ualg.pt/home/assets/files/Outros/Reg_bolsas.pdf . *Monthly maintenance allowance: *Net 1495.00£á/per month V tax free (in accordance with the grant amounts set by the Portuguese Foundation for Science and Technology).

Application deadline: Applications will be accepted until *Friday 13th May 2016*.

Application documents: Applicants should submit a letter of motivation (written in English, and explaining the experience in each evaluation criteria), a photocopy of their PhD certificate, a detailed Curriculum Vitae, a photocopy of their national identity card or passport (face-page only), and the email contacts of 3 persons who can provide academic references.

Submission of applications: Applications should be submitted by email to ccmar@ualg.pt indicating the reference CCMAR/BPD/0007/2016 (note that we can only accept applications sent through this email). You should only consider your application as validated after receiving confirmation from CCMAR by email.

Results: The results will be communicated in writing within 30 working days after the application deadline.

Selection jury members: Cymon J. Cox (Chairperson), Gareth Pearson, and Filipe de Portugal S.T. de Sousa.

Informal contact: Cymon J. Cox <cymon@ualg.pt>

CCMARs non-discrimination and equal access opportunities policy V No candidate can be privileged, benefited, jeopardised or private of any right or exempt of any claim in regards to descendent, age, gender, sexual orientation, marital status, economic situation, origin, social economy, genetic heritage, disability, chronic disease, nationality, ethnicity, territory of origin, language, religion, politics and ideological beliefs and union membership.

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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

FieldMuseum Chicago EvolutionLichenFungi

Postdoc:

Postdoctoral Research Associate, Evolutionary Biology of Lichenized Fungi

Location: Chicago, IL

The Science and Education Department (Integrative Research Center) at The Field Museum is currently looking for a full-time Postdoctoral Research Associate position focusing on diversification of lichenized fungi. We are looking for an individual with a strong interest and background in evolutionary biology. The position is for a term of 24 month, with possibility for extension.

The research entails studies on molecular evolution and diversification of lichenized fungi. The successful applicant will be involved in various aspects of lichen diversification, including studying diversification dynamics, resolving species complexes and species delimitation. Preferably, candidates should be able to demonstrate experience in phylogenetic analyses, generating and analyzing genomic datasets, competency with at least one scripting language (e.g., Perl, Python, R), and interest in applying new statistical approaches. Experience with fungal or lichen systematics is a plus. Well-developed communication (verbal and written) and organizational skills are essential. The successful candidate will also demonstrate leadership ability to assist the PI with the direction and training of graduate students.

The successful applicant is expected to publish at least one research paper as lead author within a year and collaborate as co-author in at least two further research papers. Guidance will be provided following the Postdoctoral Mentoring Plan.

Please upload application data, including a cover letter highlighting experience in aspects relevant to the research, curriculum vitae, and publication list at: https://www.fieldmuseum.org/about/careers Contact Thorsten Lumbsch for additional information: tlumbsch@fieldmuseum.org

sleavitt@fieldmuseum.org

FreieU EvolutionaryBiology

Please note: The position is available at Freie Universität Berlin, Fachbereich Biologie, Chemie, Pharmazie, Institut für Biologie, Botanik, not "Botanischer Garten und Botanisches Museum". Sorry for this mistake!

Kind regards, Eva Häffner

Auszug aus dem Stellenanzeiger der Freien Universität Berlin vom 25.04.2016 Fachbereich Biologie, Chemie, Pharmazie, Institut für Biologie, Botanik

Wiss. Mitarbeiterin / Wiss. Mitarbeiter (Postdoc) befristet bis zu 5 Jahre Entgeltgruppe 13 TV-L FU Kennung: 21224600/11/16

Aufgabengebiet:

§Mitarbeit in der Forschung auf dem Gebiet der Populationsgenetik/- genomik der Blütenpflanzen

§Erwartet wird die Mitarbeit an (bestehenden) Forschungsprogrammen, die integrativ zwischen der Arbeitsgruppe am Institut für Biologie und dem Botanischen Garten und Botanischen Museum Berlin-Dahlem realisiert werden

§Mitarbeit in der Lehre und bei allgemeinen Institutsaufgaben der AG Prof. Borsch

§Der Aufbau einer eigenen Nachwuchsgruppe und die Habilitation sollten angestrebt werden

Einstellungsvoraussetzungen:

§Promotion in Biologie Berufserfahrung: §Erfahrung in der Lehre und Betreuung der Masterkurse Erwünscht: §Ãberdurchschnittliche Promotion §Einschlägige Kenntnisse in populationsgenetischen/genomischen Arbeitstechniken einschließlich des Next Generation Sequencing sowie gentechnischer Methoden §Vertiefte Kenntnisse auf den Gebieten Bioinformatik sowie Conservation Genetics und Evolution der Blütenpflanzen §Gute Englischkenntnisse

Bewerbungen sind mit aussagekräftigen Unterlagen bis zum 16.05.2016 unter Angabe der Kennung im Format PDF und elektronisch per E-Mail zu richten an (Herrn Prof. Dr. Thomas Borsch): systbot@zedat.fu-berlin.de

Mit der Abgabe einer Onlinebewerbung geben Sie als Bewerber/in Ihr Einverständnis, dass Ihre Daten elektronisch verarbeitet und gespeichert werden.

"Häffner, Eva" <E.Haeffner@bgbm.org>

GeorgiaTech MarineMicrobiomes

Postdoc in Microbiome Research

Georgia Tech is looking for a postdoctoral scholar to apply metagenomic and metatranscriptomic methods to study environmental and animal-associated microbiomes. The postdoc will be based in the lab of Dr. Frank Stewart in the School of Biology, but will work jointly between the Stewart lab and the lab of Dr. Nicole Lopanik (Earth and Atmospheric Sciences) on a collaborative NSF-funded project. The work will involve a blend of experimental, molecular, and bioinformatic analyses, with a strong focus on comparative meta-omic analyses to test new computational approaches for quantifying microbial gene expression in marine bacteria. The postdoc will be encouraged to develop independent lines of research within the broader goals of the project, and will work collaboratively with Dr. Stewart, Dr. Lopanik, and external collaborators at Georgia State and the University of Connecticut to perform research and synthesize results for publication.

The ideal candidate will be enthusiastic, motivated by experimental and analytical challenges, proficient in genomic/meta-omic analyses and comfortable with a range of molecular microbiology techniques. Candidates should have a Ph.D. in one of these fields (or a related topic). Proficiency in Python/Perl coding, command line interfaces, and database management is highly desirable.

The School of Biology at Georgia Tech is a dynamic research environment with a strong core of researchers interested in microbial systems research and bioinformatics. The Institute offers exceptional resources for biomolecular analysis and high-performance computing, and exciting opportunities for cross-departmental collaboration, including with schools of engineering. Georgia Tech was recently voted one of the best places to work, and Atlanta is consistently ranked among the top ten places to live for young professionals.

This position begins in fall 2016. Funding is available for at least one year, with continuation contingent upon satisfactory progress in year one; applicants should express their ability to commit to the project for at least two years. Application materials should be emailed to Frank Stewart at frank.stewart@biology.gatech.edu and should include a cover letter (describing your interest in the position, work experience, and availability), CV, and contact information (name, email, phone number) for at least three references. Please include the word "Postdoc" in the subject line. Salary will be competitive and commensurate with experience and will include fringe benefits. Review of applications will begin on June 1 and continue until the position is filled.

Informal inquiries about the position can be sent to Frank Stewart at frank.stewart@biology.gatech.edu. Additional details about the Stewart lab can be found at http://marine-micro.biology.gatech.edu/ and the Lopanik lab at http://www.eas.gatech.edu/content/-lopanik-dr-nicole Georgia Tech is a unit of the University System of Georgia and an Affirmative Action/Equal Opportunity Employer and requires compliance with the Immigration Control Reform Act of 1986.

– Frank J. Stewart, Ph.D. Assistant Professor School of Biology Georgia Institute of Technology ES&T building, office #1242 311 Ferst Drive Atlanta, GA 30332-0230 office: 404-894-5819 www.fjstewart.org "frank.stewart@biology.gatech.edu"

Glasgow FishEvolution

We are seeking a postdoctoral scientist to join with a project entitled 'The predictability and limits of evolution in response to increased temperature: insights from a natural 'experiment", funded as a major initiative from the Natural Environment Research Council (NERC) to Kevin J. Parsons, Neil B. Metcalfe, Jan Lindström and Shaun S. Killen. The conceptual focus of the PI is centred on an emerging eco-evo-devo view, while the overall aim of this integrative project will be to examine the genetic, epigenetic, morphological, physiological, behavioural and developmental changes that occur in response to temperature, using freshwater populations of stickleback fish that inhabit natural geothermally heated water bodies.

You will have or be near to completing a relevant PhD and be the main person in charge of executing lab experiments, conducting physiological, behavioural and morphological assays, and taking growth measurements on populations of three-spined sticklebacks derived from contrasting thermal origins. Interest and experience with questions surrounding phenotypic plasticity would be an asset, while experience with aspects of developmental biology would also be desirable but not necessary. As part of a team funded by this NERC grant, you will work closely with another postdoctoral scientist who will focus on molecular genetic analyses, and a full-time technician who will aid in the running of the fish experiments and in maintaining the breeding programme.

Passion for research, team spirit and enthusiasm are essential. Our team is multidisciplinary with additional major projects funded by the European Research Council (ERC) and NERC. Additional PhD student projects in the lab of the PI involve collaborations with engineers, statisticians, and physicists demonstrating how the University of Glasgow is a highly active and collaborative research environment.

Informal inquiries should be made to: Kevin.Parsons@glasgow.ac.uk

Formal applications should be directed to the following address by May 22nd (job reference# 013068):

http://www.gla.ac.uk/about/jobs/vacancies/ Dr. Kevin Parsons Lecturer, Institute of Biodiversity, Animal Health, and Comparative Medicine University of Glasgow

http://www.gla.ac.uk/researchinstitutes/bahcm/staff/kevinparsons/ personal webpage: https://sites.google.com/site/kevinparsonslab/home Kevin Parsons <Kevin.Parsons@glasgow.ac.uk>

IISER-TVM India Evolution

Anumber of postdoctoral positions in biology are available with the School of Biology, IISER Thiruvananthapuram (www.iisertvm.ac.in), including in the broad field of Ecology and Evolution (www.vanasiri.in/eco-evo). Currently there are two research groups in Ecology and Evolution. Collaborations with candidates who can design projects that complement ongoing work are welcome, but we also welcome collaborations with candidates through projects on new kinds of questions, and/or new model organisms, which will enrich research in the School of Biology. The permanent campus of IISER Thiruvananthapuram is an outstanding location (see www.vanasiri.in/facilities) for ecological and evolutionary studies.

DEADLINE:15 May 2016.

RESEARCHAREAS: 1)Hema Somanathan: (Behavioural Ecology and Evolution Lab: www.iisertvm.ac.in/faculties/hsomanathan): We study plant-animal mutualisms especially those between plants, their pollinators and dispersers. Some of our current work involves understanding adaptations in pollinator visual systems in the context of angiosperm floral displays. For this, we study learning and memory in Indian honey bees and stingless bees using a combination of field studies, behavioural approaches in the lab and sensory visual models. In another project we are examining the nature of plant-pollinator-disperser interactions in small and isolated populations to understand how species persist in these populations. In yet another current study, we are examining plant-pollinator interactions in modified landscapes.

2)Ullasa Kodandaramaiah (Vanasiri Evolutionary Ecology Group: www.vanasiri.in): Ourresearch group works on various questions within evolutionary ecology including prey-predator interactions, insect-hostplant co-evolution, parasite-host co-evolution, biogeography, phylogeography, population genetics, etc. More information at www.vanasiri.in/research. Currently used model systems include insects (primarily butterflies), plants and reptiles.

Youare encouraged to contact the PIs informally (hsomanathan@iisertvm.ac.in, ullasa@iisertvm.ac.in) to discuss your ideas and their feasibility before sending in your formal application. Candidates interested in research areas other than Ecology and Evolution can contact respective research groups which are accepting Fellows during this round (see http://iisertvm.ac.in/news/read_news/298/1)

DURATION:2 years, extendable by up to one more year on the basis of performance. The preferred start date is August 2016.

FELLOWSHIP:Rs 40,000/- per month for the first two years and INR 45,000/- per month in the third year, with no other allowances. There will be a contingency grant of INR 75,000/-per year for attending conferences/workshops, etc. Candidates who have submitted their thesis and have not defended at the time of joining will be provided the Extended Senior Research Fellowship for one year.

APPLICATIONPROCEDURE AND SELECTION: Selection will be based on the scientific credentials of the applicant, quality of the research proposal and feasibility of carrying out the research proposal. The formal advertisement, including details about how to apply is here http://iisertvm.ac.in/news/read_news/298/1 LIFEIN KERALA AND THIRUVANANTHAPURAM (TRIVANDRUM): The coastal city of Thiruvananthapuram is the capital of Kerala, and has a rich cultural heritage. It is within a stone's throw away from world-famous beaches such as Kovalam and Varkala, and lovely backwater tourism areas such as Poovar. Several hill stations (e.g Ponmudi) and wildlife sanctuaries are close by. Being a major medical tourism destination, the city has excellent medical care facilities. Since it is a relatively small city, the cost of living tends to be considerably lower than in bigger Indian cities. A 2-bedroom apartment can be had for Rs 8,000 - 10,000 per month. There are plenty of options for dining out - a meal at a decent local restaurant can start from Rs 50, but a good meal with a drink even in a five-star hotel does not necessarily cost more than Rs 1000. Costs for groceries and other daily needs can be looked up here (www.kada.in). Taxis can be hired from Rs 10 per km (with a minimum fare of Rs 50), while the cost of driving your own small car (not for the faint-hearted!) is about Rs 5 per kilometer (petrol: ca. Rs 65/litre, diesel: ca. Rs 52/litre).

HemaSomanathan: hsomanathan@iisertvm.ac.in UllasaKodandaramaiah: ullasa@iisertvm.ac.in

ullasa@iisertvm.ac.in

ImperialCollegeLondon MicrobialAdaptationToWarming

Aquatic microbial ecology postdoc (3.5 years) at Imperial College London Application deadline: 25th May 2016

This is an exciting opportunity to join a multi-institute consortium that is investigating how food webs respond to warming in geothermally-warmed streams around the Arctic. This component of the project is based in the laboratory of Dr. Thomas Bell (https://bellmicrobelab.wordpress.com/), and will focus specifically on the microbial communities, whose role in Arctic food webs is virtually unknown. The position, funded by a NERC Large Grant (pounds 3.7M) led by Prof Guy Woodward in collaboration with researchers from the University of Essex, Queen Mary University, and Imperial College London and others. The successful candidate will join a large microbial ecology group based at the Silwood Park Campus, near Ascot. Previous work in the laboratory has shown that adaptation to warming (and other factors) crucially depends on the makeup of the surrounding community. The post holder will focus on understanding adaptation in complex communities, concentrating specifically on the interplay between ecological and evolutionary processes in response to a warming environment.

For details, visit: http://www.jobs.ac.uk/job/ANN425/research-associate-in-aquatic-microbial-ecology/ – Dr. Thomas Bell Imperial College London Silwood Park Campus Buckhurst Road, Ascot, Berkshire, SL5 7PY

thomas.bell@imperial.ac.uk https://bellmicrobelab.wordpress.com/ +44 (0)20 7594 2268

“thomas.bell@imperial.ac.uk” <thomas.bell@imperial.ac.uk>

IndianaU EvolutionaryGenomics

Postdoc in Evolutionary Genomics

An NSF-funded postdoctoral position is available in the lab of Matthew Hahn in the Department of Biology and School of Informatics and Computing at Indiana University, Bloomington. The work will examine the evolution of gene gain and loss through the study of gene families in a phylogenetic context. Our lab has developed the statistical and computational tools necessary to study these phenomena, and we are looking for a motivated individual to extend these methods to studies involving hundreds to thousands of genomes. The postdoctoral candidate will also be encouraged to carry out independent work in the lab.

There is a wide variety of research going on in the lab in addition to the current project. For a summary of work in the lab, please see: http://www.indiana.edu/~hahnlab/ The candidate must have a Ph.D., preferably in phylogenetics, population genetics, statistical genetics, or computer science. The position requires skills in the more computational areas of biology, and a strong record of research in these areas.

To apply, please submit (i) a letter of application, (ii) a full CV, (iii) a brief statement of research interests, and (iv) contact information for three references electronically to http://indiana.peopleadmin.com/postings/2382. Review of applications will start immediately and will continue until the position is filled. The exact start date is flexible, but best consideration to those applying before May 15, 2016. Inquiries about the position can be directed to Matthew Hahn (mwh@indiana.edu<mailto:mwh@indiana.edu>; 812-856-7001; 1001 E. 3rd St., Bloomington, IN 47405).

Indiana University has a large and active group in evolutionary genetics, and considerable resources computational resources. Bloomington is situated in scenic, hilly southern Indiana, near several parks and wilderness areas. The cultural environment provided by the University is exceptionally rich in art, music, and theater.

Indiana University is an Equal Employment and Affirmative Action employer and a provider of ADA services. All qualified applicants will receive consideration for employment without regard to age, ethnicity, color, race, religion, sex, sexual orientation or identity, national origin, disability status, or protected veteran status.

Matthew Hahn Professor Department of Biology & School of Informatics and Computing 1001 E. 3rd St. Indiana University Bloomington, IN 47405 Phone: (812)856-7001 http://www.bio.indiana.edu/facultyresearch/faculty/Hahn.html http://www.indiana.edu/~hahnlab "Hahn, Matthew William" <mwh@indiana.edu>

IowaStateU ReptileEvolutionaryPhysiology

IowaState.Reptiles.Physiology

Postdoctoral Position in Evolutionary Physiology at Iowa State

A Postdoctoral position is available in the laboratory of Anne Bronikowski at Iowa State (www.eeob.iastate.edu) to help lead projects on the comparative physiology of mitochondrial, endocrine, and immune phenotypes in diverse reptile species, examining the roles of climate, phylogeny, genotype, and plasticity in accounting for variation. These evolutionary physiology studies are part of an overarching goal to understand the integration of physiology and life-history in nature. The post-doc will coordinate sampling with a network of collaborators including evolutionary ecologists, herpetologists, wildlife biologists, and animal scientists. The postdoc will be central to most aspects of the projects and thus strong laboratory, mentoring, communication, and writing skills are essential. In addition to facilitating goals of these projects, the successful candidate will have abundant opportunities to develop her/his own independent research. The ideal applicant should have solid experience in physiology of non-model organisms, including expertise in at least one of: mitochondrial biology, evolutionary endocrinology, or immunology, as well as a strong background in ecology, evolution, and statistics.

A Ph.D. in evolutionary biology or physiology is necessary. Current funding for the position is available for as many as three years, with annual renewal contingent on performance, emphasizing progress on methods development, data collation and analysis and writing. The successful candidate must be available no later than 1 July 2016.

Examples of recent publications related to these projects include:

Gangloff et al. (2015) PBZ 88: 550-563. McGaugh et al. (2015) PNAS 112: 7055-7060 Refsnider et al. (2015) J Exp Zool A 323: 160-168 Alper et al. (2015) Exp Geron 71: 109-117 Schwartz & Bronikowski (2013) Molec Ecol 22: 739-756 Palacios et al. (2013) PBZ 86: 547-558 Palacios et al. (2012) GCE 175: 443-448

To apply, e-mail Anne Bronikowski (abroniko@iastate.edu) with (1) a brief (< 1 page) cover letter explaining your research interests, (2) a CV, and (3) contact information for three references. Review of applicants will begin immediately and end on 15 May 2016, at which point a suitable candidate will be selected.

"Bronikowski, Anne [EEOBS]" <abroniko@iastate.edu>

JohnInnesCentre Norwich EvolutionaryGenomics

Genome duplication, gene flow, and adaptation at the John Innes Centre-

We seek big-question-oriented postdocs to join us to work on fundamental problems in evolutionary genomics. We offer a highly interdisciplinary environment with remarkable institutional support and robust grant funding. Two ERC grants have just been won by the Yant lab and our very close collaborators, the Bomblies lab (also at JIC). This greatly enhances an ambitious programme in evolutionary genomics in Norwich. Additionally, we have many collaborations with diverse European groups, offering you outstanding potential for professional development.

Current projects have an explicitly phenotype-first orientation, aiming to determine the genetic basis and evolutionary repeatability of adaptation to intense, quantifiable selection pressures, both environmental and intracellular. We do this by applying large-scale population genomics to wild plant populations that have evolved to overcome demonstrable hazards. We currently focus on adaptation to genome duplication as well as adaptation to highly challenging, quantifiable environmental stressors in species ranging from Arabidopsis arenosa, to Chamerion angustifolium, to Mimulus guttatus and back throughout the Brassicaceae to A. lyrata and A. thaliana. See http://yant.jic.ac.uk for more. We strongly encourage applicants to suggest project ideas that harmonize with these general aims and we are fully committed to helping successful applicants develop their ideas for the eventual formation their own independent research groups.

Applicants with evolutionary genetic, computational, or molecular interests in adaptation are encouraged to apply. We seek candidates with initiative, mature analytical skills, and a drive to push forward on new problems in evolutionary genomics. Successful candidates will perform independent, novel analyses and will have demonstrated clear innovation during or following their PhD. To begin a meaningful conversation, we ask that you include a cover letter and a statement that indicates which research topics you are particularly interested in, and why your qualifications make you a good fit with our research.

For further information and details of how to apply, please visit our web site, http://jobs.jic.ac.uk/-Details.asp?vacancyID=3D11465. As a user of the disability symbol, we guarantee to interview all disabled applicants who meet the minimum essential criteria for this vacancy.

Early application is encouraged, but the deadline for application is 10 May 2016.

Essential Skills: Demonstrated clear innovation during or following your PhD.

Excellent communications skills.

Good interpersonal skills and ability to work with diverse team members.

A cover letter and a statement that indicates which research topics you are particularly interested in, and why your qualifications make you a good fit with our research.

Levi Yant Project Leader John Innes Centre Norwich Research Park Colney Lane Norwich NR4 7UH United Kingdom http://yant.jic.ac.uk | Tel: +44 (0)7490 253006

"Levi Yant (JIC)" <Levi.Yant@jic.ac.uk>

JohnInnesCentre UK EvolutionaryGeneticsGenomics

How can constrained system evolve to meet new challenges such as climate or genome change? Many core essential systems in cells and organisms (many of which are commonly thought of as "house-keeping" processes) may at first blush seem like things that should not evolve, and thus should lie outside the interests of evolutionary geneticists. Yet many essential processes are sensitive to perturbation, and can lead to catastrophic consequences when they are disrupted. Thus, for an organism to evolve to meet new challenges, such systems must be adjusted. But these "core" processes are often essential, and in many cases quite constrained, so how can they change at all? How the "basic biology'Â of organisms can be retuned during adaptation is an exciting and almost completely open set of questions.

Consider meiosis for example 'V the meiotic segregation of chromosomes is essential for fertility of sexual eukaryotes and therefore for the propagation of populations. The three dimensional structures and general progression of meiosis are strongly conserved even across kingdoms. Yet challenges that lineages encounter very regularly, such as changes in genome architecture and shifts in temperature, can seriously challenge the reliable progression of meiosis. This can lead to chromosome mis-segregation and infertility. It is clear from the evolutionary literature that for many known challenges to meiosis there is a species or population that is resilient to that stress, showing that it can evolve. In some cases these shifts are associated with signatures of selection having acted on core meiosis proteins. Thus it is clear that meiotic systems do evolve to cope with new challenges, and that they do so by modifying some of the essential core constituents of meiosis. But how do they do that while yet maintaining the complex multiprotein interactions and progression of three-dimensional structures that are essential for fertility? In other words, how can you change a constrained system without breaking it? Do you modify protein stability, shape, or interactions? Do changes require compensatory evolution in other proteins or systems? How many ways can meiosis be retuned as organisms face novel challenges?

