EvolDir

March 1, 2015

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

Asilomar ASN Jan10-14 SympCall

The American Society of Naturalists Call for Symposia ASN meeting at Asilomar, California 10-14 Jan 2016

A stand-alone meeting of ASN will be held at Asilomar in Monterey, California 10-14 January 2016. The Executive Council of the Society invites proposals for two half-day symposia to be held at the meeting.

Proposals should include (1) a title; (2) a description of the symposium topic (one page); (3) a tentative list of six speakers, including institutional affiliations; (4) a justification for the symposium explaining why the topic and speakers are appropriate for an ASN meeting, keeping in mind the broader goals of the society (http://www.amnat.org/about/about-the-society.html); and (5) a statement that all proposed invited speakers have agreed to participate.

Proposals must be submitted by midnight Eastern Standard Time on March 31, 2015 by email (jessica.gurevitch@stonybrook.edu) as a single pdf attachment, under subject heading: ASN Asilomar Symposium Proposal. Proposals that include women, young investigators and individuals from underrepresented groups are especially encouraged.

Please note that as with the 2014 Asilomar meeting, ASN does not have funding allocated to support these symposia, although there may be opportunities to seek external symposium funding. Speakers should assume that they are likely to have to cover their own travel costs.

The Society's selection committee will evaluate proposals based on the likelihood of attracting a substantial audience, the significance and timeliness of the topic, and on it being substantively different from recent symposia sponsored by the Society. All applicants will be notified of the decision by late April 2015.

< http://twitter.com/SnellRoodLab >

emilies@umn.edu

Bainbridge WA ChromosomeEvolution Awards

Student travel awards are available for the American Genetic Association 2015 meeting, Chromosome Evolution: Molecular Mechanisms and Evolutionary Consequences (http://www.theaga.org), to be held at IslandWood http://islandwood.org/ on Bainbridge Island near Seattle, WA.

Awards will cover registration, room and board for graduate students who would like to attend the meeting and present a poster. Applicants should submit a PDF of their poster abstract (see template at http://www.theaga.org) and have their PhD advisor submit a letter describing their qualifications, research progress, and the availability of funds for the student to attend the meeting.

Email the abstract and the letter to Anjanette Baker (AGAJOH@oregonstate.edu) by March 15, 2015. Decisions will be made before general registration opens for the meeting on April 1, 2015.

AGAJOH@oregonstate.edu

Cairns GeneticsBehaviour Aug9-14

Conference: Cairns_Australia.GeneticsBehaviourInvasion.Aug9-14

Have you heard that Behaviour 2015 (www.behaviour2015.org) will be held in Cairns, Australia and will combine meetings of the International Ethological Conference, the Australasian Society for the Study of Animal Behaviour, Australasian Evolution Society, and Australasia, New Zealand and Africa Region of Applied Ethology?

We are hosting a symposium on ?Genetic and epigenetic drivers of behaviours influencing invasiveness and native species response to invaders?. Abstracts are due on March 16th.

Description: Invasive species are a major and increasing environmental challenge worldwide, threatening biodiversity and causing substantial economic damage. Behaviours such as the long-distance dispersal or boldness have a direct impact on an organism?s ability to become a successful invader, while native species often have to evolve novel response to deal with invasive species. However, the genetic and epigenetic bases of these traits remain poorly understood. We propose a symposium to showcase emerging studies of behaviours that influence invasiveness, and the response of native species to exotic species, with a particular emphasis on the genetics and/or epigenetics underlying these behaviours.

Please consider attending Behaviour 2015 and selecting our symposium if you have a relevant abstract for this topic. We hope to see you there!

Dr. Lee Ann Rollins and Dr. Craig Sherman Centre for Integrative Ecology Deakin University Australia Lee.rollins@deakin.edu.au

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Lee Rollins <lee.rollins@deakin.edu.au>

Calgary Canada ComparativeMorphologyDev May25-29

The Comparative Morphology & Development (CMD) section of the Canadian Society of Zoologists (CSZ) invites you to attend the following symposia at the annual CSZ meeting:

May 25-29, 2015, in CALGARY, ALBERTA; GATEWAY TO THE CANADIAN ROCKIES

MAIN SYMPOSIUM: “Ten Years of the Triple Helix: Development, Morphology, Evolution” (May 27, 2015) (Celebrating the 10th anniversary of the founding of the CMD section)

JEAN BERNARD CARON (Royal Ontario Musuem) “Early body plan evolution and the Burgess Shale menagerie”

SALLY LEYS (Alberta) “Complexity and loss of complexity in the evolution of early metazoan body plans”

TIM HIGHAM (UC Riverside) “Morphological complexity and functional integration: New angles in biomechanics”

[organized by Rich Palmer, University of Alberta]

RUSSELL SYMPOSIUM: “From head to toe: Integrative vertebrate morphology and evolution” (May 26, 2015) (A symposium honouring Tony Russell’s many contributions to Zoology)

ANTHONY RUSSELL (Calgary) “Back to basics: The origin of adhesion in geckos”

MATTHEW VICKARYOUS (Guelph) “Scar-free wound healing and regeneration: Coordinating cells and environment”

AARON BAUER (Villanova) “Size, shape, function and phylogeny: Evolutionary diversity in the gekkotan skull”

HILLARY MADDIN (Carleton) “Re-evaluation of the homology of the bones of the tetrapod cranial vault”

[organized by Tim Higham, UC Riverside]

STUDENT SATELLITE SYMPOSIUM: “Techniques and technologies for better visualizing and quantifying morphology and development” (May 27, 2015)

Lead speaker: HEATHER JAMNICZKY (Calgary) “Considering the WHOLE phenotype: Emerging approaches to 3D quantitative morphology in eco-evo-devo”

[organized by U Calgary graduate students: Larry Powell, Ramon Nagesan, Leah Sparrow, Matthew Szostakiwskyj, Alexander Tinius]

FOR MORE DETAILS ABOUT THESE SYMPOSIA, SEE:

http://www.biology.ualberta.ca/CMD/home.htm TO REGISTER, OR TO LEARN MORE ABOUT THE CSZ ANNUAL MEETING, SEE:

http://ucalgary.ca/csz2015/ EARLY REGISTRATION DEADLINE: Friday, March 6, 2015

CONTRIBUTED PAPERS: Spaces are also available for contributed papers in sessions organized by the CMD section. The deadline for submitting abstracts is barely 10 days away, so don’t delay:

ABSTRACT SUBMISSION DEADLINE: Friday, March 6, 2015

FINAL REGISTRATION DEADLINE: Friday, May 1, 2015

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A. Richard Palmer, FRSC Systematics and Evolution Group Department of Biological Sciences University of Alberta Edmonton, Alberta T6G 2E9 CANADA phone: (780) 492-3633 message: (780) 492-3308 FAX: (780) 492-9234 http://www.biology.ualberta.ca/palmer/palmer.html Secretary-General Comparative Morphology & Development section Canadian Society of Zoologists: http://www.biology.ualberta.ca/CMD/home.htm rich.palmer@ualberta.ca

Cambridge EvolutionaryGeneticsGenomics Mar17

The 2015 Evolutionary Genetics & Genomics Symposium (EGGS), a Genetics Society (http://www.genetics.org.uk/) sponsored sectional interest group will be taking place in Cambridge (UK) on Tuesday 17th March 2015. The meeting is free to attend and no registration is required. The meeting aims to bring together people working on various aspects of evolutionary genetics, and has previously attracted an international line up of speakers and attendees.

We have three invited speakers:

-Josephine Pemberton, University of Edinburgh http://pemberton.bio.ed.ac.uk/josephine-pemberton -Nathan Bailey, University of St Andrews http://www.flexiblephenotype.org/ -Aoife McLysaght, University of Dublin http://www.gen.tcd.ie/molevol/ Abstract registration for talks closes in a few weeks-please email your name, institution, position (student/postdoc/PI) and abstract by the 19th Feb 2015 to eggs.symp@gmail.com

Full details can be found on the meeting website: http://www.evolutionarygenetics.group.cam.ac.uk/eggs/ eggs.symp@gmail.com

Cambridge VolvoxEvolution Aug19-22

Hello evoldir community,

Registration for the third International Volvox Conference (August 19-22, CMS, Cambridge, UK) as well as abstract submission for posters and oral presentations are now open! Focusing on the green alga Volvox and its close relatives, this conference revolves around an important model system for the evolution of multicellularity, development, and cellular differentiation.

Conference website: http://www.damtp.cam.ac.uk/-user/ah659/volvoxindex.html Registration deadline: May 15, 2015

Abstract deadline: June 15, 2015

Conference highlights: - Talks and posters on the taxonomy, ecology, development, genetics/genomics, biophysics, and evolution of Volvox and its relatives - Punting along the river Cam - Field-trip and excursion - Affordable registration (Â£250 regular, Â£180 student, includes accommodation and meals)

Thank you!

Erik R Hanschen PhD Candidate, Michod Lab Department of Ecology and Evolutionary Biology University of Arizona

http://www.eebweb.arizona.edu/grads/hanschen "Our truth is the intersection of independent lies." - Richard Levins 1966

hanschen@email.arizona.edu

Chicago Astrobiology Jun15-19

Dear colleagues,

The Astrobiology Science Conference 2015 (AbSciCon 2015) is taking place in Chicago, IL from *June 15-19, 2015*. The conference will convene scientists from all over the world who work in the interdisciplinary field of astrobiology â the study of the origin, evolution, distribution, and future of life in the universe â to report on research findings and plan future endeavors. The theme for AbSciCon2015 is "Habitability, Habitable Worlds, and Life." For more information on the purpose and scope of the conference, *click here* < http://www.hou.usra.edu/meetings/abscicon2015/-about/purpose/ >.