In my group, we combine complementary genomic, genetic, and in-depth molecular and cytological studies to understand how organisms evolve to meet new challenges. We currently focus primarily on meiosis and how it evolves in response to genome change and climate shifts, but we also digress to core transcription, cell cycle control and other processes.

The lab recently received a 5-year European Research Council to fund this work ("Adaptive evolution of meiosis in response to genome and habitat change") that opens several postdoc opportunities to creatively tackle novel questions under the broader aim of understanding the causes and consequences of the evolution of meiosis and recombination. There is room for creative individuals to join the group and develop their own projects or build on those already ongoing in the lab.

The broad focus will be on evolutionary genetics and genomics, and we seek to build a group in which people with different talents complement and inspire one another to think outside their present comfort zones. Successful applicants will have the opportunity to build their own novel research areas with which to ultimately found their own independent research careers.

Finally, the John Innes Centre is a world class research institution with excellent facilities and colleagues and Norwich England is a lovely place to live with easy access to beautiful natural areas as well as London. Our local airport provides direct connections to Amsterdam and thereby easy access to the rest of the world.

For information and to apply (by May 2): http://jobs.jic.ac.uk/Details.asp?vacancyID=11464 Also see: http://bomblies.jic.ac.uk If interested but wish to apply later, please contact Kirsten.Bomblies@jic.ac.uk

Kirsten Bomblies Project Leader John Innes Centre Norwich Research Park Colney Lane Norwich NR4 7UH United Kingdom

"Kirsten Bomblies (JIC)" <Kirsten.Bomblies@jic.ac.uk>

KielU Celegans HostMicrobiotaInteractions

Postdoc Position on the Evolution, Genetics, and Genomics of C. elegans-microbiota interactions

Basic Information

Postdoctoral Scientist position for 3-4 years, with an extension possible thereafter, salary at level TV-L E13

Area of Work

Evolution of C. elegans-microbiota interactions, using evolution experiments, phenotypic analysis, and genome analysis of both nematode and bacterial populations. The project aims at understanding the importance of associated microbes on evolutionary adaptation of the host and the entire association as a whole, including characterization of the underlying genetic and genomic processes. There is explicitly space and also time for bringing in own ideas and thus the opportunity to develop a new and original research agenda. The project is part of a larger research initiative on host-microbiota interactions (www.metaorganism-research.com), including several additional projects with the model organism C. elegans, thus providing an interactive environment for an exciting new field of research.

Expectations and Requirements

University degree and PhD in evolutionary biology and/or genomics and/or microbiota-host interactions or any related field. High competence in statistics, experimental design, and English writing is a must. Ideally comprehensive experience in genome analysis and/or work with C. elegans and/or performance of evolution experiments and/or microbiota-host analysis and/or population genetics and/or meta-analysis.

Kiel University aims at a higher proportion of women in research and education, and, therefore, specifically encourages qualified female scientists to apply. Female scientists will be preferentially considered in case of equivalent qualification, competence and achievements.

Kiel University specifically supports employment of severely handicapped people. Therefore, severely handicapped applicants will be preferentially considered in case of suitable qualification.

Kiel University specifically welcomes application from people with migration background.

Location

The position will be based in the Schulenburg group at the University of Kiel, Northern Germany. The department provides an international and interactive atmosphere, while Kiel University and connected institutes (e.g., Max Planck Institute in Ploen) offer a stimulating research environment with a particular focus on evolutionary biology and also C. elegans genetics. The city of Kiel is a medium-sized town located at the coast of the Baltic Sea. It is the capital of the most Northern state of Germany, Schleswig-Holstein. It offers many opportunities for leisure activities, including theatres, an opera, the Schleswig-Holstein classical music festival, the heavy metal festival in Wacken, sailing, surfing, cycling, and the famous festivities of the "Kieler Woche" - one of the largest sailing events in Europe.

Applications

Applications should include a motivation letter (max. 2 pages long), CV, publication list, names and contact details of two referees (who are familiar with the applicant's work), and copies of certificates. Deadline for applications is 25.05.2016. Applications should be sent as a single pdf-document by Email to Hinrich Schulenburg (hschulenburg@zoologie.uni-kiel.de).

Deadline for applications

25 May 2016

Starting date for the position

As soon as possible, ideally sometime during the summer, at the latest by December 2016

Further questions

Send an Email to Hinrich Schulenburg (hschulenburg@zoologie.uni-kiel.de).

– Hinrich Schulenburg

Zoological Institute Christian-Albrechts-Universitaet zu Kiel Am Botanischen Garten 1-9 24118 Kiel Germany Tel: +49-431-880-4143/4141 Fax: +49-431-880-2403 Email: hschulenburg@zoologie.uni-kiel.de Web: www.uni-kiel.de/zoologie/evoecogen/ Hinrich Schulenburg <hschulenburg@zoologie.uni-kiel.de>

LundU EvolutionPhylogenyThermal Adaptation

Postdoc in evolution, phylogeny and thermal adaptation (Lund University, Sweden)

I have an opening for a postdoc with background and experience in phylogenetic comparative methods for a project on micro- and macroevolution of thermal adaptation and thermal plasticity (start date: October 1 2016). This is a perfect opportunity for somebody who is interested in combining phylogenetic comparative methods and experiments, theory and empirical work.

I am seeking a qualified candidate anywhere from the world, as long as (s)he fits the required qualifications and criteria and is interested to work in my lab and in a friendly, collaborative and creative international research environment in Lund (Sweden). Please do not hesitate to contact me if you have any further questions and spread the information about this position to suitable members in your lab and in your international networks.

Information about the position and application procedure can be found here: https://lu.mynetworkglobal.com/en/what:job/jobID:99355/ Sincerely, Erik Svensson

Erik Svensson Professor Department of Biology, Evolutionary Ecology Unit Lund University SE-223 62 Lund SWEDEN Phone: +46 46 222 38 19 Fax: +46 46 222 47 16 E-mail: erik.svensson@biol.lu.se Webpage: http://www.biology.lu.se/erik-svensson Lab blog: http://exeblund.blogspot.se Researcher ID: http://www.researcherid.com/rid/E-8324-2010 New book: "The Adaptive Landscape in Evolutionary Biology" Edited by Erik Svensson and Ryan Calsbeek Available through all good bookshops, or direct from Oxford University Press at: http://ukcatalogue.oup.com/product/9780199595389.do Erik Svensson <erik.svensson@biol.lu.se>

MaxPlanck Tuebingen 5 BioinformaticsEvolutionaryGenomics

5 Postdoctoral positions available in Bioinformatics and Evolutionary Genomics

The Jones and Chan labs at the Friedrich Miescher Laboratory at the Max Planck Campus, Tübingen, Germany, are looking for *up to five* talented bioinformaticians/computer scientists/evolutionary genomicists to work on cutting edge genomics projects. The positions are available for an initial 2 years with the possibility of extension.

We work at the cross-section between functional genomics and evolutionary genetics with the aim of understanding the molecular basis of phenotypic variation in mice and stickleback fish. Both labs are funded by the Max Planck Society (MPG) and hold prestigious European Research Council Grants.

We are looking to recruit talented and motivated team members to analyse existing datasets (including DNA-, RNA-, ChIP-, ATAC-Seq). You will work closely with other wet-lab members with a focus on development of pipelines and analysis of exciting genomic datasets for the projects outlined below (please visit our websites for more details). Where applicable you may also participate actively in wet-lab data generation using our established high-throughput robotics platforms.

1. Recombination Hot- and Coldspots and Adaptive Evolution (JONES - ERC)

By shuffling parental alleles to produce novel haplotypes, recombination impacts the strength of selection on nearby polymorphisms and can influence the rate of adaptation in natural populations. We are using pedigree & population genetic methods to quantify variation in recombination hot- and coldspots across the genome, among individuals, sexes & divergent species and intersect these maps with adaptive loci to investigate how recombination shapes adaptive evolution.

2. Population Genomics: Rapid Adaptation from Standing Genetic Variation (JONES - MPG & DFG)

The type, source and availability of genetic variation can promote or constrain the speed of adaptation, and influence the future evolutionary trajectory a population. We are combining empirical population genomic analyses with theoretical population genetic models of selection-migration balance and selective sweeps from standing genetic variation in order to identify and quantify key factors that influence rapid adaptation in natural stickleback populations.

3. Comparative Functional Genomics and Genome Evolution (JONES - MPG) We are identifying and comparing functional genomic elements contributing to adaptive divergence and speciation by creating de novo assemblies and functional annotations from ChIP-seq, captureC, RNAseq, mapping panels and signatures of selection from hundreds of whole genome datasets from sequenced families and wild-caught individuals.

4. Systems biology of evolution in mice (CHAN - MPG & ERC) We have a number of mapping panels and resources, ranging from large Faroese wild mice, including whole-body morphometrics measurements, to innovative “in vitro” crosses derived from mouse interspecific hybrid stem cells. Using these resources we aim to understand the genetic architecture for adaptive traits and the evolution of gene regulatory networks.

5. Genomics of selection response in Longshanks mice (CHAN - MPG) Dr. Campbell ROLIAN at the Univ. of Calgary has performed 21 generations of artificial selection for increased tibia length in mice (2 “Longshanks” selection lines & 1 control line, >6000 individuals). We will study the selection response from multiple angles, ranging from trait mapping, population genomics, theory (in collaboration with Nick BARTON, IST Austria) to developmental genetics. With this dataset we aim to establish the dynamics of the genotype-phenotype map under strong selection.

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 training in genomics, bioinformatics or statistical genetics and in-depth research experience in these fields. You should demonstrate expertise and proficiency in one or more of the following areas:

â handling and analysis of NGS datasets (whole genome, single-cell/molecule sequencing, RNASeq, ChIP-seq, 3C/4C)

â advanced skills in statistical genomics (e.g. QTL or GWAS approaches, genotype imputation, Hidden Markov Models, and haplotype phasing of whole genome data

â de novo genome assemblies and comparative genomics.

â empirical and theoretical population genetics

â familiarity with parallel computing, visualisation of genomic datasets and associated toolkits (e.g. UCSC/Ensembl genome browsers, proficiency with web-based programming and SQL relational databases desirable)

Experience with UNIX and fluency in statistical and/or programming languages is essential (R, Python or Perl, required; C++, SQL, java knowledge desirable). Wetlab skills and experience in other types of data analysis (e.g., image processing) will be an advantage.

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McGillU Biodiversity

TheNSERC CREATE Biodiversity, Ecosystem Services, and Sustainability seeks applicants for a 2-year postdoctoral fellowship at McGill University in association with UQÃand Université Laval. Candidates could be based at any of these institutions, but would be expected to spend some time at McGill University where the program is hosted. Preference will be given to candidates with bold ideas, demonstrated research ability, and strong communication skills. A working knowledge of Spanish is essential and applicants must have obtained their PhD within the last four years.

Applicantswill be evaluated on the quality of their research proposal, their leadership and collaboration abilities, communication skills, academic excellence, and their vision to contribute to the BESS program. The successful candidate will be expected to conduct original research on core problems in the neotropical environment, foster interactions within BESS, run a seminar series, and organize a retreat.

BESSprovides partial funding for this position (~$27,000) with the rest expected to come from other sources, most often the collaborating faculty supervisor. Thus, potential applicants need to first contact one of the BESS co-PIs, in consultation with whom the applicant will prepare the following supporting documents.

1.Cover letter 2.Curriculum vitae 3.Two letters of reference 4.Scientific goals and research plan relevant to BESS - MAXIMUM TWO PAGES 5.A funding plan agreed upon with you and your proposed faculty supervisor - MAXIMUM ONE PAGE

Howto apply: Please submit your application to victoria.reed@mail.mcgill.ca before June 5th, 2016.

Forfurther information please visit our website (www.mcgill.ca/bess/bess)

FelipePérez-Jvostov BESSProgram Coordinator http://www.mcgill.ca/bess/bess RedpathMuseum, room 205 859rue Sherbrooke, Montreal, QC.

bess@mcgill.ca

Nanaimo BritishColumbia FishBarcoding

Developing metabarcoding tools for environmental DNA-based biomonitoring in aquatic ecosystems Fisheries and Oceans Canada: Pacific Biological Station, Nanaimo, British Columbia

A post-doctoral fellow with an interest in applied ecological and evolutionary genomics and aquatic ecosystems is being sought to lead the development of metabarcoding-based biomonitoring approaches to meet federal regulatory needs.

Multiple projects are underway. The successful candidate will play a lead role in a multi-disciplinary project on validating the use of environmental DNA (eDNA)-based metabarcoding (targeting meoifauna) for benthic impact assessments of salmon farms in coastal British Columbia. Salmon aquaculture causes organic enrichment of surrounding sediments which affects biodiversity and biomass of benthic fauna concomitant with sediment chemical changes. Existing environmental impact assessments rely on manual morpho-taxonomy or abiotic proxies of organic loading with uncertain accuracy. The project aims to develop an efficient and reliable lower-cost alternative based on cataloging the diversity and abundance of benthic communities through metabarcoding of environmental DNA (eDNA).

The successful candidate will also play a key collaborative role within two other projects aimed at developing metabarcoding based eDNA biosurveillance of aquatic invasive species (AIS). Aquatic invasive species (AIS) pose a major threat to freshwater aquatic ecosystems and fisheries in BC; detecting new invasions early and accurately assessing existing AIS distributions are important to maximize the chance for effective management intervention.

The successful candidate will have a PhD in ecological and/or evolutionary genomics or another relevant area and will demonstrate well-developed bioinformatics and computational skills (including programming, e.g. Perl, R, Unix, Python) as applied to the analysis of next-generation sequencing data. Experience in the preparation of samples for NGS (Illumina) and knowledge of barcoding, metabarcoding, and/or environmental DNA sampling in aquatic systems would be an asset but not a requirement. Candidates should demonstrate a strong track record of publication and be willing to work as part of a collaborative team.

A 2 year Postdoctoral Fellowship position starting by January 2017 is available with stipend funding at NSERC Visiting Fellowship rates. Applications from international candidates will be accepted. For more information and to review eligibility criteria, see: http://www.nserc-crsng.gc.ca/Students-Etudiants/-PD-NP/Laboratories-Laboratoires/index_eng.asp To be considered for this position, please send your CV and brief email text explaining your suitability to cathryn.abbott@dfo-mpo.gc.ca

Cathryn Abbott, Ph.D. Research Scientist, Pacific Biological Station

"Cathryn.Abbott@dfo-mpo.gc.ca"
<Cathryn.Abbott@dfo-mpo.gc.ca>

NHM KingsCollegeLondon 2 EvolutionaryVenomics

Posdoc:NHM_and_KingsCollege_London.EvolutionaryVenomics

Postdoctoral Research Assistants in Cnidaria and Myxozoa Venomics (2 posts) Grade 6 point 32 from £33,357 - £34,753 p.a Expected start date 20th June 2016

Two Postdoctoral Research Assistant positions are available on a 3 year fixed term Leverhulme Trust funded tripartite project between Dr Paul Long (King's College London), Prof Beth Okamura (Natural History Museum, London) and Prof Antonio Marques (University of São Paulo, Brazil). There is a lack of venom evolution studies within Cnidaria compared to other venomous animals, and our current picture of cnidarian venom evolution is highly imbalanced because almost nothing is known about myxozoan venoms. Characterising venom toxins in parasitic myxozoans and then comparing these to the toxins in free-living (non-parasitic) cnidarians will be significant because it will enable insights into how venoms have been co-opted for parasitic lifestyles. One post will be based at King's College London and it is expected that the applicants will have a PhD in bioinformatics and significant research experience in generating and analysing genomic, transcriptomic and proteomic experiments. Familiarity working with free-living cnidarians and field collection experience is desirable. The second post will be based at the Natural History Museum, London and it is expected that the applicants will have a PhD in a relevant biology subject including significant field collection and research experience working with aquatic or parasitic organisms, together with a proven track record of phylogenetic analysis and the generation and analysis of genomic and transcriptomic data. Experience in research in one or more of the following areas is also desirable: Myxozoa, venoms, ISH (in situ hybridisation), immunohistochemistry, confocal microscopy, transmission electron microscopy, proteomics. In addition, it is expected that the applicants have an excellent record of research productivity, excellent oral and written communication skills, together with excellent time management skills, and an ability to work under pressure to deadlines. The deadline for application is 29th April 2016, with interviews for both positions to be held by 6th May 2016. Applications and informal enquiries can be sent in advance of the formal advertisement directly to paul.long@kcl.ac.uk

Hanna.Hartikainen@eawag.ch

OkinawaInstSciTech 2 MoleculariToolsMuseum InsectBehaviour

Are you excited about the untapped potential of next-generation sequencing? Do you enjoy making new tools for molecular biology? If so, this postdoc if for you. The Ecology and Evolution Unit at the Okinawa Institute of Science and Technology (OIST) is looking for someone to drive the development of novel techniques for high-throughput molecular and bioinformatic population genomics analysis of non-model museum specimens. Our goal is to make reproducible and affordable tools for using historical material to study microevolutionary patterns. To this end, we are particularly focused on developing reduced representation sequencing techniques for samples with small amounts of heavily degraded DNA. We have a fully funded (for five years) laboratory with state of the art equipment. A MiSeq down the hall lets you prototype your constructs. A couple of floors down, a high-powered sequencing center can give you massive data yields, which you can analyze on one of the world's top cluster computers.The postdoc will have opportunities to interact with researchers from other disciplines, and will involve mentoring rotation students and interns, as well as additional opportunities to contribute to graduate teaching.

Contract: The postdoc will have a two year term with potential for renewal. Salary depends on the number of years since Ph.D. but ranges from 4.4 to 5.2 million yen (approximately 40 - 50 thousand US$). In addition, there are housing and commuting allowances. Relocation costs will be covered for successful candidates. While we prefer that you start some time in late August, some flexibility is possible.

About OIST: Though located in Japan, OIST is a highly international graduate university with English as its lingua franca, and students, faculty and research staff from around the world. Knowledge of Japanese is not required for work at OIST, or for life in Okinawa. OIST has a dynamic multicultural environment, and is an equal opportunity employer.

Requirements: A Ph.D. program completed by July 2016, with a track record of previous publication, as well as relevant research experience. Due university-level restrictions, only candidates within five years of their Ph.D. are eligible to apply to this position.

To apply: Please send a letter of interest, and a CV to alexander.mikheyev at oist.jp. After an initial screening over Skype, successful candidates will be asked to provide a writing sample, two letters of reference, and invited for an on-site interview in Okinawa to take place in June 2016, with all expenses for travel and accommodation paid for by the Ecology and Evolution Unit. Applications are due by May 20th, 2016, with Skype interviews to take place later that week.

Alexander (Sasha) Mikheyev Associate Professor Ecology and Evolution Unit (http://ecoevo.unit.oist.jp) Okinawa Institute of Science and Technology 1919-1 Tancha Onna-son, Kunigami-gun 904-0495 Japan

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Are you interested in the genetic architecture of behavioral traits? Do you have experience in quantitative trait mapping, or setting up insect behavioral experiments? If so, this job will be an excellent opportunity to develop your existing skills and acquire new ones. The Ecology and Evolution Unit at the Okinawa Institute of Science and Technology (OIST) has recently started a fully funded multi-year project dissecting genes involved in social behavior, using experimental crosses of honey bees as a model. The major goal is to use computer vision to characterize individual behavior, and to understand genes that underly behavioral traits. Although our principle work is on bees, we are open to the possibility of hiring someone unfamiliar with this system, and even having the postdoc work part-time on the study system of their choosing. As long as we have the crosses, we may map some non-behavioral traits as well.

Contract: The postdoc will have a two year term with potential for renewal. Salary depends on the number of years since Ph.D. but ranges from 4.4 to 5.2 million yen (approximately 40 - 50 thousand US$). In addition, there are housing and commuting allowances. Relocation costs will be covered for successful candidates. While we prefer that you start some time in late August, some flexibility is possible.

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OxfordU GuppyEvolution

Post-doc, for up to three years: We seek a post-doc to participate in a US National Science Foundation supported project entitled "The Paradox of Coexistence: The Evolution of Ontogenetic Interactions". This research is a continuation of an ongoing experimental study of the interactions between ecology and evolution in natural streams in the Northern Range Mountains on the island of Trinidad. Our project is built around four experimental introductions of guppies into previously guppy-free tributaries that contain only one other fish species - the killifish Rivulus hartii. Our prior research has characterized how each of these species evolves in response to the other and to the way the ecosystem changes after the guppy introduction. One discovery is that their interactions include bi-directional intra-guild predation. Theory predicts that such an interaction is very unlikely to be stable, yet it proves to be reliably stable in all four introductions and in all natural streams where these fish coexist. This apparent anomaly is the basis for an exploration of factors not included in theory that could lend to this stability, including the contemporary evolution of both participating species and how these interactions change with the age and size of individuals in both species. Our project is an integration of the development of new theory, new experiments to be performed in natural and artificial streams in Trinidad and the continued study of the four introductions in natural streams. The post-doc's home base will be with Joseph Travis (PI) at Florida State University but will include extensive periods of time in Trinidad, where he/she will execute experiments in natural and artificial streams. The successful applicant must have a completed PhD, publication record and extensive field experience. You can learn more about our project at our website <CNAS.UCR.EDU/guppy>. To apply, please send a CV and arrange to have at least three letters of reference sent to David Reznick at david.reznick@ucr.edu.

Cheers, Ron

Ronald Bassar <ronald.bassar@zoo.ox.ac.uk>

OxfordU StatisticalGenetics

Applications to be received by 12pm on Friday 6th of May 2016

Grade 7: 30,738 - 37,768 p.a.

We are seeking a Postdoctoral Scientist in Statistical Genomics to join an established multi-disciplinary team as part of Modernising Medical Microbiology (MMM) consortium.

The aim of the role is to develop and apply statistical methods, including genome-wide association studies, for discovering rare and common genetic variants underlying antimicrobial resistance in Mycobacterium tuberculosis. You will be given an exciting and rare opportunity to work with global Mycobacterium tuberculosis (TB) experts from five continents, statistical geneticists, clinicians, medical statisticians and software engineers; integrating statistical genetics, bioinformatics and machine learning methods with the aim of uncovering all genomic variants causing at least 1% resistance to first line anti-TB drugs.

You will hold a PhD in statistical genomics, evolutionary biology, statistics or a related subject. You will have strong statistical skills and a background in biological sequence analysis, together with an enquiring and flexible attitude and an interest in working collaboratively with researchers from different disciplines.

The post is full-time and fixed-term for up to 3 years initially.

Applications from candidates who have not yet completed their PhD may be considered, and would be appointed initially at Grade 6 (27,328 - 32,600 p.a.) with amended duties and responsibilities.

Applications for this vacancy are to be made online. You will be required to upload a supporting statement and CV as part of your online application.

To apply or for more details, please visit http://www.ndm.ox.ac.uk/current-job-vacancies/vacancy/122909-Postdoctoral-Scientist-in-Statistical-Genomics Only applications received before 12.00 midday on Friday 6 May 2016 will be considered.

Danny Wilson

– Dr Daniel Wilson Wellcome Trust/Royal Society Sir Henry Dale Fellow Associate Professor Nuffield Department of Medicine University of Oxford www.danielwilson.me.uk "daniel.wilson@ndm.ox.ac.uk" <daniel.wilson@ndm.ox.ac.uk>

Paris6U MicrobialBioinformatics

Hello,

Please find below the description of a postdoctoral position to 'Search for common 'genetic goods' in gene families and microbial communities'.

We are offering a 14 months post-doctoral position, starting on September the 1rst 2016 (see also http://www.evol-net.fr/index.php/fr/postes-a-pourvoir).

The theory of 'genetic public goods' recently postulated that genetic sequences can be exploited in various combinations, even by distantly related or unrelated evolving entities, i.e. microbial communities benefiting from the sharing of genes between their members, such as photosynthesis genes between cyanophages and cyanobacteria, or such as drug resistance genes within multispecies biofilm. Yet, the nature, size and diversity of microbial communities sharing such 'genetic goods' remain poorly known. Moreover, the rules of gene sharing also remain to be described.

A wealth of molecular data from metagenomic, single cell metagenomic, and microbial genomes projects is now available to tackle these fundamental issues. Furthermore, sequence similarity networks offer a promising complementary niche to phylogenetic methods to exploit the complexity of these data. These graphs allow for mathematical analyses of genetic diversity and similarities over dozens of millions of sequences, providing novel ways to detect 'clubs' of genomes, which have not necessarily evolved from a single last common ancestor yet exploit some common genetic material. Likewise, these networks allows for the detection of some 'sets' of gene families that exploit common pools of genetic fragments/domains.

To further develop the detection strategies of genetic public goods, our lab is now looking for a post-doctoral fellow in bio-informatics, who will be funded for up to three years by an ERC grant (for an approximate salary of 2197 euros/ month after taxes, i.e. 57 350euro before taxes for the entire post-doc). The candidate will take advantage of graph properties and algorithms from the graph theory:

-1) to improve the identification of 'clubs' of genomes /'sets' of gene and their pool of genetic goods in complex networks with a few millions nodes and dozens of millions of edges;

- 2) to analyze domains combinations in genes and gene sharing in communities, using bipartite graphs;

-3) He/she will then analyze the functions of these 'genetic goods' and their distribution across genes and genomes to test what lifestyles favors their sharing.

The candidate will work within a consortium of friendly bioinformaticians (Philippe Lopez, Eduardo Corel), evolutionary biologists (Eric Bapteste), and graph theorists (Michel Habib, Laurent Viennot), and be hosted in the University Pierre and Marie Curie in the center of Paris, France. Ideally, the candidate should have a strong interest for evolutionary biology, microbial evolution and a good background in bio-informatics, or graph theory. The position will start by September 2016, but interested candidates are invited to apply immediately.

He/she should be early in his/her carreer (i.e. holding a PhD degree for less than 2 years).

Applicants are requested to send a detailed resume, a motivation letter, a pdf copy of their PhD thesis, and the names of two scientific referees to : eric.bapteste[at]snv.jussieu.fr

The first round of applications will be closed June 1rst, 2016.

epbapteste@gmail.com

PennStateU 2 AntFungalInteractions

The Hughes Lab has two open positions on the mechanism by which fungi control ant behavior (the extended phenotype of parasites using the zombie ant system).

Postdoctoral Announcement:

The Hughes Lab is seeking a post-doctoral research to work on ant behavior and fungal parasites that affect ant behavior to enable transmission (parasite extended phenotypes). The position is available in the Center for Infectious Disease Dynamics (www.cidd.psu.edu), The Pennsylvania State University, University Park Campus but the majority of the work will take place at our field site associated with the Federal University of Vicosa, Minas Gerais, Brazil. At this field site we have accessible ant colonies and manipulated ants. The ideal candidate will be able to locate ant colonies from the wild and study ants under natural conditions. The ants are nocturnal so the work requires working in the rainforest at night, observing trails. We will also conduct experimental infections so the ideal candidate should have experience with injecting either ants or insects using standard microinjection protocols. The goal of the study is to measure changes of the fungal colony inside the ant and we will prepare samples for Serial Block Face SEM, transcriptomics and metabolomics. We are seeking a person who has experience with transcriptomics on the Illumina platform and metabolomics. Candidates should have extremely strong organizational, written, and oral communication skills; and be able to work both independently and as part of a collaborative team. Since the work is based in Brazil the candidate should be able to speak Portuguese. For further information, please feel free to contact Dr Hughes (dph14@psu.edu; +1 814- 863-6073). Interested applicants should upload a curriculum vitae, a 1-2 page statement of research interests that explicitly describes professional qualifications for this position, and contact information for three referees. Review of applicants is ongoing and the position will begin when a suitable candidate is selected. About David Hughes: Hughes, is a behavioral ecologist who has studied social insects and their diseases in 11 countries on 5 continents. He has worked with diverse diseases as well as the behavior of healthy and infected ants under field (rain- and temperate forests) and laboratory conditions. In recent years he has become interested in plant diseases. www.hugheslab.com This is a fixed-term appointment funded for one year from the date of hire with good possibility of re-funding. This work is funded thorough an NIH R01 program Modeling social behaviors.

Postdoctoral Announcement:

The Hughes Lab is seeking a post-doctoral research to work on ant behavior and fungal parasites that affect ant behavior to enable transmission (parasite extended phenotypes). The position is available in the Center for Infectious Disease Dynamics (www.cidd.psu.edu), The Pennsylvania State University, University Park Campus. The goal of the study is to measure changes in the fungal colony inside the ant and we will prepare samples for Serial Block Face SEM, transcriptomics and metabolomics. We are seeking a person who has experience with different histology approaches; ideally SEM. Experience with transcriptomics is a distinct advantage. The work requires embedding and staging samples for processing, as well as downstream data handling. The ideal candidate would also be able to do confocal microscopy. The work requires injecting ants with fungal inocula so experience using standard techniques in microinjection is a plus. The job also requires field work in South Carolina and Brazil. Candidates should have extremely strong organizational, written, and oral communication skills; and be able to work both independently and as part of a collaborative team. For further information, please feel free to contact Dr Hughes (dph14@psu.edu; +1 814- 863-6073). Interested applicants should upload a curriculum vitae, a 1-2 page statement of research interests that explicitly describes professional qualifications for this position, and contact information for three referees. Review of applicants is ongoing and the position will begin when a suitable candidate is selected. David Hughes: Hughes, is a behavioral ecologist who has studied social insects and their diseases in 11 countries on 5 continents. He has worked with diverse diseases as well as the behavior of healthy and infected ants under field (rain- and temperate forests) and laboratory conditions. In recent years he has become interested in plant diseases.www.hugheslab.com This is a fixed-term appointment funded for one year from the date of hire with good possibility of re-funding. This work is funded thorough an NIH R01 program Modeling social behaviors.

David Hughes CIDD, Dept Entomology & Biology

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PennStateU EcologicalEvolutionaryGenomics

A postdoctoral position is available in the lab of Jesse R. Lasky (laskylab.org) in the Department of Biology at The Pennsylvania State University, State College, PA. Lab goals are to understanding the processes that generate and maintain biodiversity.

In particular, the lab studies genetic and ecological mechanisms of local adaptation to environment. We are focusing on adaptation to climate and interactions between climate and biotic factors. We aim to understand the genetic basis of adaptation and the role of ecological and evolutionary dynamics in response to environmental change.

Our approach is integrative and involves patterns and processes at molecular and ecological levels. Candidates with an integrative background and interest in quantitative approaches are sought. The primary study organisms are plants; currently including forest trees, Arabidopsis, and sorghum.

Relevant recent publications include (full list: http://www.personal.psu.edu/jrl35/psu/pub.html) Lasky JR, Des Marais DL, McKay JK et al. (2012) Characterizing genomic variation of Arabidopsis thaliana: the roles of geography and climate. Molecular Ecology, 21, 5512V5529. Lasky JR, Des Marais DL, Lowry DB et al. (2014) Natural variation in abiotic stress responsive gene expression and local adaptation to climate in Arabidopsis thaliana. Molecular Biology and Evolution, 31, 2283V2296. Lasky JR, Uriarte M, Boukili V, Chazdon RL (2014) Trait-mediated assembly processes predict successional changes in community diversity of tropical forests. Proceedings of the National Academy of Sciences, 111, 5616V5621. Verslues PE, Lasky JR, Juenger TE, Liu T-W, Kumar MN (2014) Genome-Wide Association Mapping Combined with Reverse Genetics Identifies New Effectors of Low Water Potential-Induced Proline Accumulation in Arabidopsis. Plant Physiology, 164, 144V159. Lasky JR, Upadhyaya HD, Ramu P et al. (2015) Genome-environment associations in sorghum landraces predict adaptive traits. Science Advances, 1.

Penn State University has research strengths in genomics (https://www.huck.psu.edu/content/people/area-of-interest/Bioinformatics%20and%20Genomics), plant biology (https://www.huck.psu.edu/content/people/area-of-interest/Plant%20Biology), infectious disease dynamics (http://cidd.psu.edu/), and ecology (https://www.huck.psu.edu/content/people/area-of-interest/Ecology) across departments and colleges. The postdoc will have freedom to develop new projects in the lab and to build collaborations with other labs.

The ideal candidate will have expertise including population genetics, quantitative genetics, evolutionary ecology, genome-wide association studies, statistics, and computation (R, python, shell, HPC cluster). Experience in molecular genetics, host-parasite coevolution, ecophysiology and population and community ecology are also of interest. Excellent communication skills, including writing, are required, as is a strong publication record.

The position requires a PhD and is initially funded for one year. Applications must be submitted electronically. A complete application will include a cover letter detailing experience and research interests, a current CV, and contact information for three professional references. The start date is flexible. Review of applications will begin immediately and continue until the position is filled.

Apply here: https://psu.jobs/job/62448 CAMPUS SECURITY CRIME STATISTICS: For more about safety at Penn State, and to review the Annual Security Report which contains information about crime statistics and other safety and security matters, please go to http://www.police.psu.edu/clery/, which will also provide you with detail on how to request a hard copy of the Annual Security Report. Penn State is an equal opportunity, affirmative action employer, and is committed to providing employment opportunities to all qualified applicants without regard to race, color, religion, age, sex, sexual orientation, gender identity, national origin, disability or protected veteran status.

"Jesse R. Lasky" <jrl35@psu.edu>

PennState UMichigan EvolutionaryMedicine

EVOLUTIONARY RISK ANALYSES IN HUMAN HEALTH

Post-doctoral Scholars Research Associates

The evolution of drug resistance is one of the major challenges for 21st Century Medicine. One approach is to discover new drugs to replace those that are failing, but a much cheaper approach is to use the drugs we already have in ways which slow or prevent resistance emergence (stewardship). We are interested in hiring up to four people who are passionately interested in giving stewardship science a rigorous grounding in modern evolutionary theory. Projects include experimental work with drug resistance in malaria and with bacteria present in US hospitals, epidemiological and genomic analyses of hospital infections, statistical analyses of electronic health records, and the development and application of evolutionary models in health-care settings. There may also be options in cancer. Ideal candidates will have a PhD in cognate subjects (such as evolutionary biology, ecology, mathematics, statistics, epidemiology, public health, bioinformatics, genomics, microbiology). Post-Doc candidates must have up to 4 years postdoctoral experience, and a significant publication record. Research Associate candidates must have a proven record of extensive research accomplishments through publication, conference presentations, and seminars and will be expected to submit research proposals for self-support in due course.

We are looking for people whose interests coincide with ours but with skill sets that add to those already in our groups (www.thereadgroup.net, http://www.uofmhealth.org/profile/3610/robert-james-woods-md). Experience with evolution in health care settings is desirable, but more critical is a keen interest in the application of basic science to improve real-world health outcomes and the capacity to operate in a highly interdisciplinary and collaborative environment. These positions are based primarily at Penn State, but hospital-motivated projects may involve substantial time at the University of Michigan Health System http://www.uofmhealth.org/ and at the Geisinger Health System https://www.geisinger.org/. Applications must be submitted electronically at https://psu.jobs/job/62574 or https://psu.jobs/job/62580 and must include a cover letter describing research experience, interests and ambitions, a CV, and contact information for three references. Informal inquiries to Andrew Read PhD (a.read@psu.edu) or Robert Woods MD PhD (robertwo@med.umich.edu). Review of applicants will begin immediately and continue until the position is filled.

CAMPUS SECURITY CRIME STATISTICS: Penn State and State College are among the safest places to live and work in America. Federal and Pennsylvania State mandates require that all Higher Education institutions collect and publish crime statistics. For more about safety at Penn State, and to review the Annual Security Report which contains information about crime statistics and other safety and security matters, please go to http://www.police.psu.edu/clery/, which will also provide you with detail on how to request a hard copy of the Annual Security Report.

Penn State is an equal opportunity, affirmative action employer, and is committed to providing employment opportunities to all qualified applicants without regard to race, color, religion, age, sex, sexual orientation, gender identity, national origin, disability or protected veteran status.

– Andrew Read, Director, Center for Infectious Disease Dynamics, Evan Pugh University Professor of Biology and Entomology, Eberly Professor in Biotechnology, Penn State

www.thereadgroup.net Andrew Read <a.read@psu.edu>

PennsylvaniaStateU AncientDNA Archaeogenomics

Postdoctoral scholar in ancient DNA and archaeogenomics

The Department of Anthropology at The Pennsylvania State University (http://anth.la.psu.edu/) is seeking applications for a postdoctoral scholar in ancient DNA and archaeogenomics. The postdoctoral scholar will have opportunities to lead and participate in research at the intersection of archaeology, biological anthropology and human ecology. We are particularly interested in developing projects focused on human interaction with the environment and health. Please contact Douglas Kennett, George Perry or Tim Ryan with questions regarding this postdoctoral opportunity.

Candidates for this position should be experienced in both ancient DNA laboratory techniques and genomics data analysis. The position will start between July 1 and December 1, 2016 and may be renewed annually. A qualified candidate must hold a Ph.D. degree or have completed all of the requirements for a Ph.D. by the time of appointment.

To apply for this position, submit 1) a cover letter, 2) your CV, 3) the names and contact information of three people who can be contacted for letters of reference, and 4) up to three of your publications. Review of applications will begin immediately and will continue until the position is filled. Apply online at https://psu.jobs/job/-62870 CAMPUS SECURITY CRIME STATISTICS: For more about safety at Penn State, and to review the Annual Security Report which contains information about crime statistics and other safety and security matters, please go to http://www.police.psu.edu/clery/, which will also provide you with detail on how to request a hard copy of the Annual Security Report.

Penn State is an equal opportunity, affirmative action employer, and is committed to providing employment opportunities to all qualified applicants without regard to race, color, religion, age, sex, sexual orientation, gender identity, national origin, disability or protected veteran status.

grgperry@gmail.com

QueensU EvolutionaryEndocrinology

We are immediately seeking a talented and highly motivated postdoctoral associate for work on an NSF-funded study on the role of glucocorticoids in mediating responses to environmental challenges and life history tradeoffs in birds. The successful candidate will become a member of the Department of Biological Sciences at Virginia Tech in Blacksburg, Virginia, and will work closely with Ignacio Moore, Fran Bonier (Queen's University), and Mark Haussmann (Bucknell University), with opportunities for visits to each of the PI's labs. The postdoc will be based in the Bonier lab at Queen's University in Kingston, Ontario, Canada.

The project will require that the postdoc spend ~3 months in the field at the Queen's University Biological Station in Ontario, Canada from May until late July, working with a team comprised of undergraduate field assistants and graduate students. The postdoc will coordinate activities at the field sites and supervise the field team. The project will involve large-scale field experiments (manipulations of glucocorticoids, parasites, and/or reproductive effort) and measurement of effects on reproductive investment, parental behavior, immune function, and markers of oxidative stress. The postdoc will have the opportunity to be involved in all aspects of the project, and thus will receive broad training in field and laboratory methods.

*Required Qualifications: *Must have completed a PhD degree in Biology or related fields prior to the start date. Strong publication record, communication skills, organizational skills, teamwork, and leadership ability required.

*Preferred Qualifications: *Previous relevant field and lab research experience and some postdoctoral experience preferred.

This is a one-year position with possibility of renewal for an additional year. *Start date May 1, 2016.*

To apply, please send cover letter, CV, and contact information for 2 professional references to Fran Bonier: bonierf@queensu.ca

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Fran Bonier Assistant Professor Queen's University Biology Department Biosciences Complex 3523 Kingston, ON K7L 3N6 Canada

phone: 613-533-6000 x77024 email: bonierf@queensu.ca http://post.queensu.ca/ ˜ bonierf/index.html fbonier@gmail.com

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SGN Frankfurt PhylogenomicsBioinformatics

The Senckenberg Gesellschaft fÃÂ¼r Naturforschung (SGN) is a member institution of the Leibniz Association. With almost 800 employees and its headquarters in Frankfurt am Main, Senckenberg conducts natural history research with research institutions in six federal states of Germany. As an interdisciplinary institute, the Senckenberg Biodiversity and Climate Research Centre (BiK-F) focuses on the interactions between biodiversity and climate.

The working group of Prof. Dr. Axel Janke invites applications for a

Postdoc Bioinformatics Scientist in Phylogenomics (m/f)

(Full time)

There is an exciting opportunity for a talented and motivated bioinformatics scientist to join our group. The successful individual will assemble and analyse mammalian genomes from various NGS data and dissect genomic data for phylogenomic analyses. The individual is encouraged to develop own research driven activities, implement the latest methodology, and actively apply for third party funding.

Your tasks

- Understand scientific goals and identify and realize informatics solutions
- Deliver impactful bioinformatics support
- Work with MSc, PhD students and Postdocs to translate new hypotheses into phylogenomic analyses
- Engage proactively in knowledge sharing and peer support to build expertise in the tools and techniques critical to phylogenomic bioinformatics
- Maintain and expand the necessary hardware

Your profile

- PhD degree in the area of biology/bioinformatics, genetics or a related field
- Prior research experience in genomics analysis is a definite plus (minimum 3 years)
- Expertise in gene flow and selection analyses in mammals
- Expertise in genome and transcriptome assembly from mammals
- Awareness of NGS (Next Generation Sequencing) technologies and experience of NGS data interpretation
- A thorough understanding of mammalian phylogenetics or population genetics
- Strong command of programming languages for data analysis (Python / Pearl)
- Skilled in effective communication of complex genomic data to non-experts
- An excellent publication track record
- Well networked within bioinformatics communities, expertise processing and interpreting next generation

sequencing data

- Very good English skills

Salary and benefits are in accordance with a public service position in Germany (TV-H E13). The contract shall start as soon as possible and will be initially limited to a 2-year term. The Senckenberg Research Institute supports equal opportunity of men and women and therefore strongly invites women to apply. Equally qualified handicapped applicants will be given preference. The duty station will be Frankfurt am Main, Germany (exceptions might be possible due to business trips). The employer is the Senckenberg Gesellschaft fÃÂ¼r Naturforschung.

Please send your application before May 3ˆd, 2016 preferably by e-mail (attachment in a single pdf document), mentioning the reference of this position (Ref. # 6.4.16) and including a letter outlining your suitability for the post, a detailed CV, contact details of 2 references, and, if available, publications to the address below:

Senckenberg Gesellschaft fÃÂ¼r Naturforschung

Senckenberganlage 25

60325 Frankfurt am Main

recruiting@senckenberg.de

For scientific enquiries please contact Prof. Dr. Axel Janke, axel.janke@senckenberg.de.

Mit freundlichen GrÃÂ¼Ãen /Best Regards

Isabel Gajcevic, M.A.

Personalsachbearbeiterin

SENCKENBERG Gesellschaft fÃÂ¼r Naturforschung Zentralabteilung Verwaltung (ZAV) - Gruppe Personal & Soziales

Senckenberganlage 25 60325 Frankfurt/Main

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

Leiterin Personal & Soziales

- 1458 Loke, Uta

Stellv. Leiterin Gruppe Personal & Soziales

- 1319 Elsen, Carina

Mitarbeiter/in Personalbeschaffung (Recruiting)

- 1313 di Biase, Maria

- 1313 Bast, Isabell

- 1478 Gajcevic, Isabel

Fax: 0049 (0)69 / 7542-1467 Mail: recruiting@senckenberg.de Homepage: www.senckenberg.de SENCKENBERG Gesellschaft fÃÂ¼r Naturforschung (RechtsfÃÂhiger Verein gemÃÂÃ - 22 BGB) Senckenberganlage 25 60325 Frankfurt am Main Direktorium: Prof. Dr. Dr. h.c. Volker Mosbrugger, Prof. Dr. Andreas Mulch, Stephanie Schwedhelm, Prof. Dr. Katrin BÃÂ-Gaese, Prof. Dr. Uwe Fritz, Prof. Dr. Ingrid KrÃÂPrÃÂsidentin: Dr. h. c. Beate Heraeus AufsichtsbehÃÂ: Magistrat der Stadt Frankfurt am Main (Ordnungsamt)

P Before printing, think about the environment

recruiting <recruiting@senckenberg.de>

Stockholm BayesianBiodiversityAnalysis

TWO POSTDOCS in BAYESIAN BIODIVERSITY ANALYSIS

The Ronquist lab at the Swedish Museum of Natural History focuses on interdisciplinary research in systematics and evolutionary biology, usually with a strong computational or methods-development component. Our software for Bayesian phylogenetic and phylogenomic inference, MrBayes (http://mrbayes.net) and RevBayes (http://revbayes.com), is widely used across the life sciences. The lab is a major partner in the Marie Sklodowska Curie Innovative Training Network BIG 4 - Biosystematics, informatics and genetics of the four major insect orders (http://big4-project.eu). Local students work with automated identification of insects using deep learning algorithms, metabarcoding methods development with applications to large-scale studies of island biogeography, and metabarcoding and phylogenomic approaches to the evolution of gall induction in gall wasps. Other current research themes in the lab include size and composition of insect faunas, dating of phylogenies with fossils, probabilistic models of morphological evolution, and novel algorithms for Bayesian phylogenetic and phylogenomic analysis.

This project, funded by the Swedish Research Council, focuses on analyses of data from massively parallel sequencing efforts using RevBayes, our R-like computing environment, and its programming language Rev. RevBayes is based on graphical model concepts, and is primarily intended for Bayesian analysis of complex evolutionary models. The successful candidate will have great freedom in formulating her or his project within this general context and the research themes of the lab. The project can be focused on method development or empirical analyses, but should include a substantial computational component.

The ideal candidate should have a doctoral degree in evolutionary biology, bioinformatics, mathematics, statistics, or computer science. Regardless of your background, you should be familiar with biological research problems, be comfortable with mathematical and statistical reasoning, and have solid computational and programming skills. We will pay particular attention to scientific talent and potential.

The positions are for two years each, with preferred starting date in the early fall of 2016.

The Swedish Museum of Natural History (NRM) is one of the leading institutions of its kind in Europe. It combines a venerable tradition and unique collections with cutting-edge research in geology, paleontology and biology. The museum is close to Stockholm University, the Royal School of Engineering (KTH) and the Karolinska Institute. The Stockholm Phylogenomics Group (http://phylogenomics.se) engages research groups from all of these institutions.

The Department of Bioinformatics and Genetics at NRM runs a DNA sequencing facility and hosts several national and international infrastructure projects. The research includes phylogenomic, paleogenomic and population genomic studies of the evolution and population biology of mammals and birds in the labs of Love Dalén and Martin Irestedt, in addition to the research in the Ronquist lab.

The application should consist of a personal letter, a description of the planned research project (max 5 pages), and a CV. Mark your application with dnr 2.3.1-254-2016 and send it to rekrytering@nrm.se no later than May 30, 2016.

Fredrik Ronquist Professor, Dept. Bioinformatics and Genetics Swedish Museum of Natural History, Stockholm

email: fredrik.ronquist@nrm.se

Fredrik.Ronquist@nrm.se

SwanseaU EpigeneticChangesDomestication

Research Fellow position working on Epigenetic basis of fish domestication at Swansea University

Institutions: Swansea University, Cardiff University and Aberystwyth University

Collaborators: Natural Resources Wales (NRW), Cardiff Harbour Authority (CHA), Wye & Usk Foundation (WUF), Natural Aptitude, Fishgen, Skillfish, Pontus Aqua, CIBIO

We are looking for 1 Research Fellow to work on an exciting project using a multidisciplinary, cutting-edge approach to:

1. bridge, for the first time, the behavioural, genetic and environmental (epigenetic) components of fish undergoing domestication

2. disentangle the role of domestication in disease resistance in response to stress and temperature change, and

3. model pathways of introduction and dispersal of aquaculture-related invasive species (AIS) under different environmental conditions, combining state-of-the-art methods for early detection (environmental DNA) and citizen science.