We invite abstract submissions to session titled "Chance and Necessity: >From Molecules and Viruses to Cells and Populations". Researches wishing to submit abstracts should do so through the *AbSciCon 2015 website* < http://www.hou.usra.edu/meetings/-abscicon2015/ >. The deadline for abstract submission is *March 4, 2015.* Please contact session organizers for your specific questions or concerns.

Summary: Scientists have limited means with which to infer the exact evolutionary events that occurred to produce contemporary living systems. This historical limitation obscures our ability to confidently assess the relative impacts of chance and necessity upon life's origins and subsequent radiation across Earth. Are the evolutionary paths of living systems inherently random and subject to completely different outcomes if repeated under identical initial conditions? Or are the shapes of these paths predominantly constrained by internal or external controlled processes? This session will focus on inferring how evolutionary mechanisms such as chance events, population bottlenecks, genetic drift, the virus-host arms race, or environmental selection pressure affect evolutionary outcomes at the level of nucleic acids, proteins, viruses, cells, and populations. We invite studies that include perspectives from nucleic acid or protein evolution, virology, bioinformatics, molecular and synthetic biology, and culture-based analyses, with the common goal of elucidating the evolutionary mechanisms of life at both the molecular and population levels. By exploring the molecular mechanisms that led to life, as we now know it, we ultimately hope to arrive at a better understanding of why life on Earth is the way it is and how it may have developed elsewhere. This session is co-organized by Betul Kacar (NASA Postdoctoral Program/Harvard University), Rika Anderson (NASA Postdoctoral Program/University of Illinois at Urbana-Champaign), Jim Cleaves (Earth Life Science Institute), Gustavo Caetano-Anolles (University of Illinois at Urbana-Champaign), and Ken Stedman (Portland State University).

Betül Kacar <betulkcr@gmail.com>

Guaruja Brazil Evolution Jun26-30 MinorityTravelAward

Evolution 2015 (Brazil) - Minority Graduate Student Travel Award

The National Evolutionary Synthesis Center (NESCent) and the Society for the Study of Evolution (SSE), are teaming up to provide airfare and conference registration for minority graduate students attending the Evolution 2015 conference in Guarujá, São Paulo, Brazil from June 26-30, 2015. Please note that all other expenses (food, lodging, ground transportation, costs associated with visa procurement) are the responsibility of the traveler.

Applicants must be graduate students at the time of the conference (June 26-30, 2015), working towards a Masters or PhD in evolutionary science, evolutionary ecology, biogeography, evolutionary informatics, evolution education or some other field appropriate for the focus of the Evolution 2015 conference (http://www.evolution2015.org < http://www.google.com/url?q=http%3A%2F%2Fwww.evolution2015.org&sa=D&sntz=1&usg=AFQjCNHqYIKUOlFYzJJKck1saTZys39aQg >).

Applicants must be members of under-represented/under-served racial/ethnic groups, as defined by the National Science Foundation (http://www.nsf.gov/statistics/wmpd/ < http://www.google.com/url?q=http%3A%2F%2Fwww.nsf.gov%2Fstatistics%2Fwmpd%2F&sa=D&sntz=1&usg=AFQjCNHsqWMdhCsH6w9Cj87FiK6RV_pIVA >).

Applicants must be US citizens, permanent residents, or foreign nationals currently enrolled in US-based graduate programs. All applicants must be free of any restrictions which would prevent them from traveling out of the US, to Brazil over the dates of the conference.

The application package consists of basic information, a one-page Statement of Academic Interests and Career Goals, a brief biosketch, and a Letter of Recommendation from your academic advisor.

APPLICATION DEADLINE: MARCH 15TH, 2015, 5:00 PM PST

AWARDS WIL BE ANNOUNCED BY MARCH 20TH, 2015

For more information and to apply, please visit http://bit.ly/16hefaq .If you have questions, please contact Jory Weintraub (jory@nescent.org).

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

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

Guaruja Brazil Evolution Jun26-30 MSI FacultyTravel

NESCent/SSE 2015 MSI Faculty Travel Award - Evolution 2015 (Brazil)

The National Evolutionary Synthesis Center (NESCent) and the Society for the Study of Evolution (SSE), are teaming up to provide airfare and conference registration for faculty from Minority Serving Institutions (MSIs) to attend the Evolution 2015 conference in Guarujá, São Paulo, Brazil from June 26-30, 2015. Please note that all other expenses (food, lodging, ground transportation, costs associated with visa procurement) are the responsibility of the traveler.

If you are a faculty member at an MSI, HBCU or other institution with significant enrollment of under-represented minority students, you are encouraged to apply.

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

Depending on your nationality and immigration status, A VISA MAY BE REQUIRED TO ENTER BRAZIL. More information can be found at the conference website (http://www.evolution2015.org < http://www.google.com/url?q=http%3A%2F%2Fwww.evolution2015.org&sa=D&sntz=1&usg=AFQjCNHqYIKUOlFYzJJKck1saTZys39aQg >). ALL AWARD RECIPIENTS ARE RESPONSIBLE FOR FOR OBTAINING AND PAYING FOR THEIR

OWN VISA, and the conference organizers advise that it could take up to a month (or possibly longer) to obtain a visa.

For more information, or to apply, please visit http://bit.ly/1vsYWYt. If you have any questions about this program, please contact Jory Weintraub (jory@nescent.org).

APPLICATION DEADLINE: MARCH 15TH, 2015, 5:00 PM PST

AWARDS WIL BE ANNOUNCED BY MARCH 20TH, 2015

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

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

Guaruja Brazil SocSystBiol Jun26 GradTravelAwards

The Society of Systematic Biologists (SSB) invites graduate students to apply for travel awards to attend a Model-based Molecular Systematics workshop on Friday, June 26 at Evolution meetings in Guaruja, Brazil. Taking place the day before the meeting starts, this workshop will feature two parallel sessions, one focused on phylogenetics and comparative methods and the other focused on phylogeography and ABC approaches. Instructors for the former include Stacey Smith, Tracy Heath, Samantha Price, and Matt Pennell. Instructors for the latter include Bryan Carstens, Manolo Perez, and Brian O’Meara. In addition, there will be a special session on open data access presented by Karen Cranston. With generous support from the National Science Foundation, SSB will provide awards of $1750 to support travel to this meeting for 20 graduate students. Applicants must be U.S. citizens to be eligible and underrepresented groups are particularly encouraged to apply. To apply, please go to the âhow to apply’ tab on the workshop website: http://2015nsfssbworkshop.weebly.com/ Applications are due by February 20th.

Bryan C. Carstens Department of Evolution, Ecology, & Organismal Biology The Ohio State University 318 W. 12th Avenue Columbus, OH 43210-1293

web: http://carstenslab.org.ohio-state.edu/OSU/-Carstens_Lab.html < http://carstenslab.org.ohio-state.edu/ > blog: https://u.osu.edu/carstens.12/ publications: http://carstenslab.org.ohio-state.edu/-OSU/Publications.html spedeSTEM: http://-spedestem.asc.ohio-state.edu/ skype: bryan_carstens office: 614.292.6587 cell: 734.474.8527 fax: 614.292.2030

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

KansasStateU ArthropodGenomics Jun17-19 RegistrationOpen

Registration is now OPEN for the Arthropod Genomics Symposium and IGT-RCN Workshop!

--*-*-* Ninth Annual Arthropod Genomics Symposium*-*-*-*-*- June 17, 2015 to June 19, 2015 K-State Alumni Center, Kansas State University Manhattan, Kansas

REGISTRATION Please register online at the Symposium website, www.ksu.edu/agc! ABSTRACT DEADLINES IN 2015: Monday, March 9 V If you DO wish your abstract to be considered for an oral presentation/General Session talk.

Wednesday, May 20 - If you do NOT wish for your poster abstract to be considered for oral presentation and DO want to present a poster.

SPEAKERS Keynote Speaker: David A. OBrochta, Institute for Bioscience and Biotechnology Research & Department of Entomology, University of Maryland College Park

Featured Speakers: + Michelle Cilia, USDA-ARS, Boyce Thompson Institute for Plant Research, Cornell University, USA + Martin J. Donnelly, Liverpool School of Tropical Medicine and the Wellcome Trust Sanger Institute, UK + Rosemary G. Gillespie, University of California, Berkeley, USA + Sijun Liu, Iowa State University, USA + Frank Lyko, German Cancer Research Center, Heidelberg, Germany + Duane McKenna, University of Memphis, USA + Armin P. Moczek, Indiana University, USA + Amanda J. Moehring, Western University, Ontario, Canada + Daniel E. Neafsey, Broad Institute of MIT and Harvard University, USA + Greg Ragland, Kansas State University, USA + Anne-Nathalie Volkoff, INRA (UMR1333), Montpellier 1 University, France

The symposium focuses on new insights gleaned from analyzing arthropod genomes and is designed for scientists interested in genomic studies of Arthropods, both model organisms and those of agricultural or health relevance. The program will include platform presentations, a welcome reception, a gene annotation workshop using WebApollo and arthropod genomics-related poster sessions. A few poster abstract submissions will be selected for platform presentations. Postdoctoral, graduate, and undergraduate students are also encouraged to attend. Sessions conclude Friday evening, followed by an optional evening meal.

--*-*-* Pre-Symposium Workshop *-*-*-*-*- INSECT GENETIC TECHNOLOGY workshop June 17, 2015 (Wednesday morning and afternoon) Robust protocols to manipulate genes and genomes have not yet been developed for most insects other than Drosophila melanogaster, and this shortfall is limiting research progress in many aspects of arthropod genomics. The NSF-RCN on Insect Genetic Technologies (IGTRCN: 2014-2019; igtrcn.org) seeks to remedy this problem by facilitating the communication of best practice and new techniques among arthropod genomicists.