Worldwide demand for fish and shellfish has increased 9% annually over the last few decades and is expected to reach c. 180 million tons by 2015, most of which will have to come from farmed fish, as the majority of wild fisheries are either stagnant or grossly over-exploited. However, to achieve long-term sustainability and meet food security demands, aquaculture needs to diversify and to step-up the domestication of aquatic species, which will have to thrive on less food, less space, and less water, all compounded by warmer temperatures and disease.

The AquaWales Research Cluster (http://aquawales.wix.com/aquawalescluster) combines academic (Swansea, Cardiff and Aberystwyth Universities) and non-academic participants, including stakeholders and local government involved in policy and regulation, and will target these challenges by capitalising on the diverse and complementary expertise of the group (from behavioural ecology to genomics, citizen-science and fisheries policy). We use a multidisciplinary approach to disentangle the basis of domestication and the response to crowding (stress and parasite susceptibility), an aspect often neglected in breeding programs, and to investigate the potential effects of climate change on the risk of expansion and establishment of non-native aquatic species associated with aquaculture and fisheries using state-of-the-art methods.

A Research Fellow position is available from 1st July 2016 until 30 November 2018. Applicants are expected to match the following criteria:

- Have a PhD in a relevant field (e.g. Biology, Ecology, Genetics).

- Not be awarded their first PhD less than 2 years and more than 8 years prior to the starting date of the position.1

- Have published, confirmed accepted or in press, at least 5 papers in ISI accredited peer-reviewed journals by the starting date of the position. (Applicants with longer periods of postdoctoral experience will be expected to have proportionally higher numbers).

Desirable criteria are: experience working on fish behaviour, genetics/genomics background, experience programming in R/Python. The RF will be working on behavioural and epigenetic basis of fish domestication. mainly based at Swansea University in close collaboration with postdocs and PhD students at Cardiff and Aberystwyth Universities. To apply follow this link:

http://www.swansea.ac.uk/the-university/work-at-swansea/jobs/-details.php?nPostingId126&nPostingTargetIdT52&id=-QHUFK026203F3VBQB7VLO8NXD&lg=UK
Informal enquiries to: Sonia Consuegra (s.consuegra@swansea.ac.uk) or Carlos Garcia de Leaniz (c.garciadeleaniz@swansea.ac.uk).

Sonia Consuegra

Professor in Biosciences

College of Science

Swansea University

Singleton Park SA2 8PP

Swansea

Tel. +44 (0) 1792 602931

Email. S.Consuegra@swansea.ac.uk

http://www.swansea.ac.uk/staff/science/biosciences/-s.consuegra https://www.researchgate.net/-profile/Sofia_Consuegra "Consuegra S." <s.consuegra@swansea.ac.uk>

TechnicalU Denmark FishPopulationGenomics

POSTDOCTORAL FELLOWSHIP IN FISH POPULATION GENETICS/GENOMICS

Within the research area "Population Genetics" at The National Institute for Aquatic Resources, at the Technical University of Denmark (DTU Aqua) (http://www.aqua.dtu.dk/english/Research/-Population_genetics), we offer a 3-year post-doctoral fellowship in the field of fish population genetics/genomics. The starting time is negotiable, but preferably between July 1st and September 1st 2016.

The successful candidate will work on several externally funded projects within the topic fisheries genomics. The position encompasses genomic analysis of 1) archived material (scales and otoliths) from marine and anadromous fishes to describe and understand historical genetic changes. 2) Development of genomic resources and description of population structure in key commercial marine species. 3) Fisheries genetics, applying genetic tools to provide advice on pertinent fisheries management questions. A main crosscutting theme will be application of reduced representation sequencing (RAD sequencing and DNA capture) and related bioinformatics analyses. For more specific project information, please see the home page.

Qualifications We invite applications from post doc level researchers with a background in population genetics/genomics. As we aim to expand the group's competences with respect to genomic analysis, we strongly encourage applicants with previous bioinformatics experience in relation to handling and analysing genomic data. The candidate will be selected based on previous scientific track record and qualifications of relevance to the described projects. Candidates should have a PhD degree or equivalent.

Further information For further information please contact the Population Genetics research coordinator, professor Einar Eg Nielsen (een@aqua.dtu.dk), tel +45 3588 3115.

Please do not send applications to Principal Investigators, instead apply online as described below.

Application procedure: We must have your online application by 1 June 2016. Go to: http://-www.dtu.dk/english/career/job?id=3D211308e7-fc95-4c03-acf4-a096168abdae Please open the link "apply online" and fill in the application form and attach the following documents:

* A letter motivating the application (cover letter) * Your application * Curriculum vitae with publication list * Diploma * Two letters of recommendation * Other material that you would like to be included in the evaluation.

Applications and enclosures received after the deadline will not be considered. All interested candidates irrespective of age, gender, race, disability, religion or ethnic background are encouraged to apply. The purpose of DTU Aqua is to provide research, advice and education at the highest international level within the sustainable exploitation of living marine and freshwater resources, the biology of aquatic organisms and the dynamics of ecosystems as well as their integration in ecosystem-based management. DTU Aqua has 260 employees, of whom a third are scientific staff. The institute is organised into eight scientific sections which carry out the research, educational and advisory activities. In addition, the institute has a number of scientific and administrative support functions, including the research vessel DANA. DTU Aqua has employees in Charlottenlund, Hirtshals, Silkeborg as well as on Dana.

DTU is a technical university providing internationally leading research, education, innovation and public service. Our staff of 5,800 advance science and technology to create innovative solutions that meet the demands of society; and our 10,300 students are being educated to address the technological challenges of the future. DTU is an independent academic university collaborating globally with business, industry, government, and public agencies.

Einar Eg Nielsen

Professor/Reseach Coordinator DTU Aqua Coordinator of EU 7FP AquaTrace: http\aquatrace.eu Technical University of Denmark National Institute of Aquatic Resources VejlsÃvej 39 8600 Silkeborg Denmark

Direct +45 40210231

een@aqua.dtu.dk

www.aqua.dtu.dk Einar Eg Nielsen <een@aqua.dtu.dk>

TexasAMU SocialInsectPhylogenetics

Postdoc Position in social insect molecular ecology and phylogenomics in the Vargo Lab at Texas A&M University

The Vargo Lab in the Department of Entomology at Texas A&M University (http://urbanentomology.tamu.edu/) is seeking highly qualified candidates for a Postdoctoral Research Associate in social insect molecular ecology and phylogenomics. We are searching for a motivated individual to perform independent and team-oriented studies on population genetic structure and ecological genomics of insect pests of the urban environment using microsatellite markers, SNPs and DNA sequence data. A major focus of this work will be termite and ant colony breeding structure and phylogenomics of invasive pest species, including the tawny crazy ant, Nylanderia fulva, the eastern subterranean termite, Reticulitermes flavipes, the Formosan subterranean termite, Coptotermes formosansus, and the common bed bug, Cimex lectularius. In addition, there will be opportunities to develop independent research projects. The successful candidate should have experience in microsatellite and/or SNP genotyping for population genetic studies, including knowledge of population genetic analysis, especially Bayesian approaches to analyzing population genetic structure. Other desirable skills include knowledge of NextGen sequencing technologies, sequence assembly, data processing and analysis. Proficiency with R statistical software and experience writing Python scripts will be an advantage.

The full position description and instructions for application can be found at the Texas A&M jobs web site (https://greatjobs.tamu.edu/, search for NOV no. 09347).

For further information, please contact Ed Vargo (ed.vargo@tamu.edu).

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Ed Vargo

Professor and Endowed Chair in Urban and Structural Entomology Department of Entomology 2556 F&B Rd., Building 1804 2143 TAMU Texas A&M University College Station, TX 77843-2143, U.S.A.

Email: ed.vargo@tamu.edu Tel.: 979-845-5855 Fax.: 979-845-5926 Skype: ed.vargo Web page: http://urbanentomology.tamu.edu/ "Vargo, Edward L" <ed.vargo@tamu.edu>

TGAC England EvolutionaryGenomics

The Genome Analysis Centre (TGAC) currently has an exciting opportunity for a Postdoctoral Researcher join our Vertebrate and Health Genomics Group to work with Dr Wilfried Haerty.

We use comparative genomics and population genetics as well as data integration approaches to tackle the evolution of functional elements with a specific focus on those that are non-protein-coding, as there is mounting evidence that these elements are enriched for disease and trait-associated variants.

The post holder will be responsible for executing research tasks and participating in data interpretation associated with the annotation and study of functional elements within Vertebrates genomes. The main goal of the project is to investigate the evolution of functional noncoding sequences (transcribed and non transcribed) across hundreds of genomes. A specific focus will be to better understand the impact of nucleotide variation within these functional sequences and their regulatory targets both at the intraspecific and interspecific levels.

To be considered for the post, it is essential that you possess the following skills, qualifications and experience:

- PhD in Computational Biology, Population Genetics, Biology or related subject - Experience in genomics data handling and interpretation - Proficient in programming languages such as Perl, Python or R - Excellent problem solving skills with the ability to solve problems with numerous and complex variables - Experience with next generation sequencing and interpretation - Experience with genomics projects - Experience with molecular evolution and population genetics - Experience with non-coding elements annotation (desirable) - Excellent oral and written skills - Able to communicate with an interdisciplinary group including data analysts, computer scientists, proteomics specialists, clinicians and laboratory biologists

As a user of the disability symbol, we guarantee to interview all disabled applicants who meet the minimum essential criteria for this vacancy.

TGAC is a vibrant, contemporary research institute and a UK hub for innovative Bioinformatics through research, analysis and interpretation of data sets. We hosts one of the largest computing hardware facilities dedicated to life science research in Europe and our aim is to ensure that biological science in the UK has access to a skill base in genomics and bioinformatics to deliver programmes leading to improved food security, advances in industrial biotechnology and improved human health and wellbeing.

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.

For further information, including a full job description and details of how to apply, please visit http://jobs.tgac.ac.uk/Details.asp?vacancyID=3D11437 Wilfried.Haerty@tgac.ac.uk

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UAberdeen DeepSeaEvolutionaryGenomics

A research fellow is required to work with Professor Stuart Piertney, Dr Alex Douglas and Dr Alan Jamieson on a 3 year NERC-funded project that will provide the first genome-wide insights into the evolutionary adaptations that have occurred in deep-sea amphipods to cope with high hydrostatic pressure. The project will exploit a globally unprecedented sample set, use state-of-the-art analytical 'omics approaches and utilise a unique high-pressure environmental manipulation system to characterise variation in RNA sequence and secondary structure from the transcriptomes of multiple species of amphipods that cover the complete bathymetric range from surface waters to full ocean depth.

The project will involve both laboratory and bioinformatic components, and require expertise in RNA extraction and library preparation, RNAseq, phylogenetics, identifying signatures of selection from DNA sequence data, and analysis of structural polymorphism.

As this post is funded by NERC it will be offered for a period of 36 months. This appointment will be made subject to the usual terms and conditions of employment of the University.

Salary will be paid on the Grade 6 scale (£31,656 per annum), with placement according to qualifications and experience. Consideration will be given to making an appointment at Research Assistant, Grade 5 level in the first instance (£26,537 - £29,847 per annum) for individuals in the very final stages of completing their PhD.

Informal enquiries are welcome and should be made to Professor Stuart Piertney (s.piertney@abdn.ac.uk). Applications can only be made online at:

https://www.abdnjobs.co.uk/vacancy/research-fellow-256589.html Professor Stuart B Piertney Institute of Biological and Environmental Sciences University of Aberdeen Zoology Building Tillydrone Avenue Aberdeen AB24 2TZ

Tel: +44 (0)1224 272864 (Office) Tel: +44 (0)1224 272892 (Lab) Email: s.piertney@abdn.ac.uk Web: www.abdn.ac.uk/sbs/people/profiles/s.piertney Twitter: @Piertney

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"Piertney, Professor Stuart B." <s.piertney@abdn.ac.uk>

UAuckland NZ AdaptivePotential

Predicting the adaptive potential of the endangered New Zealand hihi (stitchbird; Notiomystis cincta)

We are pleased to offer an 18 month postdoctoral fellowship, funded by a Marsden Fund Grant, with Dr Anna Santure in the School of Biological Sciences, University of Auckland, New Zealand. This project is an exciting opportunity to use statistical genetic approaches to understand and predict the evolutionary potential of the endangered New Zealand hihi (stitchbird; *Notiomystis cincta*), and is a collaboration with Dr Patricia Brekke and Dr John Ewen at the Institute of Zoology, Zoological Society of London, see www.hihiconservation.com . Determining the adaptive potential of wild populations requires that we understand the genetic basis of traits that are important for survival and reproduction in these populations. We are developing a genomic toolkit to characterise the genetic basis of morphological and life history traits in the reintroduced Tiritiri Matangi Island population of hihi, in order to understand the potential of the species to respond to changing environmental pressures, including anthropogenic climate change. Hihi are an ideal study system because, in addition to being a wonderful example of eccentric New Zealand wildlife, a reintroduced population of birds on Tiritiri Matangi Island has been intensively monitored since introduction and we have a wealth of data on morphological and life history traits, social and genetic relationships, DNA samples and environmental variables. The postdoctoral fellow will be responsible for quantifying selection on morphological and life history traits, and investigating heritabilities and genetic trade-offs between traits that may constrain the adaptive potential of the species. The postdoc will also have the opportunity to contribute to linkage mapping and association analysis, and there is potential to examine signatures of selection in the draft hihi genome and test the impact of drift versus selection on the population.

We are looking for a candidate with a strong background in quantitative and / or theoretical population genetics, as well as a passion for evolution and conservation biology and a track record of publishing in leading journals. Candidates with experience in comparative genomics, statistics, bioinformatics, mathematics, computer programming or similar are also encouraged to apply.

The postdoctoral fellowship is available with a salary range of approximately NZD $79,159- $84,931 depending on experience, the start date is negotiable but ideally before September 2016. We welcome informal enquiries, please contact Anna Santure at a.santure@auckland.ac.nz.

Applications should be made through the Auckland University Careers site at: https:/ / www.opportunities.auckland.ac.nz/ psp/ ps/ EMPLOYEE/ HRMS/ c/ HRS_HRAM.HRS_CE.GBL?languageCd=ENG (select Research Fellow - School of Biological Sciences)

The University has an equity policy and welcomes applications from all qualified persons. International applicants are welcome to apply. The University is committed to meeting its obligations under the Treaty of Waitangi and achieving equity outcomes for staff and students.

asanture@gmail.com

UCalifornia LosAngeles ConservationEbony

Postdoc UCLA- Ecology and Sustainability of West African Ebony

University of California, Los Angeles, Center for Tropical Research, Institute of the Environment and Sustainability and Department of Ecology and Evolutionary Biology

We seek a highly qualified and enthusiastic individual with a background in the ecology of tropical rainforest trees or their dispersers/pollinators and an interest in the conservation and sustainability of African hardwoods to join our team. The goal of the project is to develop sustainable approaches for the production of ebony that contributes to the economic well being of local communities in Central Africa. The successful candidate will focus his/her work on 1) the ecology and life history of ebony, such as the identification of pollinators and dispersers and information important to its natural reproduction and dispersal and 2) ways to leverage this information to test alternative restoration approaches to determine the most successful methods of cultivating ebony to support local communities.

The candidate will split his/her time between UCLA (25%) and the Congo Basin Institute's Yaounde campus in Cameroon (75%)as well as the principal field site for ecological studies in the Dja Biosphere Reserve where CTR has conducted long-term research (seehttp://www.environment.ucla.edu/-ctr/research/djabiosphere.html).

The successful candidate will collaborate with scientists from UCLA, the International Institute of Tropical Agriculture (IITA), the International Bilingual Academy/Higher Institute of Environmental Sciences (IBAY SUP) and help mentor Cameroonian PhD and MS studentsworking on other elements of the project. These include: 1) creating a scalable program for the sustainable production and stewardship of ebony seedlings in rural areas 2) generation of GIS/remote sensing models of West African ebony distributions to identify suitable harvesting and planting areas and 3) testing alternative production approaches, including vegetative propagation from juvenile cuttings and tissue culture laboratory experiments to identify efficient processes and optimal conditions for cultivating ebony.

We seek a candidate with an outstanding academic background, fluency or basic knowledge of French and a passion for conservation and for finding win-win opportunities for people and biodiversity.

The postdoc will work under the supervision of Thomas B. Smith, tbsmith@ucla.edu, (http://-www.environment.ucla.edu/ctr) at UCLA, but will be expected to collaborate closely with other members of the team.The postdoc will also be encouraged to develop her/his own research focus on some aspect(s) of the project.

Application: Please send a single PDF containing a CV, a statement of research interests, and contact information for three references to Christa Gomez, cgomez@lifesci.ucla.edu; with the subject line Ebony Postdoc. Review of applications will begin August 1^st, 2016. The postdoc is for two years with the possibility that the project maybe renewed. Salary will be determined based on experience level.

Kevin Y Njabo <kynjabo@hotmail.com>

UCalifornia Merced MicrobialEvolutionaryBiology

The University of California, Merced is a dynamic new university campus in Merced, California, which opened in September 2005 as the tenth campus of the University of California and the first American research university in the 21st century. In keeping with the mission of the University to provide teaching, research and public service of the highest quality, UC Merced offers research-centered and student-oriented educational opportunities at the undergraduate, master's and doctoral levels through three academic schools: Engineering, Natural Sciences and Social Sciences/Humanities/Arts.

The Sistrom Lab seeks a Postdoctoral Scholar to participate in several projects investigating evolutionary processes in microbial systems. We work broadly across many organismal systems, with a common thread of using high throughput sequencing to investigate evolutionary processes. Our projects range from RNA virus metagenomics in plants, to microbiome studies in gastropods to comparative genomics in multi-resistant nosocomical bacteria, to experimental evolution. We seek a Postdoctoral Scholar who will build on our strengths in bioinformatics by adding microbiological laboratory experience to our group.

The Postdoctoral Scholar will be expected to contribute to existing projects in the lab, as well as developing new research. As we are a newly established lab, there is significant scope for the successful candidate to develop their own research - especially in the context of experimental evolution. The successful candidate will be expected to publish their research, assist in grant preparation, attend at least one conference annually and collaborate within and outside of the lab group.

The University of California, Merced is an affirmative action/equal opportunity employer with a strong institutional commitment to the achievement of diversity among its faculty, staff, and students. The University is supportive of dual career couples.

PhD in Evolutionary biology, Microbiology or a related field; experience in microbiological laboratory techniques and analysis of resultant data; a demonstrated record of research and publication. The ideal candidate would also have experience in bioinformatics and high throughput sequence analysis and/or experience in designing and conducting evolutionary experiments in viral and bacterial systems.

Salary is based on the University of California Academic Salary Scales.

Review of applications will begin May 6, 2016. Recruitment will remain open until the position has been filled.

Interested applicants are required to submit 1) a cover letter 2) curriculum vitae 3) a list of two references with contact information including mailing address, phone number and e- mail address 4) Diversity Statement.

Apply at: https://aprecruit.ucmerced.edu/apply/-JPF00347 For more information, please contact Mark Sistrom msistrom@ucmerced.edu.

Mark Sistrom <msistrom@ucmerced.edu>

UDenver EvolTeaching

The postdoc fellowship listed below is broad, but we particularly are interested in applicants who study evolution or evolution education.

E-STEAM (Equity in STEAM) Postdoctoral Fellowship at the University of Denver

The University of Denver Interdisciplinary Research Incubator for the Study of (In) Equality or IRISE (www.du.edu/irise) is seeking a two-year postdoctoral research fellow beginning September 1, 2016. We are looking for ways to assist transforming the culture of STEAM (Science, Technology, Engineering, Art and Math) towards an inclusive environment that integrates with societal issues. Our focus is on the national level possibly using on-campus projects and interventions as a mechanism for research study as well as transforming internal culture.

We seek candidates capable of bringing together insights from some subset of the STEAM disciplines to inform the interdisciplinary study of the relationship between racial, ethnic, and socio-economic inequality and how these factors intersect with the STEAM disciplines. More specifically, we are seeking a scholar working on issues of how to increase participation (access) and persistence of underrepresented college students in one or more of the STEAM areas. Example areas of interest:

1. Create and study the efficacy of research-based and activism-based curriculum that broadens our ideas of what science is and does. Specifically the fellow will help create a curriculum that privileges socially meaningful problems and then studies whether such an approach helps to attract and retain women and students of color.

2. Study the efficacy of various models of sustained mentorship at the K12 and postsecondary level. While many "camps" have been created, and these camps clearly do provide inspiration, women and students of color still often do not matriculate or persist in STEM areas. How should continued mentorship after such experiences be structured?

3. Many have advocated for moving STEM to STEAM by integrating the Arts. How does such an integration increase participation and persistence? What aspects of art integration are responsible for attracting and retaining students of color - design, aesthetics, social activism?

The three above area examples are meant only to be illustrative of the types of scholarship questions we hope to address and should not be viewed as limiting the scope of research areas we will consider supporting.

Depending on the fellow's background they will be housed in one of our STEAM departments, {biology, chemistry, physics, computer science, engineering, art/emergent digital practices, mathematics}, with co-supervision and mentorship by faculty from multiple other STEAM departments. Many of our STEAM faculty are working on research and outreach experiences guided towards broadening participation in STEAM. These faculty members will provide guidance and support throughout the fellowship period.

The fellow will spend the majority of time engaged in independent research, scholarship, or creative work under the guidance of departmental faculty members. Fellows will also be expected to be active in the DU community of scholars engaged in research and teaching relating to the study of inequality locally and nationally. Fellows will teach one course in their specialty the first year and two courses in their specialty the second year. The successful candidate will also be expected to attend and contribute to a weekly seminar and support other initiatives of the IRISE, such as promotion of conferences and symposia.

The ideal candidate would have training or a strong interest broadening participation in STEAM as well as disciplinary knowledge in one of the STEAM areas. Candidates should be committed to working with diverse student and community populations. We do not expect the candidate to have experience in all areas of the fellowship, as training will be provided by the mentors. In addition, because of the value of lived experiences in the investigation and understanding of inequality, we especially encourage applications from historically underrepresented groups.

Qualifications:

- PhD in Biology, Chemistry, Computer Science, Engineering, Environmental Science, Mathematics, Physics or MFA/PhD in Art, Dance, Music, Theater, or related fields.

- Applicants must have completed all requirements for their terminal degree by June 30, 2016. Candidates must also be no more than 3 years from the awarding of their degree (i.e., September 2013).

- Interest or experience addressing inequality concerns in STEAM.

- Strong methodological training and a record of successful publication in the related field(s).

Responsibilities:

- The appointment term is September 1, 2016 - August 31, 2018; however, the initial term may be renewed for an additional year.

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UEssex ComputationalGenomics

POSTDOCTORAL POSITION IN COMPUTATIONAL GENOMICS

We are looking for an enthusiastic postdoctoral researcher to work in microRNA computational genomics, in the group of Antonio Marco (http://amarco.net/) at the University of Essex.

THE PROJECT: MicroRNAs are gene regulators that bind to gene transcripts by pairwise complementarity. MicroRNA target sites are often conserved and subject to purifying selection. Recently, we found that selection against target sites is prevalent (doi:10.1534/g3.115.019497). The current project aims to explore the impact of this type of selection in humans, and its application to understand regulatory networks of complex diseases.

WHAT WE EXPECT: The postdoc will contribute to the development of new methods and software to analyse human polymorphisms at microRNA target sites. The postdoc will also analyse extensive collections of human variation data and explore complex-disease gene networks in collaboration with experimental scientists.