This IGTRCN-sponsored workshop will comprise (1) talks that showcase the latest genetic technologies, (2) discussion sessions for exchange of ideas and solutions for effective insect genetic engineering, and (3) posters. Proposals from the workshop will be integrated into the IGTRCN program of hands-on practical workshops, fellowships, and the IGTRCN KnowledgeBase. Early-career researchers are particularly encouraged to present their research at this workshop. A limited number of travel grants to attend the workshop are available for early stage investigators. Additional information on poster abstract and travel grant submission for the workshop will be posted soon on the Workshop link < http://www.k-state.edu/agc/symposium_level/workshop/index.html > of the symposium website.

TENTATIVE PROGRAM for SYMPOSIUM & WORKSHOP Wednesday, June 17 V Workshop: Insect Genetic Technology Research Coordination Network (IGT-RCN)

Wednesday evening, June 17, 7:30 pm - Arthropod Genomics Symposium begins with keynote presentation and welcome reception

Thursday, June 18 V Symposium Platform and Poster Sessions

Thursday evening, June 18, 7:00 to 9:00 pm V Workshop: Gene Annotation using WebApollo

Friday, June 19 V Symposium Platform and Poster Sessions, tentatively concluding at 5:00 pm

Friday evening, June 19 V Optional dinner at Konza Prairie Biological Station < http://kpbs.konza.k-state.edu/ > with nature hikes, bison viewing, and opportunity to collect insects.

VENUE: The 2015 Symposium is being hosted by the Arthropod Genomics Center at Kansas State University in Manhattan, Kansas. Symposium sessions will be held at the K-State Alumni Center on campus.

HOTEL/DORM ROOMS: A block of rooms has been reserved at the Holiday Inn Manhattan at the Campus. Reservation deadline for the room block discounted price is May 20. Campus dormitory rooms will also be available.

QUESTIONS: Contact Doris Merrill at dmerrill@ksu.edu.

If you would like to join the ArthropodNews to ensure receiving future notices, please send an e-mail with your name and e-mail address to dmerrill@ksu.edu.

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London StudentQuantitativeGenomics May29

Quantitative Genomics 2015

Friday 29 May 2015

Wellcome Trust Headquarters, London

We are excited to announce Quantitative Genomics 2015 (QG15), a conference for students in quantitative genomics that will take place on Friday 29th of May at the Wellcome Trust Headquarters at Euston square in the very heart of London.

The conference will focus on giving early-career researchers (Master's and PhD students) working at the forefront of mathematical and quantitative genomics a chance to present their work and learn from their peers. The conference will feature talks by Professor Brian Charlesworth < http://en.wikipedia.org/wiki/Brian_Charlesworth > from the University of Edinburgh and Nicole Soranzo < https://www.sanger.ac.uk/research/faculty/nsoranzo/ > from the Wellcome Trust Sanger Institute. Our renowned speakers represent the two sides of the spectrum of topics QG15 aims for:

from evolutionary theory and mathematical models to new omics tools applied in biomedical research. It will provide an ideal opportunity to build international networks with current and future leaders in the field in an informal and relaxed environment. Registration costs have been kept to a minimum to ensure that QG15 is accessible to all interested students.

Please refer to the QG15 website < http://-quantgen.soc.srcf.net/qg15/ > for more information and do not hesitate to contact us for further information (quantgen@damtp.cam.ac.uk). We encourage you to pre-register (open now < http://quantgen.soc.srcf.net/-qg15/sign-up/pre-registration/ >) so we can keep you updated regarding deadlines and steps for abstract submission and registration.

We hope to see you in London,

QG15 Organising Committee

Kaur Alasoo - PhD in Computational Biology, Wellcome Trust Sanger Institute/University of Cambridge, Cambridge, UK-

Rajbir Batra - Wellcome Trust PhD in Mathematical Genomics and Medicine, Cancer Research UK Cambridge Institute/University of Cambridge, Cambridge, UK-

Moises Exposito-Alonso -PhD in Evolutionary Genomics; Max Planck Institute,T^{1}bingen Germany-

Tiphaine Martin - DPhil in Genetics and Molecular Medicine; Kings College London, London, UK-

Hannah Meyer - PhD in Bioinformatics, EBI/University of Cambridge, Cambridge, UK-

Sarah Morgan - PhD in Genetics of Neurodegeneration using Next-Generation Sequencing, University College London, London, UK-

Matthias Thurner - DPhil in Genomic Medicine and Statistics, University of Oxford, Oxford, UK-

– Moises Exposito-Alonso

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Moiss Expsito Alonso <moisesexpositoalonso@gmail.com>

MexicoCity ComputBiolAlgorithms Aug4-6

2nd INTERNATIONAL CONFERENCE ON ALGORITHMS FOR COMPUTATIONAL BIOLOGY

AlCoB 2015

Mexico City, Mexico

August 4-6, 2015

Organized by:

Centre for Complexity Sciences (C3) School of Sciences Institute for Research in Applied Mathematics and Systems (IIMAS) Graduate Program in Computing Science and Engineering National Autonomous University of Mexico

Research Group on Mathematical Linguistics (GRLMC) Rovira i Virgili University

http://grammars.grlmc.com/alcob2015/ AIMS:

AlCoB aims at promoting and displaying excellent research using string and graph algorithms and combinatorial optimization to deal with problems in biological sequence analysis, genome rearrangement, evolutionary trees, and structure prediction.

The conference will address several of the current challenges in computational biology by investigating algorithms aimed at: 1) assembling sequence reads into a complete genome, 2) identifying gene structures in the genome, 3) recognizing regulatory motifs, 4) aligning nucleotides and comparing genomes, 5) reconstructing regulatory networks of genes, and 6) inferring the evolutionary phylogeny of species.

Particular focus will be put on methodology and significant room will be reserved to young scholars at the beginning of their career.

VENUE:

AlCoB 2015 will take place in Mexico City, the oldest capital city in the Americas and the largest Spanish-speaking city in the world. The venue will be the main campus of the National Autonomous University of Mexico.

SCOPE:

Topics of either theoretical or applied interest include, but are not limited to:

Exact sequence analysis Approximate sequence analysis Pairwise sequence alignment Multiple sequence alignment Sequence assembly Genome rearrangement Regulatory motif finding Phylogeny reconstruction Phylogeny comparison Structure prediction Compressive genomics Proteomics: molecular pathways, interaction networks ... Transcriptomics: splicing variants, isoform inference and quantification, differential analysis Next-generation sequencing: population genomics, metagenomics, metatranscriptomics ... Microbiome analysis Systems biology

STRUCTURE:

AlCoB 2015 will consist of:

invited lectures peer-reviewed contributions

INVITED SPEAKERS:

Julio Collado-Vides (National Autonomous University of Mexico, Cuernavaca), >From Curation of Information to Knowledge Encoding

Gaston Gonnet (Swiss Federal Institute of Technology, Zurich), Human-Dog-Mouse, Probably and Provable Non-trivial Evolution Close to the Root of the Mammalian Clade

Peter D. Karp (SRI International, Menlo Park), Algorithms for Metabolic Route Search and Determination of Reaction Atom Mappings

PROGRAMME COMMITTEE:

Stephen Altschul (National Center for Biotechnology Information, Bethesda, USA) Yurii Aulchenko (Russian Academy of Sciences, Novosibirsk, Russia) Pierre Baldi (University of California, Irvine, USA) Daniel G. Brown (University of Waterloo, Canada) Yuehui Chen (University of Jinan, China) Keith A. Crandall (George Washington University, Washington, USA) Joseph Felsenstein (University of Washington, Seattle, USA) Michael Galperin (National Center for Biotechnology Information, Bethesda, USA) Susumu Goto (Kyoto University, Japan) Igor Grigoriev (DOE Joint Genome Institute, Walnut Creek, USA) Martien Groenen (Wageningen University, The Netherlands) Yike Guo (Imperial College, London, UK) Javier Herrero (University College London, UK) Karsten Hokamp (Trinity College Dublin, Ireland) Hsuan-Cheng Huang (National Yang-Ming University, Taipei, Taiwan) Ian Korf (University of California, Davis, USA) Nikos Kyrpides (DOE Joint Genome Institute, Walnut Creek, USA) Mingyao Li (University of Pennsylvania, Philadelphia, USA) Yun Li (University of North Carolina, Chapel Hill, USA) Jun Liu (Harvard University, Cambridge, USA) Rodrigo López (European Bioinformatics Institute, Hinxton, UK) Andrei N. Lupas (Max Planck Institute for Developmental Biology, Tübingen, Germany) B.S. Manjunath (University of California, Santa Barbara, USA) Carlos Martín-Vide (chair, Rovira i Virgili University, Tarragona, Spain) Tarjei Mikkelsen (Broad Institute, Cambridge, USA) Henrik Nielsen (Technical University of Denmark, Lyngby, Denmark) Zemin Ning (Wellcome Trust Sanger Institute, Hinxton, UK) Christine Orengo (University College London, UK) Modesto Orozco (Institute for Research in Biomedicine, Barcelona, Spain) Christos A. Ouzounis (Centre for Research & Technology Hellas, Thessaloniki, Greece) Manuel Peitsch (Philip Morris International R&D, Neuchâtel, Switzerland) David A. Rosenblueth (National Autonomous University of Mexico, Mexico City, Mexico) Julio Rozas (University of Barcelona, Spain) Alessandro Sette (La Jolla Institute for Allergy and Immunology, USA) Peter F. Stadler (University of Leipzig, Germany) Guy Theraulaz (Paul Sabatier University, Toulouse, France) Alfonso Valencia (Spanish National Cancer Research Centre, Madrid, Spain)

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Montpellier CancerEvolution Mar19

< http://mike.hochberg.free.fr/ > *Evolution and Cancer conference - Montpellier, March 19th 2015*

Please join us at a one day conference on "Evolution and Cancer" at the Université de Montpellier 2. The conference is sponsored by the CNRS research consortium DarEvCan (http://www.darevcan.univ-montp2.fr/).

The objective of the conference is to foster discussion on evolutionary perspectives to understanding cancer emergence, progression and therapies. The conference will include speakers from the Centre for Evolution and Cancer (http://www.icr.ac.uk/news-features/latest-features/the-centre-for-evolution- and-cancer).

The preliminary programme can be found at this link:

Programme < http://www.darevcan.univ-montp2.fr/?page_id=221 >

If you wish to attend, then please register by email (please put: " Registration DarEvCan" in the subject header) to mhochber@univ-montp2.fr -* Registration closes on February 16th.*

Scientific committee: Pr Eric Solary (Institut Gustave Roussy), Pr. Ula Hibner (Institut de Génétique Moléculaire de Montpellier) and Pr. Michael Hochberg (Institut de Sciences de l'Evolution)

Michael Hochberg <mhochber@univ-montp2.fr>

RoyalSociety London DatingSpeciesDivergence Nov9-10

Dear All,

This meeting is free, but registration is required. Registration, at the web site, is now open. The scientific programme will be posted at the web site later.

best wishes,

ziheng yang

Royal Society discussion meeting "Dating species divergence using rocks and clocks" 9:00 am on Monday 09 November 2015 ' 5:00 pm on Tuesday 10 November 2015 at The Royal Society, 6-9 Carlton House Terrace, London

Organisers: Professor Ziheng Yang FRS, UCL, UK Professor Philip Donoghue, University of Bristol, UK

https://royalsociety.org/events/2015/11/dating-species-divergences/ The molecular clock hypothesis provides the only viable framework for integrating molecular sequence and fossil age data to establish an evolutionary timescale. However, even after five decades since its proposal, the hypothesis remains controversial. This meeting will bring together scientists from molecular systematics, palaeontology, comparative genomics, and computational biology to discuss recent breakthroughs in the field and highlight future research directions.

This event is intended for researchers in relevant fields and is free to attend. There are a limited number of places and registration is essential. An optional lunch is offered and should be booked during registration (all major credit cards accepted).

z.yang@ucl.ac.uk

Saskatoon CanSocEcolEvol May22-24

We invite you to the 10th Annual Meeting of the Canadian Society for Ecology and Evolution (CSEE) to be held in Saskatoon (SK, Canada)on 22-24 May 2015. This year, the theme of the conference is: 'Ecology and Evolution of Managed Landscapes'. We have an exciting program of symposia, invited speakers, and field trips. Please see the conference website for details: http://-csee2015.usask.ca/index.php. Conference registration and the call for presentations are now open. Early bird fees and the presentation call end March 15th!

Nous vous invitons à Saskatoon (SK, Canada), du 22 au 24 mai 2015 pour la 10e rencontre annuelle de la SCEE tenue par l'Université de la Saskatchewan. Cette année, le thème de la conférence est : ≪Ãcologie et évolution des paysages aménagés≫. Une gamme passionnante de symposia, conférenciers invités et excursions sur le terrain ont été organisés. Pour plus de détails, veuillez consulter le site internet de la conférence : http://-csee2015.usask.ca/fr/. L'inscription à la conférence et l'appel de présentations sont maintenant ouverts. Les frais d'inscription hÃtive et l'appel de présentations se terminent le 15 mars 2015!

Ciee Icee <Ciee-Icee@uregina.ca>

Scotland EMPSEB StudentEvolBiol Sep8-12

The 21st Meeting for PhD Students in Evolutionary Biology

Organized by the University of Edinburgh Location: University of Stirling - Stirling, UK Date: September 8-12th, 2015 Website: http://empseb21.bio.ed.ac.uk 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 8-10 senior scientists who are invited to give plenary talks, run discussion groups, and to provide guidance about starting your scientific career. 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: opening in spring (see updates on website)

Plenary Speakers: Rebecca Kilner, University of Cambridge Pat Monaghan, University of Glasgow Sasha Dall, University of Exeter Hannah Dugdale, University of Sheffield Jane Reid, University of Aberdeen Tiina Sarkinen, Royal Botanical Garden Edinburgh

Follow us on Facebook! https://www.facebook.com/EMPSEB21 And on Twitter! @EMPSEB

For further information or questions, please visit the conference website: http://empseb21.bio.ed.ac.uk If you have any questions, please feel free to email the EMPSEB21 committee president, Kim Prior at president.empseb21@gmail.com.

We are looking forward to welcoming you to Stirling in September 2015!

rebecca.eileen.butterfield@gmail.com

Stockholm MammalBiol Aug16-22 AbstractSubmission

The abstract submission is now open for the 7th European Congress of Mammalogy (ECM7) in Stockholm, on 16-22 August 2015. To submit an abstract for a talk or a poster, please visit the conference's webpage at: www.zoologi.su.se/ecm7 The aim of the European Congresses of Mammalogy is to foster communication between researchers working on issues of mammalian biology in the European arena, as well as providing a venue for the broad dissemination of European mammal research. The relaxed and friendly atmosphere of these congresses provides an excellent opportunity to hear the latest developments in various fields of mammalogy, to share research experience and expertise, and to develop new and closer contacts with colleagues from different countries.

The conference will cover a broad range of topics in mammal biology, including Species Interactions, Population Genetics, Conservation Biology and Ecology & Landscapes.

Early Registration will between mid-February until April 15, and Late Registration will be between 16 April and 16 June.

Love.Dalen@nrm.se

Toulouse BehaviorEvolution May18-21 CallAbsts

11th Ecology & Behaviour meeting May 18th-21th, 2015 Toulouse, France http://eb2015.sciencesconf.org/ Reminder: only 5 days before the deadline

We are pleased to announce the call for abstracts for the 11th Ecology and Behaviour meeting that will take place in Toulouse (France) from May 18th to May 21st 2015.

This international meeting is an excellent place of exchange for young researchers (Master students, PhD students and post-docs) working in the field of ecology, evolutionary biology and animal behaviour. Every year the conference gathers about a hundred participants from all over Europe and the high success of the previous editions has been the best proof of its high scientific quality.

Six thematic sessions have been defined for this 11th edition: (1) Movement ecology, (2) Cognition: memory and learning, (3) Social and sexual selection, (4) Interspecific interactions and coevolution, (5) Population ecology and individual variability, (6) Biodiversity facing global changes.

Currently, the confirmed invited speakers are: (1) Philip D. McLoughlin & Michel Baguette, (2) Randolf Menzel & Valrie Dufour, (3) Hanna Kokko & Alexis Chaine, (4) Philipp Heeb & Dennis Murray, (5) Jean-Michel Gaillard & Niels Dingemanse, and (6) Rgis Crghino.

In order to facilitate the participation of young researchers in this conference the Association of the Ecology and Behaviour Meeting will provide accommodation and lunches to the attendees. The registration for the participants presenting their work as a poster or oral communication will be either free (Master and PhD students) or for a reduced fee (post-docs).

Submit an abstract

We invite you to submit the abstract of your poster or oral communication on our website : http://eb2015.sciencesconf.org/. The deadline for online abstract submission is on Friday, February 13th 2015 (for luck purposes).

Additional information

Our website (http://eb2015.sciencesconf.org/) is regularly updated and contains all the information regarding the submission of abstracts, the registration for the conference, the scientific program, the invited lecturers, the location of housing' In case of any questions, please contact us by email: eb2015@sciencesconf.org.

Feel free to forward this message to any people that might be interested in attending the 11th edition of the Ecology and Behaviour meeting.

Looking forward to meeting you in Toulouse!

The organizers.

Arthur Kocher <arthur.kocher@gmail.com>

UCalifornia Berkeley EvoDevo Aug5-9

Registration for the inaugural meeting of the Pan American Society for Evolutionary Developmental Biology is open! Mark your calendars for the meeting dates, 5-9 August, 2015, and be sure to register before all 350 slots are filled!

The registration deadline is April 1, 2015. To register, go to http://www.evodevopanam.org/meetings–events.html . Join us in Berkeley, California for the first EvoDevo meeting in the Americas sponsored by a new professional society dedicated to supporting the EvoDevo field!

A few meeting highlights:

- Confirmed speakers: Chris Amemiya, Alexa Bely, Sean Carroll, Rachel Collin, Kim Cooper, Tamara Franz-Odendaal, Matt Gibson, Angela Hay, Vivian Irish, Catherine Linnen, Mark Martindale, Jose Xavier Neto, Natalia Pabón-Mora (Early Career Award Recipient), Richard Palmer, Rudy Raff (Pioneers Award recipient), Bob Reed, Matt Rockman, Neelima Sinha, Stacey D. Smith, Ralf Sommer, Mansi Srivastava, James Umen
- Additional speakers will be selected from submitted abstracts
- Posters will be on display throughout the entire meeting
- Poster prizes for PhD students and postdocs

All details about registration, accommodation options, child care services, and the conference program are available at the following website: http://www.evodevopanam.org/meetings–events.html Support the Society and Become a Member!! To learn more about PASEDB, visit the following website: http://www.evodevopanam.org/ The Organizing Committee and the PanAm SEDB Executive Council look forward to welcoming you to Berkeley in August!

Chelsea D. Specht, PhD Associate Professor; Departments of Plant and Microbial Biology & Integrative Biology Curator of Monocots; University and Jepson Herbaria University of California, Berkeley 111 Koshland Hall, MC 3102 Berkeley, CA 94720 510.642.5601

cdspecht@berkeley.edu http://spechtlab.berkeley.edu/ cdspecht@berkeley.edu

UNewEngland EvolutionaryGenomics Jul12-17

Applicants Now Being Accepted - See Link Below!

Ecological and Evolutionary Genomics Gordon Research Conference July 12-17 2015 at University of New England, Biddeford, MEÂ

>From Genomes to Biomes: ÂUsing Biodiversity to Explore Biocomplexity.