WHAT WE PROVIDE: The project is funded by a grant from the Wellcome Trust and will cover the salary of the successful applicant for two years (Ã31,655 per annum). We provide a vibrant and stimulating environment, mentoring schemes, advanced training programmes, and support for travelling to conferences and workshops. Our recently established Genomics Group at the University of Essex is form by seven labs with diverse interests and expertises(http://genomics.essex.ac.uk/). We have state-of-the art labs (both dry and wet), a sequencing machine and a high-performance computer cluster.

ABOUT ESSEX: The School of Biological Sciences at University of Essex has a broad-based structure, providing a strong multidisciplinary environment. Colchester campus is located at Wivenhoe Park, a picturesque and historic 200 acres parkland. It is a vibrant and international campus, hosting more than 9,000 students from more than 130 different nationalities. The campus is only two miles from the historic centre of Colchester - England's oldest recorded town, and just one hour from London.

APPLICATION: Closing date for applications: 1st June 2016 Interviews for sortlisted candidates: Week of the 20th June 2016 Expected start date: 1st September 2016

Please include in your application a cover letter (PDF, 1 page), a CV (PDF, 2-pages maximum) and contact details for three references.

For any question regarding this application please contact Antonio Marco (amarco@essex.ac.uk; amarco.bio@gmail.com).

Apply to this position from the University of Essex jobs webpage: https://jobs.essex.ac.uk/fe/tpl_essex01.asp?s=4A515F4E5A565B1A&jobid=86428,1212614836 amarco.bio@gmail.com

UFribourg PDF PhD EvolutionaryInvasionEcol

A PhD position in Dept. Biology/Ecology&Evolution at University of Fribourg, Switzerland, is available in the frame of the recently granted project on “Demographic history and recent selection in novel environments: an innovative approach to assess benefits and risks of a potential biological control agent”.

PhD Position in Evolutionary Invasion Ecology Rationale: Besides their great relevance for the environment, biological invasions have been recognized as unprecedented bio-geographical experiments to study fundamental ecological and evolutionary processes, such as local adaptation to the novel conditions in the introduced range.The proposed study capitalizes on ongoing studies in the framework of the EU-COST Action FA1203 on “Sustainable management of Ambrosia artemisiifoliain Europe” (SMARTER; ragweed.eu), and will specifically focus on the recently and accidentally introduced ragweed leaf beetle Ophraella communa into Europe. This North-American insect has also been introduced into Asia where it is successfully used as a biological control agent. The planned study complements our findings on host impact and specificity of Ophraella made so far by including genetics and genomics. It is focusing on the potential of this biological control candidate to rapidly evolve and adapt to novel abiotic (temperature: spread potential) and biotic (host plants: non-target effects) conditions in view of rendering risk-benefit assessments in biological control more predictive.

We seek a highly motivated person to perform plant-insect herbivore experiments under controlled and field conditions, do lab work and prepare samples for genomic analyses and enjoy bioinformatics and statistics analyses jointly with the PostDoc. Indeed, the project is tightly linked to a PostDoc position within the same project (cf. separate advertisement).

Requirements: Basic knowledge of experimental design and statistical data analysis is a prerequisite, and knowledge of, and experience in one or several of the following areas of research is highly desirable: population ecology, population genetics, plant-herbivore interactions, molecular techniques, genomics, bioinformatics. Good writing skills in English is a must and familiarity with-or interest to learn-French and/or Germana plus. Drivers license.

Salary and conditions: Salary dependent on age and status (gross salary in the first year about 42’000 euro).

Start date: preferentially on 1 September 2016. The PhD positionis for 3 years.

Applications: Applicants should send their CV, including publication list, a short motivation letter with a summary of research experience and interests, and the names of 3professional referees to the email address below as a single pdf-file before 22May 2016.

For further information, please contact:Heinz Muller-Scharer, Dep.Biology, University of Fribourg, CH-1700 Fribourg, Switzerland.

Tel: + (41) (0) 26-300 88 35 or : + (41) (0)79-787 35 71 E-mail: heinz.mueller@UNIFR.CH, http://www.unifr.ch/ecology/groupmueller/home specifically check out“SNSF-Summary” on: http://www.unifr.ch/ecology/groupmueller/student-opportunities A PhD position in Dept. Biology/Ecology&Evolution at University of Fribourg, Switzerland, is available in the frame of the recently granted project on “Demographic history and recent selection in novel environments: an innovative approach to assess benefits and risks of a potential biological control agent”.

PostDoc position in Evolutionary Invasion Ecology Rationale: Besides their great relevance for the environment, biological invasions have been recognized as unprecedented bio-geographical experiments to study fundamental ecological and evolutionary processes, such as local adaptation to the novel conditions in the introduced range.The proposed study capitalizes on ongoing studies in the framework of the EU-COST Action FA1203 on “Sustainable management of Ambrosia artemisiifoliain Europe” (SMARTER; ragweed.eu), and will specifically focus on the recently and accidentally introduced ragweed leaf beetle Ophraella communa into Europe. This North-American insect has also been introduced into Asia where it is successfully used as a biological control agent. The planned study complements our findings on host impact and specificity of Ophraella made so far by including genetics and genomics. It is focusing on the potential of this biological control candidate to rapidly evolve and adapt to novel abiotic (temperature: spread potential) and biotic (host plants: non-target effects) conditions in view of rendering risk-benefit assessments in biological control more predictive.

We seek a highly motivated person to explore the genetic basis of successful species invasions and subsequent local adaptation. He/she

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UHawaii PhylogeneticsBioinformatics

Postdoctoral position in phylogenetics and bioinformatics at the University of Hawaii

The Thomson Lab is looking for a postdoctoral researcher to participate in an NSF funded project that seeks to build an archive of Bayesian phylogenetic output and examine the performance of Bayesian estimation of phylogeny for large datasets. The project is a collaboration between the Thomson Lab and the Moore Lab at UC Davis and aims to improve MCMC performance, assess goodness of fit of phylogenetic models, and contribute to the field's ability to carry out robust Bayesian phylogenetic inference by developing new scientific resources and educational tools. The candidate should have demonstrated experience in phylogenetics and bioinformatics, including programming with SQL, R and/or Python. The selected candidate will join a lab that focuses on phylogenetics, bioinformatics, and conservation in UH's Department of Biology. The position is based in Honolulu, a vibrant city that is consistently recognized for its diversity, outdoor recreation, and high quality of life.

The start date is flexible, but ideally will be on or before 1 August 2016. Funding is available for two years ($54,000/year, with an additional stipend for health insurance). Application review will begin 1 May. Minimum PhD in Evolutionary Biology (or related field) is required. The University of Hawaii is an Equal Opportunity/Affirmative Action employer.

To apply, please send CV and names and contact information for three reference to Bob Thomson: thomsonr@hawaii.edu

Robert C. Thomson Assistant Professor Department of Biology University of Hawaii at Manoa Honolulu, HI 96822

808.956.6476 http://thomsonlab.org/ "thomsonr@hawaii.edu" <thomsonr@hawaii.edu>

UHeidelberg Bioinformatics

BIOINFORMATICS POSTDOC IN EVOLUTIONARY GENOMICS

Center for Molecular Biology of the University of Heidelberg (ZMBH), Heidelberg, Germany

A postdoctoral position (2 years with possible extensions) is available immediately in the evolutionary genomics group of Henrik Kaessmann.

We are seeking highly qualified and enthusiastic applicants with strong skills in computational biology/bioinformatics, ideally also with experience in data mining and comparative or evolutionary genome analyses.

We have been interested in a range of topics related to the functional evolution of mammalian genomes, including those of humans and other primates. In the framework of our research, we are generating comprehensive sets of RNA-seq data for a large collection of tissues from representatives of all major mammalian lineages (placental mammals, marsupials, and egg-laying monotremes) and evolutionary outgroups (e.g., birds). In conjunction with various high-throughput "omics" (e.g., epigenomic, metabolomic, proteomic) datasets, we perform integrated analyses to study the functional (expression) evolution of mammalian genomes across gene types, lineages, organs, cell types, developmental stages, chromosomes and sexes.

The postdoctoral fellow will be funded by a recently awarded ERC Consolidator Grant and perform integrated evolutionary/bioinformatics analyses based on data produced in our lab and available genomic data. The project will focus on analyses of new ontogenetic datasets generated in the framework of the ERC Grant, but the precise project will be developed together with the candidate.

The language of the institute is English and its members form a highly international group. The ZMBH is located in Heidelberg, a picturesque international city next to the large Odenwald forest and Neckar river. The city offers a very stimulating, diverse and collaborative research environment, with the European Molecular Biology Laboratory (EMBL), German Cancer Research Center (DKFZ), Heidelberg Institute of Theoretical Studies (HITS), and the Max Planck Institute for Medical Research located in close proximity to the University.

For more information on the group and our institute more generally, please refer to our website at the ZMBH (http://www.zmbh.uni-heidelberg.de/Kaessmann/).

Please submit a CV, statement of research interest, and names of three references to: Henrik Kaessmann (h.kaessmann@zmbh.uni-heidelberg.de).

– Prof. Dr. Henrik Kaessmann Group leader in the DKFZ-ZMBH Alliance ZMBH - Center for Molecular Biology Heidelberg University Im Neuenheimer Feld 282 69120 Heidelberg Germany –

Selected recent publications:

Carelli, F.N., Hayakawa, T., Go, Y., Imai, H., Warnefors, M., and Kaessmann, H. (2016) The life history of retrocopies illuminates the evolution of new mammalian genes. Genome Res. 26: 301-314.

Cortez, D., Marin, R., Toledo-Flores, D., Froidevaux, L., Liechti, A., Waters, P.D., Grutzner, F., and Kaessmann, H. (2014) Origins and functional evolution of Y chromosomes across mammals. Nature 508: 488-493.

Necsulea, A., Soumillon, M., Warnefors, M., Liechti, A., Daish, T., Zeller, U., Baker, J.C., Grutzner, F., and Kaessmann, H. (2014) The evolution of lncRNA repertoires and expression patterns in tetrapods. Nature 505: 635-640.

Necsulea, A. and Kaessmann, H. (2014) Evolutionary dynamics of coding and noncoding transcriptomes. Nat. Rev. Genet. 5: 734-48.

Meunier, J., Lemoine, F., Soumillon, M., Liechti, A., Weier, M., Guschanski, K., Hu, H., Khaitovich, P., and Kaessmann, H. (2013) Birth and expression evolution of mammalian microRNA genes. Genome Res. 23: 34-45.

Julien, P., Brawand, D., Soumillon, M., Necsulea, A., Liechti, A., Schutz, F., Daish, T., Grutzner, F., and Kaessmann, H. (2012) Mechanisms and evolutionary patterns of mammalian and avian dosage compensation PLoS Biol. 5:e1001328.

Brawand, D., Soumillon, M., Necsulea, A., Julien, P., Csardi, G., Harrigan, P., Weier, M., Liechti, A., Aximu-Petri, A., Kircher, M., Albert, F.W., Zeller, U., Khaitovich, P., Grutzner, F., Bergmann, S., Nielsen, R., Paabo, S., and Kaessmann, H. (2011) The evolution of gene expression levels in mammalian organs. Nature 478: 343-348.

Henrik Kaessmann <Henrik.Kaessmann@unil.ch> Henrik Kaessmann <Henrik.Kaessmann@unil.ch>

UHelsinki EvolutionaryGenomics

Post-doc position in Evolutionary Genomics (1.5 years) at University of Helsinki

The postdoctoral researcher will be a part of the Ecological Genetics Research Unit (EGRU; http://www.helsinki.fi/biosci/egru/index.html) lead by Prof. Juha Merila. The assignment can start in June 2016 (start date is flexible - early start preferred) and continue until end of December 2017.

The post-doctoral fellow to be employed is expected to work with projects addressing broad and generally interesting problems relating to processes of population differentiation and genetics of adaptation as inferred from already available whole genome sequence datasets. The model system in these studies is the nine-spined stickleback (Pungitius pungitius) and its relatives, and their computational genome analysis is a collaboration with the bioinformatics group of Dr. Ari Loytynoja (http://www.biocenter.helsinki.fi/bi/loytynoja).

An ideal candidate for this position would have a broad interest in evolutionary biology and a background in one or several of the following fields: bioinformatics, evolutionary genomics, statistical or population genetics/genomics, animal or plant breeding sciences. We are looking for an individual who is highly motivated and can work both independently and in a team. Capacity to face intellectual challenges, willingness to learn new skills, and to explore new intellectual territories are qualities expected from a strong candidate. A demonstrated track-record in research, and experience in bioinformatics analysis of next- generation sequencing data are required.

An appointee to the position of post-doctoral researcher shall hold a doctoral degree, have the ability to conduct independent scholarly work.

The working language will be English. An overview of our past and current research can be found at http://www.helsinki.fi/biosci/egru/publications/index.html The salary will be based on level 5 of the demands level chart for teaching and research personnel in the salary system of Finnish Universities. In addition, the appointee will be paid a salary component based on personal work performance (total salary will be approximately 3050-3400 EUR per month).

The application should include (i) CV, (ii) Publication list, (iii) statement of research interests and motivation for applying this position not exceeding two pages and (iv) contact information of two reference persons who have agreed to provide a written statement on behalf of the applicant.

Applications should be addressed to the Department of Biological Sciences, P. O. Box 65 (Viikinkaari 1), FIN-00014 University of Helsinki, and sent to juha.merila@helsinki.fi The deadline for applications is May 15 2016. More information on this position is available from Prof. Juha Merila (e-mail: juha.merila@helsinki.fi).

Juha Merila Ecological Genetics Research Unit Department of Biosciences PO Box 65 (Biocenter 3, Viikinkaari 1) FIN-00014 University of Helsinki Finland E-mail: juha.merila@helsinki.fi Gsm: +358-(0)50-416 0561 Fax: +358-9-19157694 www: http://www.helsinki.fi/biosci/egru/ ResearchGate: https://www.researchgate.net/profile/Juha_Merilae?ev=3Dhdr_xprf Publons: https://publons.com/author/341551/juha-merila#profile Juha Merilä <juha.merila@helsinki.fi>

UInnsbruck SpeciationPhylogeography

PostDoc: UInnsbruck.EcologicalNicheModelling

MOLECULAR ECOLOGY, INSTITUTE OF ECOLOGY, UNIVERSITY OF INNSBRUCK PostDoc position We have an open position to be filled ASAP for a PostDoc with extensive training in ecological-niche modelling (ENM). The position is for 9 to 11 months at the Molecular Ecology group of the Institute of Ecology, ending in March 2017. Centering on the Alpine Space, the group's mission is interdisciplinary research, embedded in international collaboration networks. A list of research topics and projects can be found at: http://www.uibk.ac.at/ecology/forschung/molecular_ecology.html.en The successful candidate will be involved in several projects (see link above) dealing mainly with invertebrate taxa. These projects are currently in an advanced state, with extensive genomic, morphometric, and distributional data already acquired and data analysis in progress. The candidate will become part of an established team as ENM specialist and, due to the extensive groundwork, gather momentum rapidly. Papers on topics related to the successful candidate's tasks include: Wachter et al (2016) Molecular Ecology, doi:10.1111/mec.13634; Dejaco et al (2016) Systematic Biology, doi:10.1093/sysbio/syw003; Schlick-Steiner et al (2010) Annual Review of Entomology 55: 421-438; Schlick-Steiner et al (2006) Molecular Phylogenetics and Evolution 40:259-273.

Responsibilities 1. ENM for several multidisciplinary projects (speciation, phylogeography, integrative species delimitation) 2. participation in manuscript writing 3. contact and collaboration with a range of scientists at the Faculty of Biology in Innsbruck, at other Austrian research facilities, and internationally

Selection criteria A. PhD degree in biology B. published research experience and excellent skills in ENM C. ability to work as part of a multi-disciplinary team D. ability to work independently E. very good knowledge of English

Salary The annual gross salary is about Euro 50,260. The contract includes health insurance and vacation. Details upon request.

How to apply To apply, please submit by E-mail to <birgit.schlick-steiner@uibk.ac.at>: a cover letter, systematic point-by-point replies as to your readiness for the responsibilities and how you meet the selection criteria, brief statement of research interests, curriculum vitae, and complete list of publications. Also, arrange for at least one letter of recommendation to be sent to <birgit.schlick-steiner@uibk.ac.at> Applications must be written in English. Review of applications will begin immediately and continue until a suitable candidate has been found. The University of Innsbruck is striving to increase the percentage of female employees and therefore invites qualified women to apply. In the case of equivalent qualifications, women will be given preference. An offer of employment is contingent on a satisfactory pre-employment background check.

The research institution and its environment Detailed information about the Molecular Ecology group can be found at http://www.uibk.ac.at/ecology/forschung/molecular_ecology.html.en. The University of Innsbruck has a long-standing and internationally renowned tradition in life sciences and offers a vibrant research atmosphere. The university has more than 28,000 students and 4,500 staff members. Innsbruck is situated in the heart of the Alps and very close to Switzerland, Germany and Italy; scenery and outdoor recreation are fantastic.

More information needed? For more information, please contact: Birgit Schlick-Steiner <birgit.schlick-steiner@uibk.ac.at>

Birgit C. Schlick-Steiner Professor of Molecular Ecology

Institute of Ecology University of Innsbruck Technikerstr. 25 6020 Innsbruck, Austria Phone: +43 512 507-51750 Fax: +43 512 507-51799 http://www.uibk.ac.at/-ecology/forschung/molecular_ecology.html.en "Schlick-Steiner, Birgit" <Birgit.Schlick-Steiner@uibk.ac.at>

ULausanne TheoEvolutionaryBiol

1 postdoctoral position in Lausanne: Theoretical evolutionary biology, social evolution, and human evolution

A theoretical evolutionary biology postdoctoral position for 1 year (extensible for 2 more years) is open in the research group of Laurent Lehmann at the Department of Ecology and Evolution of the University of Lausanne (https://www.unil.ch/dee). We study social evolution from a mathematical and computational point of view with a current focus on human evolution and address the following type of questions:

How did large-scale stratified human societies emerge from small-scale egalitarian societies? Is this the result of an increase in the technologies of production and exchange (invention of agriculture and trading) or in the technology of appropriation (intensification of warfare)? What are the selection pressures on increased lifespan and cognition in the human lineage? Is this the result of an ecological or a social pressure? How does the determinants of behavior evolve in social environments? Should behavior be genetically driven, acquired by social learning, or is free choice of actions delegated to the individual?

Applicants with a strong interest in these research questions are encouraged to apply. Applicants should have a Ph.D. in a relevant area (e.g. evolutionary biology, economics, anthropology, physics, or mathematics), with strong mathematical and computing skills, and a vivid interest in fundamental research.

Inquiries and applications should be sent to laurent.lehmann@unil.ch by April 31th. They should include a CV, a statement of research interests, and names of 2-3 referees. Only applications with all these information will be considered. Starting date is negotiable, from May 2016 onwards.

Laurent Lehmann <Laurent.Lehmann@unil.ch>

ULeicester EvolutionGenomicImprinting

The Mallon Lab in the Department of Genetics at the University of Leicester (http://www2.le.ac.uk/-departments/genetics/people/mallon) is seeking highly qualified candidates for a Postdoctoral Research Associate in insect epigenetics.

We are searching for a motivated individual to perform independent and team-oriented studies on epigenetics of the bumblebee, Bombus terrestris using whole genome/transcriptome sequence data.

A major focus of this work will be to independently test the major theory for the evolution of genomic imprinting, by examining the parent of origin allele specific expression of genes important for bumblebee worker reproduction. In addition, there will be opportunities to develop independent research projects.

You should have experience in routine molecular biology and next generation sequencing data generation and analysis. Proficiency with R statistical software and experience writing Python scripts will be an advantage.

http://www.jobs.ac.uk/job/AUE426/research-associate/ Informal enquiries are welcome and should be made to Dr Eamonn Mallon on ebm3@le.ac.uk.

The closing date for applications is midnight 23rd May 2016. Also we are very keen to host a Marie Curie Fellow within the general field of Insect Epigenetics. If you are interested and eligible (http://ec.europa.eu/research/mariecurieactions/-about-msca/actions/if/index_en.htm) please contact me (ebm3@le.ac.uk)

Dr. Eamonn Mallon Lecturer in Evolutionary Biology Room 220 (inside lab 219) Adrian Building Department of Genetics University of Leicester Tel 01162523488 ebm3@leicester.ac.uk

"Mallon, Eamonn B. (Dr.)" <ebm3@leicester.ac.uk>

ULille France Coevolution MatingSystems Models

Crossing the fitness valley : coevolution and diversification in structured populations

We offer a 2-years post-doctoral position funded by an ERC Consolidator grant to theoretically investigate how population structure affects the rate of diversification and patterns of coevolution in a two-components genetic system.

Background.

Our main model is self-incompatibility (SI) in the flowering plants, a molecular recognition system preventing inbreeding and enforcing outcrossing. SI phenotypes are generally determined by two linked sets of alleles: one for pollen, the other for stigma. Tight coevolution is expected between the genes controlling pollen and stigma specificities because mutations at one of the two genes only would prevent proper recognition, thus allowing selfing, which in this system represents an important valley of fitness because of the expression of inbreeding depression. Despite this evolutionary constraint, dozens of different SI alleles are typically observed in natural populations, suggesting that novel SI alleles have emerged repeatedly. How evolutionary constraints and large allelic diversities can be reconciled remains a largely open question in evolutionary biology, for which the specific case of SI is a case-study. Previous work in our group and others showed that coevolution and diversification of SI alleles is possible in a panmictic population, but it constitutes a self-attenuating process that fails to explain the large observed allelic diversity (Uyenoyama et al. 2001, Gervais et al. 2011). The goal of the post-doc will be to determine to what extent population structure would help solve the puzzle. The question is not trivial because the mode of selection acting on SI, negative frequency-dependent selection (aka ≪ advantage of the rare ≫), increases the effective migration rates, which should largely eliminate genetic structure and thus impede allopatric diversification.

Profile

The successful candidate should have theoretical skills and the ability to develop and analyze population genetics models, both deterministic and stochastic. The hired person will interact with people generating genetic and genomic data within the same ERC project. Mathematical and/or programming skills are a plus. The hired post-doc will benefit from an excellent scientific environment, with people with expertise in various domains ranging from population genetics and genomics, to mathematics and bioinformatics.

Conditions

The monthly raw salary will range between 2,500 and 2,800â¬*dependingonexperience.Thepositionwillstartduringearlyfall*
Eco−Paléo(CNRS,UniversityofLille),France.Workinglanguagein

Application procedure

To apply send a CV, a one-page statement of research interest and contact information of three people who can provide references. The application package should be sent to Sylvain.Billiard@univ-lille1.fr and Vincent.Castric@univ-lille1.fr <mailto:Vincent.Castric@univ-lille1.fr>

Sylvain Billiard and Vincent Castric

sylvain billiard <sylvain.billiard@univ-lille1.fr>

UMichigan YeastEvolutionaryGenomics

Two Postdoctoral Positions in Experimental Yeast Evolutionary Genomics at University of Michigan

Two postdoctoral positions are available in the laboratory of Jianzhi "George" Zhang at University of Michigan, Ann Arbor, Michigan. Ideal candidates will use the budding yeast *Saccharomyces cerevisiae* and its relatives as model organisms to study evolutionary processes. Potential topics include but are not limited to (1) the fitness effects of various types of mutations including gene duplication, (2) genic/genomic basis of reproductive isolation, (3) evolution of dominance, (4) genetic mechanisms of heterosis, (5) position effects on protein expression level and noise, and (6) evolution of gene expression. The positions require motivated individuals with an interest in evolutionary genetics and experience in molecular genetics or genomics. Prior training in yeast genetics will be a plus. For further information about the Zhang lab, see http://www.umich.edu/~zhanglab/. Applicants should email a short statement of research interests, CV, and contact information of three references to jianzhi@umich.edu.