>From genomes to biomes, from microbes to plants and animals, the 2015 Gordon Research Conference on Ecological and Evolutionary Genomics will highlight how genome-enabled approaches are helping to rapidly advance our understanding of the complicated relationship between genotype, phenotype and the environment. Topic areas such as population genomics, adaptation & speciation, symbiosis and interacting organisms, biodiversity & phylogenomics, community & ecosystem genomics, genetic and ecological networks, methods & non-model organisms, genomics & animal behavior, and applications of ecological and evolutionary genomics, will highlight how biodiversity can be used to illuminate complex biological relationships and inform ecological and evolutionary processes and molecular mechanisms of adaptation to changing environments. The conference will also feature emerging approaches and technologies to aid further exploration of the genomes from organisms that span the tree of life. Gordon Conferences are famous for fostering in depth interactions that yield new insights in a collegial atmosphere.

Co-chairs, Jack Werren (University of Rochester) and Michael Herman (Kansas State University) along with

Vice-chairs Felicity Jones (Max Plank Institute, Tubingen) and Michael Pfrender (University of Notre Dame) invite you to join us on the ocean-side campus of the University of New England in Biddeford, Maine for a stimulating conference. We are assembling a diverse group of established and early career investigators to discuss their latest work.

Discussion leaders and symposium speakers for "Young Investigators: Advances in Eco and Evo Genomics" session will be chosen from among the registrants. The organizers are actively seeking funds to assist students and others attend the meeting. Applications for attendance will be accepted until the meeting is full, so don't delay!

Applications to attend are now open and information can be found atÂhttps://www.grc.org/programs.aspx?id=13135 Symposim Topic Areas & Speakers - Advances in Computational and Genomic Approaches to Non-Model Organisms (Steven Salzberg, Wes Warren, Beth Shapiro) - Applications of Ecological and Evolutionary Genomics (John Colbourne, Sherry Flint-Garcia, Joseph Shaw) - Behavioral Ecology Meets Genomics (Laurent Keller, Amy Toth, Todd Schlenke) - Biodiversity and Phylogenomics (Holly Bik, Casey Dunn, Davide Pisani) - Community and Ecosystem Genomics (Jack Gilbert, Blake Matthews, Jenn Schweitzer) - Networks: From Genes to Ecosystems (Karoline Faust, Cedric Feschotte, Alvaro Sanchez, Patricia Wittkopp) - ÂPopulation Genomics, Adaptation and Speciation (Andrew Clark, Asher Cutter, Elodie Ghedin, Josephine Pemberton) - ÂSymbiosis and Interacting Organisms (Siv G. Andersson, Angela Douglas, Takema Fukatsu, Wayne Potts) - Young Investigator Presentations: Advances in Ecological and Evolutionary Genomics (TBA, from submitted abstracts)

Please plan on joining us in Biddeford in 2015!

Michael Herman Professor Division of Biology Kansas State University 266 Chalmers Hall Manhattan, KS Â66506 Office: (785) 532-6741 Lab: (785) 532-6773 FAX (785) 532-6653 Email :Âmherman@ksu.edu http://www.k-state.edu/hermanlab mherman@ksu.edu

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UOxford Systematics Aug26-28 StudentBursaries

A number of bursaries are available for students to attend the forthcoming Systematics Association biennial conference 'Systematics - the science that underpins biology' that will be held at the University of Oxford from 26-28 August 2015.

This three-day meeting comprises four thematic sessions (The value of long term monitoring plots for plant systematics and ecology in the tropics; Comparative approaches to the origin of biodiversity; Accelerating the pace of taxonomy; Rooted in deep time: Palaeontological contributions to systematics) and contributed papers on any aspect of systematics.

Five bursaries of £200 sponsored by the Linnean Society of London are open to students wishing to present a contributed talk or poster.

In addition, the British Ecological Society Tropical Ecology Group (BES-TEG) have sponsored bursaries for students wishing to attend the symposium on 'The value of long term monitoring plots for plant systematics and ecology in the tropics'. Two bursaries of £1500 are available for PhD students from tropical forest countries and 5 bursaries of £200 are open to all PhD students. Applicants are expected to attend the entire meeting as well as the specific symposium, and are encouraged to offer a contributed talk.

The deadline for bursary applications is midnight (23:59 GMT) 30th April. The closing date for contributed papers is (23:59 GMT) 1st July.

Further details can be found on the Systematics Association website at http://www.systass.org/biennial2015/ Dr Mark Carine Plants Division, Department of Life Sciences The Natural History Museum Cromwell Road London SW7 5BD United Kingdom

Tel: 020 7942 5541

M.Carine@nhm.ac.uk

Vienna SMBE2015 AbstractDeadline reminder

Hello evoldir community,

abstract submission for oral presentations at SMBE 2015 (July 12-16) in Vienna, Austria, closes on February 8.

Join us in one of the most beautiful cities at the spectacular Imperial Palace (Hofburg) in the heart of Vienna!

A few meeting highlights:

- All posters will be on display throughout the entire meeting.

- At least four poster sessions

- 27 symposia on cutting edge topics suggested by SMBE members and one Open Symposium for which 5 featured speakers will be selected though the Local Organising Committee (LOC).

- Plenary speakers: Doris Bachtrog (UC Berkeley), Joe Felsenstein (Univ. of Washington), Johanna Schmitt (UC Davis) and Diethard Tautz (MPI for Evolutionary Biology).

- Heavily subsidized child care

- many awards (https://www.smbe.org/smbe/-AWARDS.aspx): — Poster prize for postdocs and PhD students — Fitch prize — Young investigator travel awards — Junior and mid career research awards — Child Care Travel Awards

- affordable accommodation (starting from euro 19,- /night. Also many double rooms are available for euro 60,- /night incl. breakfast)

Early bird registration by March 1 will also benefit from up to 30% reduced registration fee and full consideration of submitted abstracts.

All details about registration, accommodation options and travel discounts are available at the conference website: www.smbe2015.at The Local Organising Committee is looking forward to welcome you to Vienna in July!

julia.hosp@gmail.com

Vienna SMBE2015 Jul12-16 AbstDeadlineSunday

Hello evoldir community,

abstract submission for oral presentations at SMBE 2015 (July 12-16) in Vienna, Austria, closes THIS SUNDAY.

Join us in one of the most beautiful cities at the spectacular Imperial Palace (Hofburg) in the heart of Vienna!

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julia.hosp@gmail.com

Vienna SMBE2015 Jul12-16 EarlyBird ClosingSoon

Hello evoldir community,

don't miss the early bird deadline - register by the end of the month to save up to 30% on the registration fee for SMBE 2015, held in one of the most beautiful cities at the spectacular Imperial Palace (Hofburg) in the heart of Vienna!

A few meeting highlights:

- All posters will be on display throughout the entire meeting.

- At least four poster sessions

- 27 symposia on cutting edge topics suggested by SMBE members and one Open Symposium for which 5 featured speakers will be selected though the Local Organising Committee (LOC).

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julia.hosp@gmail.com

Vienna SMBE2015 Jul12-16 OralContributions StillAccepted

Dear evolDir community,

one last unforeseen chance to submit your abstract to be considered for an oral contribution at SMBE 2015 in Vienna (July 12-16):

The abstract system caused delays due to the required separate registration. Therefore, we will accept submissions for oral contributions until Sunday, Feb 15!

Register for SBME 2015 here: http://smbe2015.univie.ac.at/home/ Please register separately for the abstract system (the link to abstract submission will be sent to you in the conference registration confirmation).

The Local Organising Committee is looking forward to welcome you to Vienna in July!

A few meeting highlights:

- All posters will be on display throughout the entire meeting.

- At least four poster sessions

- 27 symposia on cutting edge topics suggested by SMBE members and one Open Symposium for which 5 featured speakers will be selected though the Local Organising Committee (LOC).

- Plenary speakers: Doris Bachtrog (UC Berkeley), Joe Felsenstein (Univ. of Washington), Johanna Schmitt (UC Davis) and Diethard Tautz (MPI for Evolutionary Biology).

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- affordable accommodation (starting from 19,- /night. Also many double rooms are available for 60,- /night incl. breakfast)

Early bird registration by March 1 will also benefit from up to 30% reduced registration fee and full consideration of submitted abstracts.

julia.hosp@gmail.com

Vienna SMBE July12-16 AdaptiveEvolution

Dear evoldir members,

I would like to remind you that the abstract submission deadline for the Annual Meeting of the SMBE is on Sunday February 8th, at the end of this week. Please do not hesitate to contact us if you need any information about the symposium “Adaptive and non-adaptive evolution of gene expression and regulation”.

Original announcement below:

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As a part of the Annual Meeting of the Society for Molecular Biology and Evolution (SMBE), that will be held in Vienna on July 12-16 2015, we are pleased to announce a symposium on the topic “Adaptive and non-adaptive evolution of gene expression and regulation”. Abstract submissions for oral presentations are open until February 8th.

Symposium summary:

Identifying the substrate of adaptive evolution is a key question in evolutionary biology. It was proposed early on that much of adaptive evolution may occur at the level of gene expression, by means of positive selection acting on the genetic variation naturally occurring at regulatory elements. Comparisons of gene expression patterns and regulatory mechanisms are now possible within and between species, allowing evolutionary biologists to reveal the genetic mechanisms of adaptations. However, non-adaptive forces are also expected to shape the genetic variation of regulatory modules and to drive the evolution of gene expression. Therefore, mechanisms such as genetic drift, biased gene conversion, variability in mutation rates have to be carefully taken into account when reconstructing the evolutionary history of gene expression and regulation. In this symposium we propose to bring together researchers from the fields of population genetics, functional and evolutionary genomics and systems biology to discuss issues related to the functional characterization of the genetic variation within regulatory elements and the statistical inference of evolutionary forces driving the evolution of gene expression. We encourage submissions that examine adaptive and non-adaptive mechanisms underlying different aspects of gene expression evolution, including alternative splicing, non-coding RNA expression, as well as transcriptional and post-transcriptional regulation.

Invited speakers: Prof. Laurent Duret (http://lbbe.univ-lyon1.fr/-Duret-Laurent-.html?lang=en) and Prof. Yoav Gilad (http://giladlab.uchicago.edu/).

Please note that travel awards and childcare support are available to allow young scientists and parents to attend the conference. Please go to http://smbe2015.at/ for additional information and registration.

For more details, please don’t hesitate to contact us.

Stefan Laurent stefan.laurent@epfl.ch Jeffrey Jensen jeffrey.jensen@epfl.ch Anamaria Necsulea anamaria.necsulea@epfl.ch Mehmet Somel msomel@metu.edu.tr

– Anamaria Necsulea SNSF-Ambizione fellow Swiss Institute for Experimental Cancer Research (ISREC) Ecole Polytechnique Fédérale de Lausanne (EPFL) EPFL-SV-ISREC-UPDUB SV2842 Station 19 CH-1015 Lausanne Switzerland

Phone +41 21 693 06 05 anamaria.necsulea@epfl.ch

Vienna SMBE SpeciationGenomics Jul12-16

SMBE Speciation genomics - Vienna, July 12-16th 2015

Dear colleagues

We would like to invite you to join a symposium on Speciation genomics at the next SMBE meeting in Vienna. PLEASE NOTE: Abstracts for oral presentations can still be submitted until 8th of February. Deadline for abstracts for poster presentations 29th March.

Speciation is a fundamental evolutionary process: this process involves every living organism and its rates mirror atmospheric and geological changes on Earth, but its mechanisms are still largely a mystery. Usually, speciation is defined by mating barriers, which can arise ether slowly, due to growing divergence between geographically or ecologically separated groups, or immediately, due to ploidy change.

Speciation research covers a broad array of scientific fields, starting from molecular and cellular biology to evolutionary biology. A rapidly growing amount of assembled genomes and transcriptomes make possible to study speciation in much more detail than before. Looking at patterns of genomic divergence, identifying footprints of selection, or mapping genes that are involved in reproductive isolation are just a few of the powerful genomic approaches that recently become available to study speciation. Today it is not rare that speciation research pushes the existing knowledge to frontiers of technologies and advanced algorithms.

This symposium will welcome research in model and non-model species integrating emerging themes and novel approaches, together with a reassessment of more traditional methodologies in order to understand why and how organisms diversify.

The invited speakers that will open the symposium are Luca Comai (UC Davis) and Christian Lexer (University of Fribourg). We encourage submissions from researchers active in this area working on any system. Students and postdocs are particularly welcome. Check submission details on the SMBE 2015 webpage http://-smbe2015.at/ Please contact us with any questions.

Polina Novikova (polina.novikova@gmi.oeaw.ac.at)

and

Ovidiu Paun (ovidiu.paun@univie.ac.at)

ovidiu.paun@univie.ac.at

WashingtonDC PteridologySystematicsEvolution Jun1-5

Registration is now open and abstracts are currently being accepted for:

Next Generation Pteridology: An International Conference on Lycophyte & Fern Research

1-5 June 2015 in Washington D.C. National Museum of Natural History & United States Botanic Garden

http://botany.si.edu/sbs/ The past decade has seen remarkable advances in our understanding of fern and lycophyte biology. New sources of data have emerged and novel methods for analyzing these data are being developed. At the same time, many traditional approaches have been revitalized as their unique and specific contributions are more fully realized. With a recent influx of students and early career researchers, the international pteridological community continues to grow. Through more widespread and far-reaching collaborations, the pace of scientific discovery is accelerating, new parts of the globe are being included, and the conservation of these important species in a rapidly changing world is being investigated. This conference aims to bring together the world's pteridologists to celebrate the progress to date and to forecast developments still on the horizon.

The early registration and abstract submission deadline is 1 April 2015. If you have questions, or would like to be added to the distribution list for conference-related announcements, please email sbs@si.edu

Eric Schuettpelz Research Botanist National Museum of Natural History Smithsonian Institution Department of Botany MRC 166 PO Box 37012 Washington DC 20013-7012 Telephone 202.633.0914 Fax 202.786.2563 E-mail schuettpelze@si.edu

"Schuettpelz, Eric" <SchuettpelzE@si.edu>

Yosemite Symbiosis May1-3 RegistrationExtended

EARLY BIRD REGISTRATION EXTENDED FOR ONE MORE WEEK:

REGISTRATION link: http://snri.ucmerced.edu/-symbiosis Dear Colleagues,

The Fifth annual Symbiosis Workshop will take place on May 1-3, 2015 at the Sierra Nevada Research Station, Yosemite National Park.

This has become a great venue for a diversity of symbiosis researchers, so we hope to continue to attract a diverse group

Keynote speaker 2015: Dr. Ellen L. Simms from the University of California, Berkeley.

Information about our meeting:

Why: Our goal is to better integrate scientists that focus on symbiosis research. We plan to continue annual workshops at Yosemite as this site is both beautiful and secluded. This will be our 5th annual meeting and we are now attracting scientists from all over the country and overseas.

Who: The meeting is small by design (~50 participants) and we seek to focus on scientists interested in both cooperation and symbiosis. In the past we have covered a range of symbiosis topics from ecology and evolution to molecular mechanisms in different model and non-model systems. We would like to make room for a diverse group of people so we will initially accept up to 3 lab members per group (including the PI) on a first come first served basis.

When: The talks and formal meeting will be held May 2-3, 2015, though we make accommodation arrangements available for attendees to arrive on Friday the 1st to provide opportunities to enjoy the park. Since time at the conference is limited, we ask attendees to submit an abstract and a preference (talk versus poster). Priority will be given to those presenting. Abstract and early bird registration are due on January 31st, 2015.

Where: SNRS has a set of cabins in Wawona and all within a short walk of the conference room. Costs: See details in the registration page. We will only be able to accept credit card payments this year.

Link to meeting information: http://-www.sachslab.com/symbiosis-2015.php=-3D0ARegistration REGISTRATION link: http:/-/snri.ucmerced.edu/symbiosis Please direct any questions to the organizers: Joel Sachs joels@ucr.edu A. Carolin Frank cfrank3@ucmerced.edu Becca Fenwick (SNRS Director) bfenwick@ucmerced.edu

Joel L. Sachs Associate Professor #310 Science Labs I Department of Biology University of California Riverside, CA 92521

Mailing Address: Sachs Lab UC Riverside 3401 Watkins Dr. 1229 Spieth Hall Riverside, CA 92521

Office (951) 827-6357 Fax (951) 827-4286 www. sachslab.com http://www.biology.ucr.edu/people/faculty/-Sachs.html=3D0A joel.sachs@ucr.edu

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Zurich EvolutionaryMedicine Jul30-Aug1

Dear colleagues

May I draw your attention towards the Evolutionary Medicine Conference 2015 (30. July - 01. August) at the Institute of Evolutionary Medicine (IEM).

This international conference will bring together distinguished keynote speakers (2008 Nobel Laureate Harald zur Hausen and others, see attachment) as well as experts from different research areas (including medicine, anthropology, molecular/evolutionary biology, paleopathology, archaeology, epidemiology, and other fields) to debate the evolutionary origins of diseases and on how the knowledge of the past informs the present and the future. Furthermore, the specific implications of interdisciplinary research in the understanding and management of human health issues will be addressed.

- Registration open now - Deadline for mini-symposia: Feb 16, 2015 - Deadline for abstracts: Mar 30, 2015

Find all relevant information on http://-www.iem.uzh.ch/evolmedconf2015.html Best regards,

Kaspar Staub“

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: +41446355702 kaspar.staub@iem.uzh.ch http://www.iem.uzh.ch/people/kasparstaub.html Kaspar Staub <kaspar.staub@iem.uzh.ch>

GradStudentPositions

BangorU SoilBiodiversity

A fully funded PhD studentship focusing on soil biodiversity is available at Bangor University, UK, closing date March 1st, 2015.

Does Soil Biodiversity Matter? Soil biodiversity is at a true scientific frontier and unravelling its complexities lies at the heart of understanding how ecosystems work and how they can be effectively managed and restored. In this context, we are looking for an enthusiastic and committed PhD candidate to work in the area of soil biology in relation to soil functioning and the delivery of ecosystem services. The work aligns with efforts in Defra and the European Commission to better manage soils and to understand their response and resilience to anthropogenic perturbation (in terms of both degradation and restoration), and is linked to a flagship research programme which has been responsible for the metabarcoding of >1000 soil samples to date. Uniquely, we are also capturing a vast array of other data associated with these samples including above-ground biodiversity (plants, birds, insects), land management, surface water quality and a range of soil quality indicators (e.g. pH, total C and N, texture, available P, water repellency). Hence, this PhD studentship will focus on examining the relationship of key soil organisms (bacteria, fungi, archaea, protists) with other components of the ecosystem (birds, insects, vegetation, climate), land use and management regime, and other soil quality indicators. You will use a combination of both bioinformatics and laboratory analysis of soil microbial communities. The studentship directly aligns with NERC's recent Most Wanted Skills in UK Science Review thereby providing the candidate with training for life in an area with great career potential. The studentship is based at Bangor University and will be co-supervised by the Centre for Ecology and Hydrology, as well as Welsh Government. You will contribute to a growing and enthusiastic multidisciplinary research team and to the next generation of soil scientists within the NERC Doctoral Program STARS team.

The necessary links for the project, details and NERC DTP are available here:

http://mefgl.bangor.ac.uk/news/new-funded-phd-studentship-available-does-soil-biodiversity-matter-21810 http://www.starsoil.org.uk/portal/projects/-002426/does-soil-biodiversity-matter Funding Notes: Applicants should be a UK resident and hold a minimum of an UK Honours Degree at 2:1 level (or equivalent Masters) in a subject area such as microbiology, ecology, biology, environmental or natural sciences. The student should be statistically numerate, have experience in carrying out laboratory practical work, bioinformatics and have a passion for understanding ecosystem biodiversity.