– Jianzhi "George" Zhang Marshall W. Nirenberg Collegiate Professor Department of Ecology and Evolutionary Biology University of Michigan 1075 Natural

Science Building 830 North University Avenue Ann Arbor, MI 48109-1048 Phone (office): 734-763-0527 Phone (lab): 734-763-0514 Fax: 734-763-0544 Email: jianzhi@umich.edu Home page: www.umich.edu/~zhanglab Jianzhi Zhang <jianzhi@umich.edu> Jianzhi Zhang <jianzhi@umich.edu>

UMontana EvolutionSymbiosis

EVOLUTIONARY CELL BIOLOGIST. The McCutcheon lab at the University of Montana seeks a postdoctoral research associate interested in evolutionary cell biology. Our lab values diversity in thought, experience, and personel, and as such individuals from many different backgrounds are appropriate for this position. However, experience in eukaryotic cell biology and a willingness to work in non-model insect systems are required. An ideal candidate would have experience with immunologically based electron or fluorescence microscopy. The position will remain open until filled but could start immediately.

Read more about our lab, our research, and Montana here: http://mccutcheonlab.org Read the full job ad, and apply, here: http://bit.ly/1495umdbs Please email John McCutcheon with any questions (john [DOT] mccutcheon [AT] umontana [DOT] edu)

"McCutcheon, John" <john.mccutcheon@mso.umt.edu>
"McCutcheon, John" <john.mccutcheon@mso.umt.edu>

UNevada Reno EvolutionaryPhysiology

A postdoctoral position in evolutionary endocrinology is available in the laboratory of Dr. Jenny Ouyang, Assistant Professor in the Dept. of Biology at the University of Nevada, Reno. A competitive starting salary plus benefits will be provided. Preferred start date is September 1, 2016.

In the Ouyang lab, we are interested in understanding how animals are physiologically adapted to changing environments. We empirically test, in natural and laboratory avian populations, how, and at what rate, hormonally-regulated traits can evolve. Current field sites include various locations in Reno and the UNR main station field lab with 1000 acres of prime farmland. More information about the lab can be found at www.jennyouyang.com . The University of Nevada, Reno is a Tier I institution offering a highly productive research environment. The Biology Department is home to 25 tenure-ladder faculty members who maintain nationally recognized, extramurally funded research programs and who mentor ~ 50 graduate students.

Reno is located in the Sierra Nevada Mountains near Lake Tahoe and has been recently rated as one of the best small cities in the US for outdoor recreation and overall quality of life.

To apply and for more information, please submit requested application materials at https://www.unrsearch.com/postings/20567 The University of Nevada, Reno is committed to Equal Employment Opportunity/Affirmative Action in recruitment of its students and employees and does not discriminate on the basis of race, color, religion, sex, age, creed, national origin, veteran status, physical or mental disability, and sexual orientation, or genetic information, gender identity, or gender expression. The University of Nevada, Reno employs only United States citizens and aliens lawfully authorized to work in the United States. Women, under-represented groups, individuals with disabilities, and veterans are encouraged to apply.

Jenny Ouyang Assistant Professor University of Nevada, Reno

http://www.jennyouyang.com/ 1664 N Virginia Street Department of Biology, ms 314 Reno, NV 89557 1-775-784-6089

Jenny Q Ouyang <jouyang@unr.edu>

UUtah EvolutionaryGenomicsDevBio

Postdoctoral positions are available in the laboratory of Dr. Mike Shapiro in the Department of Biology, University of Utah. We seek highly motivated and creative colleagues to study the genetic and developmental basis of evolutionary diversity. Our current research focuses on:

1. Genomics and developmental genetics of morphological variation in the rock pigeon (epidermal, skeletal, and muscle identity and patterning; local collaborations

with laboratories of Mark Yandell, Gabrielle Kardon, and others).

2. Genomics of rapid adaptation of ectoparasites to changes in host conditions (experimental evolution in pigeon lice; local collaborations with laboratories of Dale Clayton and Sarah Bush).

Specific projects will be tailored to the strengths and interests of successful candidates. Please visit our home page for more information about the lab and recent publications.

REQUIREMENTS 1. Ph.D. in genetics, genomics, developmental biology, evolutionary biology, or a closely related field. Applicants with fewer than 2 years of postdoc experience are strongly preferred. 2. Track record of productivity. 3. Demonstrated ability and willingness to work both independently and collaboratively. 4. Excellent written and oral English communication skills.

A strong background in experimental developmental biology and/or analysis of high-throughput sequencing data is preferred.

TO APPLY Please submit the following materials:

1. CV, including a list of publications 2. Statement that includes your research experience and interests, as well as your preferred approximate start date 3. Names of three referees who will be willing to submit letters of reference upon request

Please email application materials in PDF format to Dr. Mike Shapiro: shapiro@biology.utah.edu

Informal inquiries are welcome prior to formal application.

SCIENTIFIC AND CULTURAL ENVIRONMENT The Department of Biology comprises a diverse and vibrant group of laboratories, with research interests ranging from environmental biology to biochemistry. The genetics and developmental biology communities are strong on the University of Utah main and medical school campuses and offer numerous opportunities for collaboration. The growing interdepartmental evolutionary genetics and genomics community is especially interactive.

The University of Utah is located in beautiful (and affordable) Salt Lake City, with easy access to world-class entertainment and recreation. Salt Lake City and nearby Park City are home to the annual Sundance Film Festival and a year-round cinema and arts scene, as well as outstanding restaurants, coffee houses, and brewpubs. Several national parks are located within a just few hours' drive, and the university is within a 40-minute drive of at least six major alpine skiing and snowboarding resorts, including venues of the 2002 Olympics. Hiking and mountain biking trails begin essentially on campus. Outside Magazine recently called Salt Lake City "one of the nation's most underrated outdoor meccas." The city is also a major airline hub, with non-stop flights throughout North America and Europe (Paris, London).

NONDISCRIMINATION & ACCESSIBILITY STATEMENT The University of Utah does not discriminate on the basis of race, color, religion, national origin, sex, age, status as a disabled individual, sexual orientation, gender identity/expression, genetic information or protected veteran's status, in employment, treatment, admission, access to educational programs and activities, or other University benefits or services.

Mike Shapiro Associate Professor, Department of Biology Adjunct Associate Professor, Department of Human Genetics University of Utah 257 S 1400 E Salt Lake City, UT 84112 (801) 581-5690, fax (801) 581-4668 http://www.biology.utah.edu/shapiro/ @MikeDShapiro

"shapiro@biology.utah.edu"
<shapiro@biology.utah.edu>

UVermont SocialInsectGenomics

The Helms Cahan lab is seeking a post-doctoral scholar with expertise in genomic analyses interested in using high-throughput sequencing and bioinformatics analyses to investigate the roles of genetic, regulatory, and structural genome evolution in phylogeographic and phenotypic diversification in ants. The position offers the opportunity to get involved in our ongoing projects on the origins, evolution and mechanisms of alternative forms of reproductive caste determination in the harvester ant genus Pogonomyrmex, as well as joining in the development of a new project on the role of genome structural variation on patterns of diversification in the North American ant genus Aphaenogaster. Much of our work involves next-generation SNP genotyping and transcriptome profiling, with the imminent arrival of several newly-sequenced ant genomes. We are looking for a colleague who will complement our existing expertise in ecology, behavior, and molecular ecology and allow us to leverage the immense data resources generated by high-throughput genomics projects to answer new and exciting questions.

We have a small but enthusiastic group of PhD, MS, and undergraduate students, along with a network of collaborators across the US and internationally. The candidate would also be able to interact with a vibrant and growing research community in Ecological Genomics at the University of Vermont.

This post-doctoral position is designed to provide mentorship and training for scientists ultimately interested in a faculty position at an institution that emphasizes both research and teaching. In addition to independent research, the candidate will gain classroom experience by teaching 1-2 courses per year, first in a team-taught environment, but with the opportunity to later design and teach their own course at the undergraduate or graduate level. Funding is available for a total of two years, with a starting date of August 22, 2016.

To apply for the position, please submit a cover letter, CV, brief statements of research and teaching interests, and names of three potential references to: scahan@uvm.edu<mailto:scahan@uvm.edu> . I am happy to discuss the expectations and project details informally by e-mail (at the above address) as well. Formal review of applications will begin May 26th, 2016.

Sara Helms Cahan Associate Professor and Chair Department of Biology University of Vermont Burlington, Vermont 05405 (802)656-2962 scahan@uvm.edu

Sara Cahan <scahan@uvm.edu>

UWashington StatisticalGenetics

Postdoc Opportunity in Forensic Statistical Genetics

A postdoctoral position is available immediately in the Department of Biostatistics at the University of Washington. The appointee will work with Dr Bruce Weir and with Dr Glendon Parker of the Lawrence Livermore National Laboratory. The project involves an investigation of the statistical genetic issues surrounding the use of genetically variable peptides for human identification. Applicants should have a PhD in statistics or genetics or a related field. An appreciation of forensic uses of DNA profiles would be an advantage. The appointee will join a large statistical genetics community at the University of Washington. Send a letter of interest, a CV and the names of three references to Bruce Weir by email to bsweir@uw.edu, by May 1, 2016.

– Bruce Weir Department of Biostatistics University of Washington Box 359461 Seattle, WA 98195-9461 Phone: (206) 221-7947

Bruce Weir <bsweir@uw.edu>

VirginiaTech MolecularEvolution

An NSF-funded postdoctoral position is available in the lab of Joel McGlothlin in the Department of Biological Sciences at Virginia Tech. The successful candidate will collaborate with Dr. McGlothlin on a project investigating the evolution of voltage-gated sodium channels across birds and reptiles. The project will use DNA target enrichment to capture and sequence the sodium-channel gene family in a wide variety of species in order to characterize the evolutionary history of resistance to tetrodotoxin and other prey defenses. The postdoc will be responsible for both bioinformatic analyses of existing genomes and the generation and analysis of new sequences. The ideal candidate will possess both laboratory skills in molecular evolutionary genetics and experience mining and analyzing large genetic datasets.

Minimum qualifications include a Ph.D. in biology, ecology and evolutionary biology, or a related field; strong oral and written communication skills; the ability to work independently and as part of a research group; and a demonstrated ability to efficiently produce strong peer-reviewed publications. Candidates who have not yet defended will be considered, but successful defense of the Ph.D. is required by the start date.

Candidates with a background in molecular evolution or bioinformatics will be given preference.

Interested candidates should submit a curriculum vitae, statement of interest along with two letters of recommendation at < http://listings.jobs.vt.edu/postings/-65745 > http://listings.jobs.vt.edu:80/postings/65745. Review of applications will begin on May 11, 2016.

Virginia Tech does not discriminate against employees, students, or applicants on the basis of age, color, disability, gender, gender identity, gender expression, national origin, political affiliation, race, religion, sexual orientation, genetic information, veteran status, or any other basis protected by law. For inquiries regarding non-discrimination policies, contact the executive director for Equity and Access at 540-231-8771 or Virginia Tech, North End Center, Suite 2300 (0318), 300 Turner St. NW, Blacksburg, VA 24061. If you are an individual with a disability and desire accommodation, please contact the hiring department.

Additional information: McGlothlin lab: http:/-

/www.mcglothlin.biol.vt.edu Application link: < http://listings.jobs.vt.edu/postings/65745 > http://listings.jobs.vt.edu:80/postings/65745 Biological Sciences at VT: http://www.biol.vt.edu/ Ecology, Evolution, and Behavior at VT: http://www.biol.vt.edu/eeb/index.html Joel W. McGlothlin Virginia Tech, Dept. of Biological Sciences Derring Hall 2125, 1405 Perry St. Blacksburg, VA 24061 http://www.mcglothlin.biol.vt.edu Email: joelmcg@vt.edu Phone: (540) 231-0046 Office: Derring Hall 4002

Joel McGlothlin <joelmcg@vt.edu>

WageningenU DynamicModellingSystemsBiology

Postdoc Position in Dynamic modelling in Systems Biology at Wageningen University & Research

We are looking for an enthusiastic, motivated Postdoc on Systems Biology with a strong background in mathematical modelling of dynamic systems, expertise in modelling metabolism and/or host-pathogen interactions being a bonus. The candidate should apply the concepts of systems biology to enhance our understanding of the fundamental principles of signalling, regulatory and most prominently metabolism in living organisms, to generate a mechanistic understanding leading to new hypothesis and model driven experimentation.

Using an interdisciplinary approach the candidate should be able to build detailed dynamic models accounting for key elements of bacterial organisms, specifically of Mycoplasma pneumoniae. The final goal is integrating the generated models in a modelling framework associating genotype and phenotype and leading to the development of testable hypothesis to transform M. pneumoniae in an optimal chassis for synthetic biology. The candidate should have working experience in mathematical modelling of dynamic systems, experimental design, and analysis of systems exhibiting complex dynamic behaviour.

Furthermore, experience and willingness to interact with colleagues on large-scale genome engineering and refactoring, and interactions between the mammalian host and the pathogen (eg. through omics and detailed biochemical measurements) will be a substantial bonus.

We ask For this position we request: - Proficiency with mathematical modelling of dynamic systems and experimental design (experience in modelling host-pathogen interactions and/or mammalian cell systems being a bonus) - A sound knowledge of physiology, biochemistry and Systems Biology - Computational competences in Python, Matlab and/or R - Experience in interacting with experimentalists - A solid background in Maths and/or Physics - A PhD in Computational, Systems, Mathematical Biology or related fields - Fluent in English, both written and spoken - The candidate will collaborate in a team with scientists at the chair of Systems and Synthetic Biology and with members of an EU funded consortium devoted to the study of M. pneumoniae

We offer We offer you a temporary position for a period of 2 years with possibility for extension of 1 year. Gross salary €2920,- to €3400,- based on a fulltime employment and dependent on expertise and experience. We not only offer a competitive salary but also good (study) leave and a pension of the ABP Pension Fund.

More information For more information about this position, please contact Prof. Vítor Martins dos Santos, chair Systems and Synthetic Biology, telephone number +31 317482865. For more information about the contractual aspects, please contact Mrs. J. van Meurs, HR advisor, telephone number +31 317480101

Interested? You can apply online at http://www.wageningenur.nl/career until 1st May 2016 or through direct link: http://www.wageningenur.nl/en/Jobs/Vacancies/Show/Postdoc-Position-in-Dynamic-modelling-in-Systems-Biology.htm We are Systems Biology is one of the spearheads of the Wageningen UR, which invests considerably in this area. The mission of the Laboratory of Systems and Synthetic Biology is to contribute to the elucidation of the mechanisms underlying basic cellular processes, evolution and interactions among microbes and between microbes and their environment (including the human host) and to translate this knowledge into applications of biotechnological, medical and environmental interest.

The Agrotechnology & Food Sciences Group is part of Wageningen UR where fundamental and applied sciences complement each other. As an important European player, we carry out top-level research and work alongside authoritative partners within the international business world as well as the government on Healthy food in a biobased society. We have a crucial role in innovations within the market. Entre preneurship and professionalism are what define us. In short, we are an interesting, international employer of stature.

Wageningen University & Research Delivering a substantial contribution to the quality of life. That's our focus each and every day. Within our domain, healthy food and living environment, we search for answers to issues affecting society such as sustainable food production, climate change and alternative energy. Of course, we dont do this alone. Every day, 6,500 people work on the quality of life, turning ideas into reality, on a global scale.

Could you be one of these people? We give you the space you need.

"Pinkster, Carolien" <carolien.pinkster@wur.nl>

WashingtonStateU ComputationalEvolutionaryGenomics

Postdoc Position: Computational Evolutionary Genomics at Washington State University

A postdoctoral position is available in the laboratory of Dr. Joanna Kelley, in the School of Biological Sciences at Washington State University in Pullman, WA (labs.wsu.edu/genomes). The research goals of the laboratory are to use genomic and computational methods to understand the genomic basis of adaptation to extreme environments. We are interested in understanding how genetic and environmental variation interact to drive population differentiation and adaptive evolution. The School of Biological Sciences at Washington State University has a strong research presence in evolution and ecology research and there are many opportunities for interaction and collaboration. The postdoctoral position is a computational genomics position studying phenotypic plasticity in the mangrove rivulus, Kryptolebias marmoratus. The candidate will lead an exciting research project studying genome, transcriptome and phenotypic data from many lineages of this primarily self-fertilizing hermaphroditic fish.

The ideal candidates will have recently completed or be completing a PhD degree in Genetics, Genomics, Computational Biology or related disciplines. We welcome applications from candidates with diverse backgrounds. Applicants must have at least one strong first-author publication. A computing background is desired, especially experience with Linux, and knowledge in at least one programming language. Prior experience with handling large-scale data and with the use of bioinformatics and statistical tools would be an advantage. Candidates should have strong organizational, written, and oral communication skills; and be able to work both independently and as part of a collaborative team. Applicants will be encouraged to develop and lead independent projects.

The appointment is for two years. Salary is competitive and commensurate with experience, and benefits are included. Applicants should email Joanna Kelley at joanna.l.kelley@wsu.edu and include a (i) cover letter that includes a statement of research interests that explicitly describes your professional qualifications for the position, (ii) curriculum vitae, and (iii) contact information for three references. Applications will be accepted through May 15th. The desired start date is August 2016.

Joanna L. Kelley, PhD Assistant Professor, School of Biological Sciences Member, Center for Reproductive Biology Washington State University joanna.l.kelley@wsu.edu http://labs.wsu.edu/genomes Phone: 509-335-0037

"Kelley, Joanna.l" <joanna.l.kelley@wsu.edu>

WashingtonStateU LandscapeGenomics

We are seeking a postdoctoral researcher to work on landscape genomics and transcriptomics of Tasmanian devils and Tasmanian devil facial tumor disease. This NSF-funded international collaboration builds on over 15 years of research tracking the spread of this unique infectious tumor across Tasmania and consequent endangerment of the iconic Tasmanian devil. Reference genomes are available for both tumor and devil and population genomic data have already been collected for >3500 Tasmanian devil individuals. The successful applicant will have an unprecedented opportunity to analyze thousands of devil individuals and hundreds of tumor samples taken both before and after epizootics to test for selection, coevolution, patterns of resistance, etc, across Tasmania. We will then use these data to predict the course of disease in uninfected populations. The position is centered in the lab of Dr.

Andrew Storfer (www.wsu.edu/˜storfer) at Washington State University, in close collaboration with Dr. Paul Hohenlohe at the nearby University of Idaho (8 miles away). Both universities have genomics core facilities, including the Institute of Bioinformatics and Evolutionary Studies (IBEST;http://www.uidaho.edu/research/-ibest) with state-of-of-the art equipment, computational facilities and staff support.

Review of applications will begin on May 2, 2016 and continue until the position is filled. A Ph.D. in Biology or a related discipline and genomics and bioinformatics experience is required. Desired qualities also include a background in population genomics, infectious disease evolution, and/or cancer genomics. Start date is negotiable, but anticipated to be between June 1 and September 1, 2016. Salary and benefits are competitive. Position is for 1 year, with continuation for an additional year pending satisfactory progress. To apply, please send in pdf format a CV, and names, addresses and email addresses of 3 references, a research statement, and up to 3 representative reprints via email to: Andrew Storfer (astorfer@wsu.edu).

WSU is an Equal Opportunity/Affirmative Action/ADA educator and employer.

Andrew Storfer, PhD Eastlick Distinguished Professor Associate Director for Graduate Studies School of Biological Sciences Washington State University Pullman, WA 99164 USA Phone: (509) 335-7922 Fax: (509) 335-3184 astorfer@wsu.edu www.wsu.edu/~storfer Andrew Storfer <andrew.storfer@gmail.com>

WashingtonStateU PlantMicrobes

A postdoctoral position in plant-microbe symbiosis and biological invasions is available in the Porter lab at Washington State University, Vancouver. The postdoc will join an NSF-funded project to examine the ecological and evolutionary forces reshaping plant-microbe symbioses during biological invasions (DEB-1355216). This research will leverage genomic tools in the model symbiosis between leguminous plants and nitrogen-fixing symbiotic rhizobium bacteria to examine ecological dynamics and the evolution of cooperation in natural and experimentally evolved invasions.

Project opportunities: plant and bacterial population genomics in the Medicago-Ensifer model system, quantitative genetic cross-inoculation experiments in the greenhouse, and/or studies of ecological dynamics in the field. Research will be conducted in collaboration with the Friesen lab at Michigan State University (http://friesen.plantbiology.msu.edu/) and funding will be provided for the postdoc to travel to MSU as needed. The postdoctoral researcher will lead-author peer-reviewed scientific articles and funding will be provided to give national conference presentations.

Location: the postdoc will join the new Microbial Symbiosis Lab at Washington State University, Vancouver. WSUV is a vibrant, rapidly growing institution located within the greater Portland/Vancouver metropolitan area, near the Columbia River, Cascade Mountains and coastal ocean, and as such offers an exceptional quality of life. For more information see:

https://labs.wsu.edu/stephanie-porter/ Qualifications:

PhD in evolutionary ecology, genomics, microbial biology, and/or plant biology &

Demonstrated excellent written and oral English communication skills, including strong record of scientific publication.

Appointment is for one year at full time plus benefits; expectation of renewal for a second year pending quality performance. The start date for this position is flexible.

Application review will begin May 15th, and applications will continued to be reviewed on a rolling basis until the position is filled. To apply, please send a single pdf email attachment with "Microbial Symbiosis Postdoc" in the email subject line. Include a 1-page statement of research interests and experience, a curriculum vitae, copies of relevant publications, and contact information for 3 references, to:

Stephanie S. Porter Assistant Professor, School of Biological Sciences Washington State University, Vancouver stephanie.porter@wsu.edu

"stephanie.porter@wsu.edu"
<stephanie.porter@wsu.edu>

WashingtonStateU TasmanianDevilGenomics

POSTDOCTORAL RESEARCHER

Washington State University

School of Biological Sciences

We are seeking a postdoctoral researcher to work on landscape genomics and transcriptomics of Tasmanian devils and Tasmanian devil facial tumor disease. This NSF -funded international collaboration builds on over 15 years of research tracking the spread of this unique infectious tumor across Tasmania and consequent endangerment of the iconic Tasmanian devil. Reference genomes are available for both tumor and devil and population genomic data have already been collected for >3500 Tasmanian devil individuals. The successful applicant will have an unprecedented opportunity to analyze thousands of devil genotypes and hundreds of tumor samples taken both before and after epizootics to test for selection throughout both genomes, coevolution, patterns of resistance, etc, across Tasmania. We will then use these data to predict the course of disease in uninfected populations. The position is centered in the lab of Dr. Andrew Storfer (www.wsu.edu/˜storfer) at Washington State University, in close collaboration with Dr. Paul Hohenlohe at the nearby University of Idaho (8 miles away). Both universities have genomics core facilities, including the Institute of Bioinformatics and Evolutionary Studies (IBEST;http://www.uidaho.edu/-research/ibest) with state-of-of-the art equipment, computational facilities and staff support.

Review of applications will begin on May 2, 2016 and continue until the position is filled. A Ph.D. in Biology or a related discipline, combined with genomics and bioinformatics experience is required. Desired qualities also include a background in population genomics, infectious disease evolution, and/or cancer genomics. Start date is negotiabl between June and August, 2016. Salary and benefits are competitive. Position is for 1 year, with continuation for an additional year pending satisfactory progress. To apply, please send in pdf format a CV, and names, addresses and email addresses of 3 references, a research statement, and up to 3 representative reprints via email to: Andrew Storfer (astorfer@wsu.edu).

WSU is an Equal Opportunity/Affirmative Action/ADA educator and employer.