Funded by the Natural Environment Research Council (NERC), Lancaster University leads the STARS initiative, which brings together eight institutions with an excellent track record in soil science: the Universities of Nottingham, Bangor, and Cranfield, the Centre for Ecology and Hydrology, the British Geological Survey, the James Hutton Institute, and Rothamsted Research.

For informal enquiries, please contact either Si Creer (s.creer@bangor.ac.uk), or Davey Jones (d.jones@bangor.ac.uk) for further details.

Cheers and best wishes

Si Creer

Simon Creer Senior Lecturer Molecular Ecology and Fisheries Genetics Laboratory School of Biological Sciences Environment Centre Wales Bangor University Gwynedd LL57 2UW Tel: +44(0)1248 382302 Fax: +44(0)1248 382569 web: http://mefgl.bangor.ac.uk/-si.php Skype: spideycreer Twitter: @spideycreer

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

Bonn InsectSystematics

A PhD student position funded by the European Union (European Union's Horizon 2020 research and innovation programme under the Marie Sk^{3}odowska-Curie acts) is available in the Diptera Section of the Zoologisches Forschungsmuseum Alexander Koenig (ZFMK). The fellow will investigate the genera Asarkina and Allobaccha (Diptera: Syrphidae), both occurring in the Afrotropical, Oriental and Australasian Regions. The project aims to perform a taxonomic revision, as well as to resolve phylogenetic placement of these taxa with the development of a workflow for Ultra-Conserved Elements or Anchored Hybrid Enrichment technique. The main academic advisor is X. Mengual, but the project is co-advised by F. Ronquist (Swedish Museum of Natural History) and N. Wahlberg (Lund University). At the same time all students will be part of the BIG4 international cross-disciplinary training consortium (BIG4: 'Biosystematics, Informatics and Genomics of the 4 big insect groups') funded by the European Union Marie Sk^{3}odowska-Curie Innovative Training Network Program. The project combines classical methods of systematics with innovative techniques and approaches and it involves travels and field work. The position is for 3 years (36 months) at the ZFMK with very competitive salary, additional family allowance for married students, and sufficient research funds.

We are looking for a highly motivated candidate with an excellent academic track record. A MSc degree (or equivalent) in a related discipline is desirable. The successful candidate is expected to be able to demonstrate some previous experience with evolutionary or taxonomic studies. Experience with next generation sequencing methodology and/or Diptera taxonomy are a plus, but excellent organization and communication skills are a must. Due to the requirements of the Marie Sk^{3}odowska-Curie Program applicants should not hold PhD degree and, at the time of enrollment in the PhD program in Germany, should have less than 4 years of research experience (counted as time of employment in research since receiving a degree allowing enrollment in the PhD program). Additionally, at the time of recruitment applicants must not have resided or carried out his/her main activity (work, studies, etc.) in the country of the host (Germany in this case) for more than 12 months in the 3 years before his/her recruitment for the PhD project. The working language in our laboratory is English; however, German skills will be helpful for everyday life in Bonn.

BIG4 stands for "Biosystematics, Informatics and Genomics of the 4 big insect groups'. It is an international training consortium funded by the European Union-based Marie Sk^{3}odowska-Curie Innovative Training Network Program (EU ITN) that mainly targets PhD education. BIG4 unites established researchers from 7 academic institutions with 3 business companies in Europe and 11 other support institutions around the globe. The main idea of BIG4 is to bring together experts with complementary taxonomic and methodological strengths for training a lucky cohort of young systematic entomologists in broad sense. BIG4 targets the biggest insect groups such as Coleoptera, Hymenoptera, Diptera and Lepidoptera. It tackles a long standing problem of amalgamation classical systematics with innovative methods in phylogenetics, bioinformatics, genomics, advanced sematic biodiversity publishing, and Citizen Science into competitive cross- disciplinary profiles. For every BIG4-based PhD student attached to either of the core BIG4 organizations, the consortium opens learning opportunities additional to their respective academic advisor or home lab. Secondments are planned from a few weeks to a few months to other BIG4 partner labs, and a series of thematic workshops held for all BIG4-based PhDs. Non-academic members of BIG4 bring opportunities in science-related business or industry and give students additional skills to succeed there, since not every PhD graduate lands in academia.

To be considered please send your application per email to x.mengual@zfmk.de including your CV, a two pages letter of motivation describing why are you personally interested in this position, and the names and contacts of three academic referees. Incomplete applications will be disregarded. Screening of applications will begin immediately and we will try to assess all applicants within 2-3 weeks after the deadline. The latest preferred start date is April 1st, 2015.

Dr. Ximo Mengual Head of the Diptera Section Zoologisches Forschungsmuseum Alexander Koenig Leibniz Institut für Biodiversität der Tiere Phone: 0049 (0)228 9122 292 x.mengual@zfmk.de https://www.zfmk.de/en/-zfmk/ximo-mengual Zoologisches Forschungsmuseum Alexander Koenig - Leibniz-Institut für Biodiversität der Tiere - Adenauerallee 160, 53113 Bonn, Germany www.zfmk.de

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CharlesU Prague LepidopteraPollinationCameroon

A Ph.D. studentship

Butterflies and moths as pollinators along an Afrotropical altitudinal gradient

We are seeking a highly motivated Ph.D. student to join a project assessing studies of plant-pollinator relationships between butterflies and moths (Lepidoptera) with selected groups of flowering plants (Rubiaceae and Acanthaceae) on Mt. Cameroon. The student will process already collected material, as well as actively participate on field sampling (at least two times during the study) of data and their subsequent processing in collaboration with international specialists. The length of the study is 4 years.

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

Offered

- attractive scientific topic in an established international team

- standard university scholarship (up to 114,000 CZK annually according to discharging of the study responsibilities) together with the support of the STARS project (120,000 CZK annually; http://www.stars-natur.cz) for four years, it sufficiently covers living expenses in the Czech Republic

Required

- enthusiasm in nature and ecological science

- ability to lead a field research in challenging conditions of tropical environments

- fluency in English

- a MSc degree in biology or related fields

Desirable (but not necessary)

- previous experience of collaboration in scientific projects evidenced by a (co)authorship of research papers or conference contributions

- previous experience with insects and/or plants

- basic knowledge of French

All applicants will apply for the position online through http://www.stars-natur.cz/. The deadline for application is the 28th February 2015, the successful candidate will be selected till early April. The position is available from the beginning of 2015/2016 academic year.

All questions should be sent directly to Robert Tropek (robert.tropek@gmail.com).

Robert Tropek <robert.tropek@gmail.com>

CNRS Nice DevelopmentalPlasticity

Graduate position: Developmental plasticity and evolution of the germline in Caenorhabditis nematodes (CNRS, Nice, France)

A PhD fellowship is available in the Braendle lab at the Institute of Biology Valrose in Nice. The candidate will be involved in one of our on-going research projects aiming to integrate mechanistic and evolutionary understanding of how gene-environment interactions shape development and evolutionary processes. We address this problem using the nematode Caenorhabditis elegans, focusing on molecularly well-characterized systems, such as the development of the hermaphrodite germline.

These analyses combine developmental and quantitative genetic approaches and are further complemented by experimental evolution assays and ecological studies. A current key research focus is the mapping of natural genetic variation in C. elegans developmental plasticity.

Applicants are expected to be highly motivated and participate in the planning of the project. Candidates with a background in quantitative genetics, bioinformatics, or C. elegans biology are particularly encouraged to apply. This 3-year position is open to all nationalities and will start in October 2015.

Our team belongs to the Institute of Biology Valrose (IBV), an international research institute hosting over 20 research groups working on diverse topics in development, genetics and cell biology. The institute, located in the city centre, has excellent research facilities and provides an interactive, stimulating scientific environment.

To apply, send a summary of your research motivation and interests, CV, names and contact information for three references to Christian Braendle (braendle@unice.fr) in a single PDF file. Application deadline: March 20, 2015.

For more information, please visit: http://www.braendlelab.net http://ibv.unice.fr Christian Braendle Institute of Biology Valrose CNRS UMR7277 - INSERM U1091 Universite Nice Sophia Antipolis Parc Valrose 06108 NICE cedex 2 France Tel +33 (0) 4 92 07 68 97 Fax +33 (0) 4 92 07 68 34 braendle@unice.fr http://www.braendlelab.net http://ibv.unice.fr Christian.BRAENDLE@unice.fr

Europe 13 Biocontrol

13 Graudate positions in Europe for Biocontrol

Graduate position: BremenU.WaspVariationReproductiveTraits

A PhD student position within the EU-funded Marie Sk^{3}odowska-Curie Innovative Training Network BINGO (Breeding Invertebrates for Next Generation Biocontrol) is available at the Population & Evolutionary Ecology Laboratory at Bremen University, Germany. The candidate will work on clutch size, sex ratio, and differential mortality in the Bracon hebetor / B. brevicornis species complex. Probably due to global warming, the European corn borer recently became able to produce two generations per year instead of just one, thereby drastically increasing its destructive potential in some areas. Wasps of the genus Bracon are very promising additional biocontrol agents against this important pest. By quantifying and mapping genetic variation for important traits, such as clutch size or sex ratio produced, we will be able to select for the most suitable Bracon populations.

The main objectives of this project are (i) to analyse the natural variation and heritability in the above mentioned traits, (ii) to map the genomic variation for understanding phenotype/genotype links (SNP), to analyse differential developmental mortality using transmission ratio-distorting loci (TRDLs) and (iv) to analyses the trade-offs involved in phenotype expression. For more details on this position, see http://bit.ly/1BgIUmm We seek a bright, highly motivated, and enthusiastic person able to work both as part of a team and independently. The ideal candidate shall have a master degree in natural science, preferably with a good background in entomology, ecology, genetics and/or biological control. Good skills in statistical data analysis (R) are a plus, but training will be provided. The language in the lab is English, and a high standard of spoken and written English is required. Basic knowledge of the German language and a valid driving license will be useful for the fieldwork.