Andrew Storfer, PhD Eastlick Distinguished Professor Associate Director for Graduate Studies School of Biological Sciences Washington State University Pullman, WA 99164 USA Phone: (509) 335-7922 Fax: (509) 335-3184 astorfer@wsu.edu www.wsu.edu/˜storfer

andrew.storfer@gmail.com

WoodsHole EvolutionaryConservationAgeing

Postdoctoral Scientist - Genetic and Epigenetic Mechanisms of Aging

Marine Biological Laboratory | Woods Hole, MA | Salary commensurate with experience and qualifications

Position Summary: A postdoctoral position is available in the laboratory of Dr. Kristin Gribble at the Marine Biological Laboratory in Woods Hole, MA, to study the molecular mechanisms of the biology of aging. Our work focuses on understanding the mechanisms of plasticity in health and lifespan in response to environmental changes and interventions, and the evolutionary conservation of these mechanisms. We are specifically investigating the genetic and epigenetic mechanisms of maternal effects in determining offspring health and lifespan (Aging Cell 13:623 2014). This project takes a multidisciplinary approach, using phenotypic, transcriptomic, genetic, genomic, epigenetic, biochemical, imaging, RNAi, and next-generation sequencing methods in an exciting new animal model system, the monogonont rotifer. The successful applicant will have the opportunity for independent and novel research in an innovative new laboratory.

For more information about the laboratory, please see the lab website, http://www.mbl.edu/jbpc/gribble/ or contact Dr. Gribble at kgribble@mbl.edu.

Basic Qualifications: Applicants should posses a Ph.D. and/or M.D. in molecular biology, cell biology, biochemistry, genetics, bioinformatics, or a related field. The ideal candidate will have a record of scientific rigor, productivity, and creativity; the ability to work both independently and as part of a team; and a strong publication record. Excellent oral and written communication skills are required. Highly motivated individuals with experience in other model systems and a background in biochemistry, cell/molecular biology, epigenetics, and/or bioinformatics are encouraged to apply.

Terms: The position is available immediately, and is renewable annually depending upon progress and funding.

Special Instructions to Applicants: To apply, send, please submit:

(1) A cover letter describing your research goals and motivation for joining the lab;

(2) a CV;

(3) a 1-2 page research statement; and

(4) contact information for three references

Kristin Houtler <kgribble@mbl.edu>

WorkshopsCourses

Barcelona GeneticBasisOfShape Sep6-9

Dear colleagues,

There are a few places still available for the course “From Phenotype to Genotype: The Genetic Bases of Shape - 3rd Edition”; September 6-9, 2016.

Instructors: Dr. Neus Martínez-Abadías (Centre for Genomic Regulation, Spain) and Dr. Nicolas Navarro (Ãcole Pratique des Hautes Ãtudes, France).

Site: Premises of Sabadell of the Institut Catalá de Paleontologia Miquel Crusafont (Barcelona, Spain).

Course Webpage: http://www.transmittingscience.org/courses/gen/quant-gen-shape/ The aim of this course is to provide participants with an overview of quantitative genetics, with specific application to shape analysis and decomposition of phenotypic variation into components of genetic and environmental variation. The basic theoretical concepts of resemblance between relatives, heritability, estimates of selection, and geometric morphometrics will be introduced. Practical lessons will enable participants to learn to use user-friendly (and not so user-friendly) software packages to estimate heritability, phenotypic and genetic variance covariance matrices, response to hypothetical selection, actual selection and QTL mapping.

Participants are encouraged to bring their own data for analysis and discussion in the course. Morphometric data involves any kind of quantitative shape data collected on individuals, such as linear measurements and/or 2D or 3D landmark coordinates. Pedigree files usually consist of text files with a list of three columns (individual ID, father ID, mother ID). Specific details about formatting these files will be provided during the practical lessons.

This course is co-organized by Transmitting Science and the Institut Catalá de Paleontologia M. Crusafont. Place are limited and will be covered by strict registration order.

Please feel free to distribute this information between your colleagues if you consider it appropriate.

With best regards

Sole

Soledad De Esteban-Trivigno, PhD. Scientific Director Transmitting Science www.transmittingscience.org soledad.esteban@transmittingscience.org

Denver CO EvolutionInCognition Jul21

Workshop:Denver_CO.EvolutionInCognition.July21

Evolution in Cognition Workshop July 21 to be held as part of the

2016 Genetic and Evolutionary Computation Conference (GECCO-2016) July 20-24, Denver, Colorado, USA

Organized by ACM SIGEVO http://gecco-2016.sigevo.org Webpage: http://lis2.epfl.ch/-events/workshops/GECCO2016/ Submission Deadline extended: April 12th, 2016

=== Topic =Evolution by natural selection has shaped life over billions of years leading to the emergence of complex organism capable of exceptional cognitive abilities. These natural evolutionary processes have inspired the development of Evolutionary Algorithms (EAs), which are optimization algorithms widely popular due to their efficiency and robustness. Beyond their ability to optimize, EAs have also proven to be creative and efficient at generating innovative solutions to novel problems. The combination of these two abilities makes them a tool of choice for the resolution of complex problems.

Even though there is evidence that the principle of selection on variation is at play in the human brain, as proposed in Changeux's and Edelman's models of Neuronal Darwinism, and more recently expanded in the theory of Darwinian Neurodynamics by Szathmáry, Fernando and others, not much attention has been paid to the possible interaction between evolutionary processes and cognition over physiological time scales. Since the development of human cognition requires years of maturation, it can be expected that artificial cognitive agents will also require months if not years of learning and adaptation. It is in this context that the optimizing and creative abilities of EAs could become an ideal framework that complement, aid in understanding, and facilitate the implementation of cognitive processes. Additionally, a better understanding of how evolution can be implemented as part of an artificial cognitive architecture can lead to new insights into cognition in humans and other animals.

The goals of the workshop are to depict the current state of the art of evolution in cognition and to sketch the main challenges and future directions. In particular, we aim at bringing together the different theoretical and empirical approaches that can potentially contribute to the understanding of how evolution and cognition can act together in an algorithmic way in order to solve complex problems. In this workshop we welcome approaches that contribute to an improved understanding of evolution in cognition using robotic agents, in silico computation as well as mathematical models.

Keywords: Evolutionary Computation, Evolution, Cognition, Darwinian Neurodynamics, Neuronal Darwisnism, robotics.

=== Invited speakers = - Prof. Eörs Szathmary - Prof. Jeff Krichmar - Prof. Arne Dietrich

=== Organizers = - Prof. Stéphane Doncieux, University Pierre and Marie Curie, France - Dr. Joshua Auerbach, EPFL, Switzerland - Prof. Richard Duro, Universidade da Coruna, Spain - Dr. Harold P. de Vladar, Parmenides Foundation, Germany

=== Workshop format This is a half day workshop with invited talks and a session dedicated to posters, videos and demonstrations. The session will start with a short teaser of posters and demonstrations. Videos will also be displayed afterwards.

=== Submissions and deadlines =Submission: extended abstracts (2-4 pages) following ACM template should be sent in electronic form (pdf) to eic_2016@isir.upmc.fr - April 3rd, 2016: Papers Submission Deadline - April 20th, 2016: Notification of Acceptance - May 4th, 2016: Camera-Ready Paper Submission - July 21st, 2016: Workshop

Each accepted abstract will be presented in one or more of the following formats: - poster - 2-minutes video - demonstration

Your submission email should specify in which of these formats you would like to present.

Original works, position papers as well as overviews of author's recent work are all welcome.

All abstracts will be included in the GECCO workshop proceedings, unless explicitly required by the authors (for copyright reason, for instance).

GECCO is sponsored by the Association for Computing Machinery Special Interest Group on Genetic and Evolutionary Computation (SIGEVO). SIG Services: 2 Penn Plaza, Suite 701, New York, NY, 10121, USA, 1-800-342-6626 (USA and Canada) or +212-626-0500 (Global).

Stéphane Doncieux, Josh Auerbach, Richard Duro and Harold P. de Vladar

Harold P. de Vladar

Center for the Conceptual Foundations of Science. Parmenides Foundation. Kirchplatz 1, 82049 Pullach, Germany

hpvladar.wordpress.com www.parmenides-foundation.org "Harold P. de Vladar" <Harold.Vladar@parmenides-foundation.org>

Edinburgh EvolutionaryQuantGenetics Oct31-Nov4

Short course in EVOLUTIONARY QUANTITATIVE GENETICS

The course: This course will give a comprehensive review of modern concepts in Evolutionary Quantitative Genetics. The contents of the course are basic statistics, population genetics, quantitative genetics, evolutionary response in quantitative traits, estimating the fitness of traits and mixed models and their extensions.

Course dates: 31 Oct - 4 Nov 2016.

Location: The Roslin Institute < http://www.roslin.ed.ac.uk/ >, The University of Edinburgh, Scotland, UK.

Instructor: Dr Bruce Walsh < http://eeb.arizona.edu/people/dr-j-bruce-walsh >, Department of Ecology & Evolutionary Biology, University of Arizona.

Brief programme: Monday, Oct 31- Background: Basic stats, population genetics. Tuesday, Nov 1- Basic Quantitative Genetics. Wednesday, Nov 02- Evolutionary response in quantitative traits. Thursday, Nov 03- Estimating the fitness of traits. Friday, Nov 04- Mixed Models and their extensions.

A more detailed syllabus can be downloaded here.

Participants: Participation at the course is open to all.

Course fees: Level 1 - 300 - Internal University of Edinburgh students and staff. Level 2 - 400 - External academics. Level 3 - 500 - Industry.

The course fee includes tuition, lunch and light refreshments.

Registration: Pre-registration is now open, please email Maria Sanchez <Maria.Sanchez@ed.ac.uk> subject Walsh course EQG.

Hosts: John Hickey < http://www.alphagenes.roslin.ed.ac.uk/group-members/john-hickey/ >, Division of Genetics and Genomics, The Roslin Institute, University of Edinburgh.

Josephine Pemberton < http://pemberton.bio.ed.ac.uk/home >, Institute of Evolutionary Biology, University of Edinburgh, University of Edinburgh.

Chris Haley < http://www.hgu.mrc.ac.uk/people/c.haley.html >, MRC Human Genetics Unit, MRC IGMM, University of Edinburgh.

For any further information please contact Maria Sanchez <Maria.Sanchez@ed.ac.uk>.

http://www.alphagenes.roslin.ed.ac.uk/short-course-in-evolutionary-quantitative-genetics/ HICKEY John <John.Hickey@roslin.ed.ac.uk>

Faro Portugal StatisticalGenetics Ext Deadline

Please note, the application period has been extended until 8th April 2016.

Please apply to ccmaratt@ualg.pt

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ADVERTISEMENT WEBSITE: http://att.ccmar.ualg.pt/statistical_genetics_2016 WORKSHOP IN STATISTICAL GENETICS - taught by BRUCE WEIR - Professor of Biostatistics, and Director of the Institute of Public Health Genetics at the University of Washington. Bruce Weir is the author of the textbook "Genetic Data Analysis" (3rd edition in preparation) and he has directed the Summer Institute in Statistical Genetics since 1996. http://www.gs.washington.edu/faculty/weir.htm, http://www.ncbi.nlm.nih.gov/pubmed/?term=Bruce+Weir DESCRIPTION: A unified treatment for the analysis of discrete genetic data, starting with estimates and sample variances of allele frequencies to illustrate genetic vs statistical sampling and Bayesian approaches. A detailed look at Hardy-Weinberg and linkage disequilibrium, including the use of exact tests with mid-p-values and a new look at X-chromosome Hardy-Weinberg testing. A new characterization of population structure with F-statistics, based on allelic matching within and between populations with individual relationship estimation as a special case. Analyses illustrated with applications to forensic science and association mapping, with particular reference to rare variants.

VENUE: Centre of Marine Sciences, University of the Algarve, Faro, Portugal. http://ccmar.ualg.pt - Google maps: https://goo.gl/cM78fp

DATE: 8th-9th September 2016

FORMAT: 2-day workshop, lectures and hands-on practical sessions (attendees will need to bring laptops). The course is equivalent to 3 European ECTS credits.

INTENDED AUDIENCE: PhD students, post-doctoral and advanced researchers (but no formal restriction)

REGISTRATION FEE: 240 euro

Registration does not include travel and lodging. Faro has an international airport located 4 km from the Gambelas Campus of the University of Algarve where the course will take place.

HOW TO APPLY: Applications in the form of a CV and motivational letter should be sent to ccmaratt@ualg.pt by *8th April 2016*. Applicants will be selected on merit and successful applicants will be informed by 10th April 2016.

SCHOLARSHIPS: At least 2 scholarships to cover registration fees will be awarded to PhD students; applicants should indicate if they would like to be considered and must send proof of student status.

ACCOMMODATION: Recommended: Hotel Aeromar at Faro beach (http://www.aeromar.net/en) has temporarily reserved (until 31st May) and discounted 8 double rooms, priced 62.5 euro and 80 euro, double and single occupancy, respectively (mention CCMAR reservation when booking). Additional accommodation at the beach and in Faro centre: http://goo.gl/mgG85g. A minibus service will run between the beach, town centre, and campus.

CONTACTS: Ester SerrÃ£o - Assistant Professor, UALG/CCMAR - eserrao@ualg.pt Cymon J. Cox - FCT Coordinating Researcher, CCMAR - cymon@ualg.pt

Advanced Technologies and Training programme @ CCMAR 2016 ccmaratt@ualg.pt <ccmaratt@ccmar.ualg.pt>, att.ccmar.ualg.pt/statistical_genetics_2016

The Centre of Marine Sciences (Centro de Ciências do Mar, CCMAR) is an independent multidisciplinary, non-profit institute located on the Gambelas campus of the University of the Algarve in Faro with ~250 members and a mission to promote research and education in the marine sciences. Faro (http://www.algarve-tourist.com/Faro-portugal-guide.html) is the capital city of the Algarve region of southern Portugal and borders the Ria Formosa National Park (http://www.formosamar.com/en). The Algarve (http://www.visitalgarve.pt/?idioma=uk) boasts > 300 days of sun per year, stunning beaches and mountain vistas, opportunities for diving, golf, and other sporting activities, and a unique traditional regional cuisine (esp. seafood). A variety of optional social activities will be organised to coincide with the course and special events can be organised upon request for participants and/or accompanying persons (diving, surf, stand-up paddle, windsurf, kayaking, horse-riding, tennis, bird-watching, nature walks, boat guided tours, fishing, etc).

Bruce Weir - Recent Publications:

Zhu ZH, Bakshi1 A, Vinkhuyzen AAE, Hemani G, Lee SH, Nolte IM, van Vliet-Ostaptchouk JV, Snieder H, The LifeLines Cohort Study, Esko T, Milani L, Mägi R, Metspalu A, Hill WG, Weir BS, Goddard ME, Visscher PM,

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Hafjel Norway Selection Jun6-10 reminder

Dear colleagues,

This is a reminder for the workshop on *"Optimal Contribution Selection"*

arraged by The Nordic Genetic Resource Center (NordGen) in Hafjell (Ãyer municipality north of Lillehammer), Norway 6th-10th of June 2016.

The main goals of the workshop are:

- to introduce the theory and implementation of Optimal Contribution Selection in sustainable management of breeding and conservation programs

- to promote the independent use of EVA (EVolutionary Algorithms) software with hands-on exercises

To maximize the learning experience of all participants, the workshop is divided into two parts. Participants may choose to register for *both* *or only one* of the consecutive parts: "*Part I - Introductory"* and "*Part II - Advanced"*. The maximum number of participants in Part I and Part II are 20 and 25, respectively. There are still few places left on both parts.

For a more detailed description of the workshop program, registration and practical information please follow the link below:

https://sites.google.com/a/nordgen.org/workshop-optimal-contribution-selection/ Feel free to distribute this invitation amongst your colleagues and other institutions.

Best regards

Anne Kettunen

Dr. Anne Kettunen Senior Scientist NordGen - Nordic Genetic Resource Center P.O. Box 115, NO-1431 Ãs, Norway Street address: Raveien 9, NO-1430 Ãs, Norway Phone: +47 9036 5249, mobile: +47 9778 0903 anne.kettunen@nordgen.org www.nordgen.org Anne Kettunen <anne.kettunen@nordgen.org>

Hinxton UK HumGenomeAnalysis JUL20-26 DEADLINE APR8

Last Call for Applications and Bursaries: Closes FRIDAY 8 April!

Human Genome Analysis: Genetic Analysis of Multifactorial Diseases 20-26 July 2016, Wellcome Genome Campus, Hinxton UK Application and Bursary Deadline: 8 April

Summary: This intensive, computational course is aimed at scientists actively involved in genetic analysis of multifactorial traits. The programme provides a comprehensive overview of the statistical methods currently used to map disease susceptibility genes in human populations.

Bursaries: Limited bursaries are available (up to 50% of the course fee) and are awarded on merit. URL: https://registration.hinxton.wellcome.ac.uk/events/item.aspx?e=3D566 COURSE INSTRUCTORS

Daniel Weeks (University of Pittsburgh, USA) Heather Cordell (Newcastle University, UK) Simon Heath (Centre Nacional d'Analisi Genomica (CNAG), Barcelona, Spain) Janet Sinsheimer (UCLA, USA) Eric Sobel (UCLA, USA) Joe Terwilliger (Columbia University, USA)

GUEST SPEAKERS for 2016

Richard Duerr (University of Pittsburgh, USA) Andrew Morris (University of Liverpool, UK) Nicole Soranzo (Wellcome Trust Sanger Institute, UK) Timothy Thornton (University of Washington, USA) Chris Wallace (University of Cambridge, UK)

Full details at: www.wellcomegenomecampus.org/coursesandconferences "JanetS@mednet.ucla.edu" <JanetS@mednet.ucla.edu>

LakeBalaton Hungary ConservationGenetics May30-Jun10 Deadline

SHORT TITLE

Registration Deadline - CONGEN2016 Lake Balaton Hungary

LONG TITLE

Deadline approaching - Recent Advances in Conservation Genetics Course (ConGen2016)at Lake Balaton, HUNGARY www.congen2016.com Dear Conservation Genetics Community:

Please note that the Registration deadline for ConGen2016 is approaching (April 15).

The 2016 Recent Advances in Conservation Genetics Short Course (ConGen2016) will be held at Balaton Limnological Institute of the Hungarian Academy of Sciences near Budapest, Hungary over May 30-June 10, 2016. The course will host 25-30 students dedicated to conservation and about 20-25 faculty from around the world.

The course will be directed by Dr. Stephen J. O'Brien, and taught by renowned scientists in methods, interpretation, and applications of molecular genetic analyses for conservation of endangered species, who will also share a variety of their personal experiences in this important field. ConGen2016 faculty (http://congen2016.com/home/congen2016-faculty/) is an amazing group of people who come from all around the world and will be teaching, sharing their conservation stories and interacting with students during the course.

For the first time in its ore than 25 year history Congen is coming to Europe. The 2016 course will be organized in collaboration with the Balaton Limnological Institute on the shores of this charming freshwater lake in Hungary. It is one of the largest freshwater lakes, and one of the region's foremost tourist destinations. The mountainous region of the northern shore is known both for its historic character and as a major wine region, while the flat southern shore is known for its resort towns. Due in no small way to the scientific efforts of the Balaton Institute researchers, Lake Balaton is today one of the most intensively studied lakes of the world.

Who should apply?

Applicants should be conservation-minded scientists (advanced graduate students, post-docs, teachers, and researchers with advanced degrees) from academia, government, NGOs, or industry who are studying the genetics of endangered species and who will apply the knowledge gained from this course to the conservation of such species.

Please submit your registration here: http://congen2016.com/home/registration/ Registration Cost:

Early Registration - paid before March 1, 2016: The cost per participant will be US$2,150 and will include your accommodation, all meals and travel from and to the airport.

Late Registration - paid after March 1 and before April 25, 2016: The cost of late registration per participant will be US$2,350 and will include your accommodation, all meals and travel from and to the airport.

Application forms: Please complete the application form below and submit together with a CV. Successful applicants will be notified via email and will be sent additional course information and they must ensure that they check the following list. Payment must be made in full using the PayPal link that will only be made available to the successful applicants have been notified or by direct bank deposit (SWIFT).

Scholarships:

Partial or full scholarships may be awarded to registered students, subject to availability. The scholarship application is a separate process and will be coordinated with our sponsors. To be eligible for a scholarship, please apply on this page http://congen2016.com/home/registration/scholarship-application/ . Please note: Scholarships will be allocated based on need, scholastic potential , likelihood of conservation translation, the applicant's CV, and other information contained in the application form. Scholarships will be awarded as a complete or partial refund of the tuition for those applicants who have already submitted their deposit.

Course Faculty

- Stephen J. O'Brien: Chief Scientific Officer at the Theodosius Dobzhansky Center for Genome Bioinformatics , St. Petersburg State University, RUSSIA

- Scott Baker: Professor and Associate Director, Marine Mammal Institute, Oregon State University, OREGON, USA

- Oliver Ryder: Director of Genetics and Kleberg Chair of San Diego Zoo's Institute for Conservation Research, CALIFORNIA, USA

- Joan Pontius: Senior Bioinformatics Scientist at ESAC Inc, Rockville MARYLAND, USA

- Harris Lewin: Vice chancellor for research at the University of California, Davis, CALIFORNIA, USA

- Dennis Larkin: Reader in Comparative Genomics Veterinary College, London, ENGLAND, UK

- Bridget von Holdt: Assistant Professor, Ecology and Evolution, Princeton University, NEW JERSEY, USA

- Augosthinho Antunes: CIMAR, Centro Interdisciplinar de InvestigaÃÂ§ÃÂ£o Marinha e Ambiental, Laboratory of Ecotoxicology,

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Lisbon Portugal Biodiversity Lichens

Subject: Portugal-cE3c-Course: two advanced courses with deadlines May 2016 cE3c - Centre for Ecology, Evolution and Environmental Changes is organizing several Advanced Courses: see below the two with closer deadlines.

Additional informations at: http://ce3c.ciencias.ulisboa.pt/training/?cat=1 cE3c - Centre for Ecology, Evolution and Environmental Changes Advanced Course Natural History Collections and Biodiversity taught by Maria Judite Alves, Raquel Barata, Cristiane Bastos-Silveira et al. | May 30 - June 3 @ Lisbon, Portugal

Objectives Natural history museums are privileged spaces for seminal research on different subjects of biological sciences such as biodiversity, evolution, ecology, biogeography and taxonomy. This crucial role is due to the fact that they represent biological diversity repositories becoming huge libraries of information on Earth living organisms. The long-term sampling through various decades renders to natural history collections an historic perspective that allows reconstructing a "memory", sometimes secular, of natural patterns and processes. This aspect gains particular relevance nowadays because of the increasing rate of species extinctions and biodiversity decrease. This course aims to: - evidence the importance of natural history collections for the study of biodiversity. - show new tools and approaches to extract and disseminate biodiversity data from natural history collections - increase awareness of young researchers for the scientific and culture value of Natural History Museums.

Course coordinator Maria Judite Alves (mjalves@fc.ul.pt) Researcher at the Centre for Ecology, Evolution and Environmental Changes (cE3c), Faculty of Sciences of the University of Lisbon (http://ce3c.ciencias.ulisboa.pt/teams/user/?id=211)

Intended audience This five days intensive course will be open to a maximum number of 16 participants, being directed to PhD or MSc students in Biology, Evolution, Ecology or related areas, and postdocs and other professionals working in related topics. Minimum formation: Bachelor in Biology or related area.

The course is free for 1st year PhD students in the Doctoral programme in Biology (FCUL), Biodiversity, Genetics and Evolution (UL; UP) and Biology and Ecology of Global Changes (UL, UA). For information of fees for other participants see the programme details (access link below).

Deadline for applications: May 9, 2016

Candidates should send a short CV and motivation letter to Maria Judite Alves (mjalves@fc.ul.pt)

For additional details about the course and to know how to register, click here: http://ce3c.ciencias.ulisboa.pt/training/ver.php?id For more information about the course, please contact by email: Maria Judite Alves (mjalves@fc.ul.pt)

cE3c - Centre for Ecology, Evolution and Environmental Changes Advanced Course Lichens as a tool for interpretation of environmental changes taught by Cristina Maguas, Cristina Branquinho, Sofia Augusto et al.| July 11-15 2016 @ Lisbon, Portugal

Objectives: With this course, we aim at providing the participants with the basics of lichen biology and ecology, biomonitoring and data analysis methods to allow the use of lichens for the interpretation of the environmental conditions and the development of a responsible scientific-based environmental management.

Course coordinator Cristina Maguas (cmhanson@fc.ul.pt) Associate Professor at the Faculty of Sciences of the University of Lisbon, Researcher at the Centre for Ecology, Evolution and Environmental Changes (cE3c) (http://ce3c.ciencias.ulisboa.pt/teams/user/?id=145)

Intended audience This course will be open to a maximum number of 18 participants, being directed to PhD or MSc students in Ecology, Environmental Studies, Geography or related areas, and postdocs and other professionals working in related topics. Minimum formation: Bachelor in Biology, Natural Science or related areas.

The course is free for 1st year PhD students in the Doctoral programme in Biology (FCUL), Biodiversity, Genetics and Evolution (UL; UP) and Biology and Ecology of Global Changes (UL, UA). For information of fees for other participants see the programme details (access link below)

Deadline for applications: May 13, 2016

Candidates should send a short CV and motivation letter to lichenscourse@fc.ul.pt

For additional details about the course and to know how to register, click here: http://ce3c.ciencias.ulisboa.pt/training/ver.php?id For more information about the course, please contact by email: Cristina Máguas (cmhanson@fc.ul.pt)

Margarida Matos, PhD Associate Professor

Researcher ID: K-2365-2012

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Maynooth Ireland Phylogenomics May29-Jun3

PHYLOGENOMICS SUMMER SCHOOL 2016 (MAY 29TH - JUNE 3RD)

http://mcinerneylab.com/evolution/phylogenomics-summer-school-2016-may-29th-june3rd/ (Est. 1999)

What?: Week-long, intensive phylogenetics course covering all aspects of bioinformatics and phylogenetics/phylogenomics. Where?: Department of Biology, National University of Ireland Maynooth. This is approximately 40 minutes from Dublin Airport (Serviced by Aer Lingus, British Airways, Ryanair, American Airlines, Lufthansa, Air France, etc.) , 25km from the centre of Dublin, Ireland. When?: Sunday May 29th - Friday June 3rd (inclusive), 2016.

Who is it for?: This course starts with the basics of bioinformatics - unix computer usage, genome assembly, gene prediction and genome annotation.

The course then leads on to phylogenetic reconstruction and deals with all the major methods and all kinds of data from genes to genomes. Therefore, it is particularly suited to researchers that have a keen interest in phylogenetic reconstruction, but have little or no practical experience or theoretical background (ideally suited to new Masters/PhD students/post-docs, but also investigators moving into this area of research).

We welcome organismal phylogeneticists or genome scientists who are trying to make sense of the evolutionary history of any kind of gene or genome.

Who has taken this course in the past?: Researchers from every continent and every stage of their career, from early-stage Masters students, to Professors with 40 years experience in research.

Course structure: Every day will begin with formal lectures covering all parts of phylogenetic reconstruction. The afternoons will be taken up with practicals. In addition, the course will have specific lectures that demonstrate "use cases" for phylogenetics, with examples from prokaryotes, animals, plants, protozoans and fungi.

Student involvement: All students are expected to give a five minute presentation of their research agenda. This will happen towards the beginning of the week, in order to encourage discussions during the course.

Course fee: 750. This includes a welcome reception on Sunday May 29th, all coffee breaks and all lunches during the week and the course dinner on Thursday evening. It does not include accommodation.

Accommodation: If you are accepted on the course, we will make several recommendations for inexpensive (27 - 70 per night) or more luxurious accommodation (100-250 per night). You must organise and pay for your own accommodation.

Application process:

You first place an order for a place on the course (email phyloinformatic@gmail.com). You must include your CV and a half-page letter of interest, stating your position and why you want to do the course. You will get a yes/no answer within two working days and if the answer is yes, you will get a link to a BACS payment system. You will then have five working days to make the payment. Your place on the course will be held for that time. Please email us at phyloinformatic@gmail.com if you need more information.

Note 1: All students will be presented with a certificate of completion for this course and it can be used as part of post-graduate studies.

Note 2: We have found it better if students bring their own laptops. Please let us know if this is a problem for you and we will supply a laptop.

Programme 'V tentative and subject to change

Day 1 (Sunday May 29th, 2016) 'ÂMeet and Greet'Â

Meeting with students.(8:00PM) 'Âintroductions and refreshments'Â

Day 2 (Monday May 30th, 2016) 'Âthe scene'Â

Lecture I (9.00 'V 10.30): James McInerney 'V 'Âto Gene and Genome Evolution'Â

Coffee break (10.30 'V 10.45) (Provided by the course)

Student introductions and presentations I (10.45 'V 12.30)

Lunch (12.30-1.30) (Provided by the course)

Student introductions and presentations II (1.30 'V 3:00)

Coffee Break (3.00 'V 3.15) (Provided by the course)

Practical session I (3.15 'V 5.00): David Fitzpatrick (leading demonstrator) 'V 'Âpipelining and the automation of analyses in comparative genomics and phylogenomics I'Â

Seminar I (5.00 'V 5.45): Mary O'Connell 'V 'Âand the Evolution of Function'Â

Day 3 (Tuesday May 31st, 2016) "Putting Order On The Data"

Lecture II (9.00-10.30): James McInerney - "BLAST - sequence similarity, database searching and statistics"

Coffee break (10.30 - 10.45) (provided by the course)

Practical session II (10.45 - 12.30) David Fitzpatrick (leading demonstrator) - "Short read assembly using Velvet"

Lunch (12.30-1.30) (Provided by the course)

Practical session III (1.30-3.00) David Fitzpatrick (leading demonstrator) - "Gene prediction using GeneMark"

Coffee break (3.00 - 3.15)

Practical session IV (3.15-5.00) David Fitzpatrick (leading demonstrator) - "Genome annotation using Interpro"

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Norway NonmodelOrganismHTS May31-Jun10

PhD course: High throughput sequencing of non-model organisms DR425F - 2016

The Faculty of Biosciences and Aquaculture at Nord University 31 May 2016 - 10 June 2016

The Faculty of Biosciences and Aquaculture at Nord University takes great pleasure in inviting you to the annual PhD course "High throughput sequencing of non-model organisms" (DR425F) 31 May - 10 June 2016. High throughput sequencing (HTS) technologies are being applied to a wide range of important topics in biology. However, the analyses of non-model organisms, for which little previous sequence information is available, pose specific problems. This course will address the specific strengths and weaknesses of alternative HTS technologies, the computational resources needed for HTS, and how to analyze non-model species using HTS. The course consists of practical training in preparing and running fragment libraries, HTS bioinformatics training, and lecturing/seminars of HTS approaches specifically targeting non-model organisms.

A detailedcourse description is availablehere [http://www.nord.no/en/studies/programmes-courses/find-programmes-courses/2016h/1/Pages/DR425Fv1.aspx] . We will accept a maximum of 10 students. The closing date for applications is April 29.

If you have questions regarding the course, please contact Prof. Truls Moum at truls.b.moum@nord.no

"\"Alexander Jüterbock\"" <Alexander-Jueterbock@web.de>

Portugal NicheModelling Jul18-22

INTRODUCTION TO NICHE MODELLING SECOND EDITION 18-22 July 2016 Observatorio Astronomico Prof. Manuel de Barros Faculty of Sciences o University of Porto Alameda do Monte da Virgem, Vila Nova de Gaia, Portugal

Do you want to know what is an Niche Model and how to calculate it? Do you want to use ecological niche models to support a species' description? Or to evaluate niche conservatism inside a taxonomical group? This course will teach you the base theory of ecological niche modelling and its main methodologies. By the end of this 5-day practical course, you will have the capacity to perform ecological niche models and understand their results. You will be able to choose and apply the correct methodology depending in the aim of your study and type of datasets.

This course is orientated to PhD and MSc students, as well as other students and researchers working on biogeography, evolutionary biology, systematists, or related disciplines. Participants will receive a diploma of course attendance, copies of presentations and materials used, one selection of the most relevant articles on Niche Modelling, and a copy of programs and other tools used in the course.

The course will be mainly practical, with some theoretical lectures. All modelling processes and calculations will be performed with R, the free software environment for statistical computing and graphics (http://www.r-project.org/). Students will learn to use modelling algorithms like Maxent, Bioclim, Domain, and logistic regressions, and R packages for computing ENMs like Dismo and Biomod2. Also, students will learn to compare different ecological niche models with Ecospat package.

** Recommended Background Basic knowledge in Geographical Information Systems and R statistical package is necessary.

** Course Format The first course day will be mainly theoretical. The following days will be mainly practical with some short theoretical presentations. The course will be lectured in English.

** Lecturer Neftali Sillero Assistant Researcher Centro de Investigac,ao em Ciencias Geo-Espaciais (CICGE), Faculdade de Ciencias, Universidade do Porto

** Course Information and Registration On *l* y 24 inscriptions! The registration fee is 150EUR. Registration deadline: 1/7/2016. Students must bring their own laptops!

Dates: 18-22 July 2015. Venue: Observatorio Astronomico Prof. Manuel de Barros, Alameda do Monte da Virgem, Vila Nova de Gaia (Portugal). https://goo.gl/maps/Xaxfe ** More information in: https://www.facebook.com/pages/Introduction-to- Ecological-Niche-Modelling/359229247606906 https://sites.google.com/site/neftalisillero/Home/enm-course – Neftali Sillero

Assistant Researcher https://sites.google.com/site/neftalisillero/ https://scholar.google.pt/citations?user=yJHOX7IAAAAJ&hl=en http://na2re.ismai.pt/ neftali.sillero@gmail.com

CICGE: Centro de Investigac,ao em Ciencias Geo-Espaciais Faculdade de Ciencias da Universidade do Porto Observatorio Astronomico Prof. Manuel de Barros Alameda do Monte da Virgem 4430-146 Vila Nova de Gaia, Portugal

Life is too short to eat bad chocolate

Neftalí Sillero <neftali.sillero@gmail.com>

Scotland GeneticDataAnalysis Exploration Aug16-20

“Genetic data analysis/exploration using R”

Delivered by Dr. Thibaut Jombart

http://prstatistics.com/course/genetic-data-analysis-using-r-gdar/ This course will run from 16th - 20th August, Millport Field Station, Ilse of Cumbrae, Scotland

This course will provide an extensive overview of exploratory methods for the analysis of genetic data using the R software and aim to equip participants with powerful resources for tackling increasingly common challenges in genetic data analysis. It is aimed at PhD students, research postgraduates, and practicing academics as well as persons in industry working with genetic data in fields such as molecular ecology, evolutionary biology, and phylogenetics. This course will provide a comprehensive introduction to various statistical approaches for the analysis of genetic data.

Course content is as follows

Day 1 Introduction to phylogenetic reconstruction

- Lecture 1a: Reconstructing phylogenies from genetic sequence data. Three main approaches covered: distance-based phylogenies; maximum parsimony; and likelihood-based approaches.

- Lecture 1b: Short R refresher.

- Practical 1: Phylogenetic reconstruction using R. Three main approaches plus rooting a tree; assessing/testing for a molecular clock; and bootstrapping.

Main packages: ape, phangorn.

Day 2 Introduction to multivariate analysis of genetic data

- Lecture 2: Key concepts in multivariate analysis. Focus on using factorial methods for genetic data analysis.

- Practical 2: Basics of multivariate analysis of genetic data in R. Topics include: data handling, population genetic tests of population structure (PCA, PCoA).

Main packages: adegenet, ade4, ape.

Day 3 Exploring group diversity

- Lecture 3: Approaches to identifying and describing genetic clusters. Topics include: hierarchical clustering, K-means, population-level multivariate analysis (between-group-PCA, DA, DAPC).

- Practical 3: Applying the approaches covered in morning lecture and emphasising their strengths and weaknesses.

Main packages: adegenet, ade4.

Day 4 Spatial genetic structure

- Lecture 4: Discussing the origin and significance of spatial genetic patterns, and how to test or them.

- Practical 4: Visualising and analysing spatial genetic data. Topics: spatial density estimates, Moran/Mantel tests, mapping principal components in PCA, spatial PCA.

- Main packages: adegenet, glmnet.

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Day 5 Using R for reproducible science

- Lecture 5: Using R for reproducible science.

- Practical 5: Practical session based on morning lecture

- Main packages: knitr, Sweave, rmarkdown

- Option to discuss own data (time permitting)

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

ADVANCING IN STATISTICAL MODELLING USING R (May)

TIMES SERIES DATA ANALYSIS FOR ECOLOGISTS AND CLIMATOLOGISTS (May)

INTRODUCTION TO PYTHON FOR BIOLOGISTS (May)

ADVANCES IN SPATIAL ANALYSIS OF MULTIVARIATE ECOLOGICAL DATA (July)

ADVANCES IN DNA TAXONOMY USING R (August)

INTRODUCTION TO BIOINFORMAITCS USING LINUX (August)

INTRODUCTION TO BAYESIAN HIERARCHICAL MODELLING (August)

MODEL BASED MULTIVARIATE ANALYSIS OF ECOLOGICAL DATA USING R (October)

LANDSCAPE (POPULATION) GENETIC DATA ANALYSIS USING R (October)

APPLIED BAYESIAN MODELLING FOR ECOLOGISTS AND EPIDEMIOLOGISTS (October)

PHYLOGENETIC DATA ANALYSIS USING R (November)

SPATIAL ANALYSIS OF ECOLOGIC AL DATA USING R (November)

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

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PR˜Statistics

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SimBioQUBES FacultyMentoring

SimBio (http://simbio.com) and the Quantitative Undergraduate Biology Education and Synthesis (QUBES) project invite applications for a Faculty Mentoring Network (FMN) focused on using SimBio's SimUText Ecology as a platform to incorporate more active learning into ecology courses. Participants in this FMN will each pick two SimBio chapters to implement in their course, and will work together with SimBio authors to develop and implement in-class activities to accompany those chapters with the goal of providing increased active-learning opportunities to their students.

The FMN will have two main objectives:

1. To develop, localize, and test in-class activities for ecology classes that can be shared with other faculty, and

2. To promote group-learning and sharing around implementation strategies for the in-class activities.

The Faculty Mentoring Network is a mentored, long-term community interaction on the QUBES site. The group will begin working online in July, with a set of three online two hour meetings. Applicants must be teaching ecology or an equivalent course in Fall 2016 and be able to commit to 1-2 hours per week, including online meetings. Participants will receive a stipend for participation. Upon completion of the Faculty Mentoring Network participants will post their materials and teaching guidelines for sharing with other ecology faculty.

SimBio will be hosting 20-30 minute webinar sessions at the following times to discuss the FMN project with instructors who may be interested in participating:

-Friday April 8th @ 9am pacific, 10am mountain, 11am central, 12pm eastern

-Friday April 8th @ 11am pacific, 12pm mountain, 1pm central, 2pm eastern

-Friday April 15th @ 10am pacific, 11am mountain, 12pm central, 1pm eastern

Please visit http://simbio.com/simutext-ecology-FMN to register for a session or https://qubeshub.org/groups/simbiofmn for more information.

Questions? Contact Eli Meir (emeir@simbio.com) or Alison Hale (anm116@pitt.edu)

“Hale, Alison Nicole” <anm116@pitt.edu>

Toronto MappingGenomicFeaturesClinicalTraits Jul18-Jul19

Canadian Bioinformatics Workshops present: Next Generation Methods for Mapping Genomics Features and Clinical Traits

Course Dates: July 18 - 19

Instructors: Philip Awadalla (Ontario Institute for Cancer Research) and Stephen Montgomery (Standford University)

Location: Downtown Toronto, ON

Registration: https://bioinformatics.ca/workshops/2016/next-generation-methods-mapping-genomic-features-and-clinical-traits-2016 This 2 day workshop focuses on the genetics and analysis of genomes and quantitative traits in human populations, with emphasis on population genetic inference, genetic mapping, estimation and prediction analysis of discrete (diseases) and quantitative traits using genomic resources. Principles and pitfalls of prediction analyses using genetic markers and eQTL mapping will also be discussed.

Participants will gain practical experience and skills to be able to:

* Estimate population genetic parameters using partial or whole-genome data * Infer relatedness from genomic data * Evaluate GWAS data for quantitative traits * Use GWAS data to estimate and partition genetic variance * Infer Gene x Environment interactions using multi-omic approaches (eg. eQTL mapping)

Course Outline

Day 1

Module 1 - Concepts in Population Genomics (2016)

Basic concepts in population genomics (drift, structure, inbreeding) Parametric and Non-parametric Inference in population genetics for inferences of mutation

Lab Practical: The following lab exercises will be done in R

Hapmap/genotyping data vs. whole genome/sequencing data Simulations V coalescent, forward simulations MCMC V extensions of the coalescent, capturing and estimating mutation and recombination events/rates

Module 2 - Extensions in Population Genomics (2016)

The coalescent Extensions of the coalescent including inferences of recombination and population structure

Module 3 - QTLs (2016)

Basic concepts in QTL mapping in inbred populations and outbred populations Linkage analysis for quantitative traits

Lab Practical:

Principals of linkage analyses (PLINK, Merlin) Analytical treatment of discrete (binary) outcome data versus continuous data

Day 2

Module 4 - More QTLs (2016)

Whole genome linkage analysis GWAS for quantitative traits Imputation

Lab Practical:

GCTA, Replication and Multiple testing correction Covariates and relatedness

Module 5 - Gene x Environment (2016)

Basic concepts in gene expression analysis: RNAseq, eQTLs inferences Integrating phenotypic and environmental data

Module 6 - Functional Annotation of Mutations & Haplotypes (2016)

Impact of selection and disease on mutations Classical approaches to mapping mutations and genes under selection or potentially damaging/associated with disease Constraint and selection,- polyphen, SIFT, GERP, etc.

Lab Practical:

Modeling dominance and functional impact Inferences using whole genome data of constraint Simulations and analyses of mutation trajectories and impact on linked loci

Registration and Travel awards available.

Ann Meyer <Ann.Meyer@oicr.on.ca>

UTennessee Knoxville NIMBioSTutorial EvolQuantGenetics Aug8-12

Please spread this announcement to colleagues:

NIMBioS Tutorial Evolutionary Quantitative Genetics 2016 Meeting dates: August 8-12, 2016 Location: NIMBioS at the University of Tennessee, Knoxville Organizers: Stevan J. Arnold, Integrative Biology, Oregon State Univ.

Joe Felsenstein, Genome Sciences, Univ. of Washington, Seattle Objectives: This tutorial will review the basics of theory in the field of evolutionary quantitative genetics and its connections to evolution observed at various time scales. Quantitative genetics deals with the inheritance of measurements of traits that are affected by many genes.

Quantitative genetic theory for natural populations was developed considerably in the period from 1970 to 1990 and up to the present, and it has been applied to a wide range of phenomena including the evolution of differences between the sexes, sexual preferences, life history traits, plasticity of traits, as well as the evolution of body size and other morphological measurements. Textbooks have not kept pace with these developments, and currently few universities offer courses in this subject aimed at evolutionary biologists. There is a need for evolutionary biologists to understand this field because of the ability to collect large amounts of data by computer, the development of statistical methods for changes of traits on evolutionary trees and for changes in a single species through time, and the realization that quantitative characters will not soon be fully explained by genomics.

This tutorial aims to fill this need by reviewing basic aspects of theory and illustrating how that theory can be tested with data, both from single species and with multiple-species phylogenies. Participants will learn to use R, an open-source statistical programming language, to build and test evolutionary models. The intended participants for this tutorial are graduate students, postdocs, and junior faculty members in evolutionary biology.

The content of this tutorial will be similar to the tutorial held at NIMBioS in 2015.

For general information, access the web page of the tutorial at this address: http://www.nimbios.org/tutorials/-TT_eqg2016 Co-sponsor: American Society of Naturalists Instructors: Stevan J. Arnold, Integrative Biology, Oregon State Univ. Marguerite Butler, Department of Zoology, Univ. Hawaii Patrick Carter, Evolutionary Physiology, Washington State Univ., Pullman Joe Felsenstein (by video link), Genome Sciences, Univ. of Washington, Seattle Adam Jones, Biology, Texas A&M Univ. Emilia Martins, Biology, Indiana Univ., Bloomington Brian O'Meara, Ecology & Evolutionary Biology, Univ. of Tennessee Patrick Phillips, Institute of Ecology and Evolution, Univ. of Oregon Josef Uyeda, Bioinformatics and Evolutionary Studies, Univ. of Idaho, Moscow

A descriptive flyer can be accessed at this address: http://www.nimbios.org/ifiles/TT_eqg2015_flyer.pdf Application deadline: May 1, 2016 To apply, you must complete an application on our online registration system:

Use this link to access the system: https://-adnimb.nimbios.org/pages/home Login or register Complete your user profile (if you haven't already) Find this tutorial event under Current Events Open for Application and click on Apply

Food and lodging. Breakfast and lunch will be provided at NIMBioS each day of the tutorial, as well as coffee and mid-morning and mid-afternoon snacks. NIMBioS is not covering dinner, travel, or lodging expenses for participants. A block of rooms at a group rate will be reserved at the Four Points by Sheraton Knoxville Cumberland House Hotel. More information will be available here soon about room rates and how participants can make reservations.

Joe Felsenstein <joe@gs.washington.edu>

Vairao Portugal Speciation May9-13

This advanced course has as main goals to:

1) (re-)introduce the students to some of the canonical literature concerning the process of speciation; and

2) discuss the paradigm of divergence-with-gene-flow represented by the web-of-life metaphor.

The second goal will be accomplished by discussion sections using Mike's new book (Arnold, M.L. 2016. Divergence With Genetic Exchange. Oxford University Press), as a distillation of many studies of natural hybridization, lateral exchange and viral recombination.

Click here to see the PROGRAMME for the course.

INTENDED AUDIENCE This course will be open to a maximum number of 20 participants.

Priority will be given to:

- 1st year PhD students attending the BIODIV Doctoral Programme;

- other BIODIV PhD students;

- PhD students attending other courses;

- other post-graduate students and researchers.

REGISTRATION Registration deadline: April 12, 2016.

Participation is free of charge for BIODIV students | Registration fee for other participants: euro 150,00. To register, please send an e-mail accompanied by a short CV to Maria Sant'Ana at post.graduation@cibio.up.pt. Please refer your status (PhD student, MSc Student, Other) and the University to which you are affiliated.

For more information about the course, please contact: post.graduation@cibio.up.pt.

CIBIO - Centro de Investigacao em Biodiversidade e Recursos Geneticos

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Zagori Greece ConservationBiology Jun27-Jul8

8th Greek Summer School in Conservation Biology - Biodiversity Theory and Practice - Zagori, Greece, 27 June to 8 July, 2016

This international course which is held under the aegis of SCB-Europe (Society for Conservation Biology) and of HELECOS (the Hellenic Ecological Society) aims to equip participants with an understanding of the principles of modern biodiversity theory and its role in Conservation Biology. They will learn practical skills for biodiversity fieldwork including sampling design and monitoring. Students will learn how to analyze ecological data with R using some of the main packages for biodiversity data analysis and have the opportunity to try these out on their own datasets.

Further details can be found on the website: http://gss.bat.uoi.gr/ Application deadline: 22 April 2016

– Dr. Martin Wiemers Department of Community Ecology Helmholtz Centre for Environmental Research - UFZ Theodor-Lieser-Str. 4 06120 Halle Germany Tel. +49 345 558-5322 e-mail: martin.wiemers@ufz.de http://www.ufz.de/index.php?en=31235 Martin Wiemers <martin.wiemers@univie.ac.at>

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.