Candidates must be, at the time of recruitment by the host organisation, in the first four years (full-time equivalent) of their research careers and have not yet been awarded a doctoral degree. This is measured from the date when they obtained the degree which would formally entitle them to embark on a doctorate. Eligible candidates may be of any nationality but must not, at the time of recruitment have resided or carried out their main activity (work, studies, etc) in Germany for more than 12 months in the 3 last years immediately prior to the recruitment date.

The BINGO-ITN is funded by the EU Horizon 2020 programme and involves 12 partners from academia, non-profit organizations and biocontrol industry located in the Netherlands, Germany, France, Spain, Czech Republic, Austria, Switzerland, Greece and Portugal. BINGO's approach is multidisciplinary, encompassing a broad range of scientific disciplines, including the application of state-of-the-art population genomics. The BINGO programme combines integrated training workshops and internship opportunities across the network, with career opportunities in academia, public or the private sectors.

You will work in close cooperation with PhD students and researchers involved in related BINGO research projects. Secondments are planned to other BINGO participants. For more information about the BINGO project and other PhD vacancies see www.bingo-itn.eu To apply, please provide a letter of motivation and a detailed CV by e-mail to: 1. Dr. Andra Thiel, thiel@uni-bremen.de 2. CC to: info@bingo-itn.eu 3. Add subject: BINGO-Application RP4 We will be considering applications until 31 March 2015, the envisaged starting date is 1 May 2015

Margreet Bruins | info@bingo-ITN.nl |

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Graduate position: CABI.Switzerland.BiocontrolWaspRiskAssesment

A PhD student position within the EU-funded Marie Sk^{3}odowska-Curie Innovative Training Network BINGO (Breeding Invertebrates for Next Generation Biocontrol) is available at the CABI Centre in Delémont, Switzerland. The candidate will work on the benefits and risks of using native parasitoids for augmentaive biological control of the invasive pest Halyomorpha halys in Europe. The invasive heteropteran pest Halyomorpha halys is a rising threat to fruit crops in Europe but control measures are lacking. Native European egg parasitoids have started to adopt the new host H. halys and thus, show potential for augmentative biological control. The main objective of the project is to develop an innovative, environmentally safe control strategy such as biological control.

A thorough risk-assessment strategy and subsequent monitoring of the released organisms are key components of modern and environmentally safe biological control procedures. The PhD candidate will conduct laboratory and field experiments to quantify the risk of direct and indirect

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KAUST SaudiArabia MarineBiodiversity

Ph.D. Fellowship Opportunity at the Red Sea Research Center, KAUST, Saudi Arabia.

**Impacts of UVB Radiation on Red Sea biota - Ph.D. Thesis to be co-supervised by Profs. Susana Agusti, Carlos M. Duarte, and Christian R. Voolstra

The Red Sea is an ultraoligotrophic environment characterized by highly transparent waters to damaging UVB radiation along with very high temperatures. Recent evidence suggests that Red Sea biota is highly vulnerable to UVB radiation, which is exacerbated by high temperature. However, UVB impacts have yet been assessed only for zooplankton and picoautotrophs. This project will characterize the impacts of UVB radiation on key Red Sea biota, encompassing keystone species in benthic (such as seagrass and corals) and pelagic (such as phyto and zooplankton and meroplankton) habitats. It will do so through field observations and field and laboratory experiments assessing impacts of UV radiation at multiple levels: molecular, cellular, physiological, organismal, holobiont and population levels. The project will also assess complex interactions mediated by UV for selected model species, including UV-driven constraints on organismal life history mediated by ontogenetic variability in their vulnerability to UV radiation as well as possible benefits of UV radiation on Red Sea biota driven by antagonistic effects resulting from UV impacts on pathogens, parasites, and predators.

Key qualifications (in addition to general KAUST requirements, see below): Prior research experience ideally including publications in international journals, SCUBA diving, solid underpinnings in marine and molecular ecology.

**About KAUST and the Red Sea Research Center

King Abdullah University of Science and Technology (http://www.kaust.edu.sa) has been established as a world-class international graduate-level research university dedicated to inspiring a new age of scientific achievement in Saudi Arabia that will also benefit the region and the world.

Inaugurated in early 2011, with the striking blue waters visible from its laboratory windows, the Red Sea Research Center (http://rsrc.kaust.edu.sa < http://rsrc.kaust.edu.sa/ >) is well-positioned and well-equipped to study the Red Sea with state-of-the-art facilities and world-class researchers. The Red Sea Research Center has delved into the volume of research necessary to formulate a comprehensive understanding of the Red Sea to conserve its rich ecology. The incredible biodiversity of the Red Sea holds untapped potential and serves as a model for understanding biological systems and adaptation to extreme environments.

Successful students should apply to KAUST, indicating that they already have an offer from their supervisors (see below), as these positions are contingent on the students being admitted to KAUST. The application term is open and incoming applications are reviewed three times per year (see http://www.kaust.edu.sa/application-form-kaust.html for details on the application process).

All students admitted to KAUST will receive a very generous fellowship for the duration of their graduate studies. The benefits of the KAUST Student Fellowship include:

- Full tuition support - Monthly living allowance (ranging between $20,000-30,000 annual) - Free housing - Medical and dental coverage - Relocation support - One return ticket home every year

**Application

Applicants for this position are expected to have a high GPA (>3.5 of a maximum of 4), experience and background knowledge in the field and impeccable English (oral and writing).

Please send - CV - List of Publications - Letter of Motivation (why you wish to conduct a Ph.D., what is your understanding of what a Ph.D. involves, why you want to undertake this project) - Names of 2 References

by March 30, 2015 to christine.nelson@kaust.edu.sa

Christian R Voolstra <christian.voolstra@kaust.edu.sa>

NewcastleU 2 PlantAdaptation

The School of Biology has an exciting opportunity for a PhD studentship, starting Oct 2015. The strongest student applying to any of the eight proposed plant-based projects will be given the RB Cook studentship. The studentship covers fees and maintenance for UK/EU students.

Two of the proposed projects are in the area of evolution and ecology, complementing ongoing research in the research group of Kirsten Wolff.

Living on the edge: can adaptation at the edge of a species range accommodate rapid climatic change in a long-lived species? http://www.ncl.ac.uk/biology/study/postgrad/projects/adaptation.htm Genetic diversity and evolution of nuclear restorer genes in gynodioecious Plantago species http://www.ncl.ac.uk/biology/study/postgrad/projects/plantago.htm For how to apply: http://www.ncl.ac.uk/biology/study/postgrad/phds.htm Deadline: 20 March 2015.

Further enquiries about these two projects: please email with kirsten.wolff@ncl.ac.uk

Dr Kirsten Wolff Reader in Evolutionary Genetics Newcastle University, School of Biology Devonshire Building 5th floor Newcastle NE1 7RU, UK Phone: 0191 2084852 (internally 84852) email: kirsten.wolff@ncl.ac.uk www.staff.ncl.ac.uk/kirsten.wolff/ http://research.ncl.ac.uk/tiliageneticsresearch/ Kirsten Wolff <kirsten.wolff@newcastle.ac.uk>

NewZealand YersiniaEvolution

A graduate position is available in New Zealand to work on the ecological and evolutionary genetics of a curiously fascinating insecticidal species of Yersinia and its grubby host. Applicants need to be highly skilled in thinking, writing and communicating. Being a whiz at the bench helps. Details here: https://careers.sciencenewzealand.org/jobdetails/ajid/67Vw7/PhD-Studentship-in-Disease-Dynamics-of-a-Novel-Insect-Pathogen,10532.html Paul Rainey

paul.rainey@espci.fr

NHM Oslo PlantSpeciation

Natural History Museum Doctoral Research Fellowship in Evolutionary Biology (Plant Speciation)

One 4-year PhD position (SKO 1017) is available at the Natural History Museum (NHM), University of Oslo.

The Natural History Museum, University of Oslo, is the largest of its kind in Norway and has approximately 150 employees engaged in research, teaching, curating of collections and public outreach in botany, mycology, zoology, paleontology and geology. The museum is located in the beautiful Botanical Garden close to the city centre of Oslo.

Job Description

The position is connected to the project SpArc (High speciation rates in Arctic plants: genomic mechanisms and relevance to the latitudinal diversity gradient), funded by the Research Council of Norway for four years from 2015. The successful applicant will be part of a strong project team including researchers at the University of Oslo and international collaborators with long relevant experience. We will design the PhD project to contain a reasonable balance between high- and low-risk components, and between relatively independent work and work conducted in close collaboration with two postdocs. The successful applicant is expected to carry out part of the research in the laboratory of one of our international collaborators.

The SpArc project follows up recent discoveries in arctic diploid plants, showing that there are many cryptic biological (i.e. reproductively isolated) species within what has traditionally been recognized as well-defined, single taxonomic species. In this project, we will identify the genomic mechanisms of postzygotic reproductive isolation in two arctic systems, and test whether more southern floras contain similarly high, but hitherto undetected, cryptic biological species diversity. Based on crossing experiments and high-throughput DNA sequencing we will address whether selfers contain more cryptic species than outcrossers when controlled for lineage age, and whether polyploid formation from a diverse pool of recently diverged, cryptic diploid species can help explain why the Arctic harbours one of the most polyploid-rich floras on Earth. The project will provide new and potentially ground-breaking insights into both the dynamics of the latitudinal diversity gradient and the fundamental process of species divergence.

The PhD fellow will participate in work to identify the genetic mechanisms resulting in frequent reproductive isolation using genome sequencing and high-throughput QTL mapping approaches. She/he will also participate in work to test whether the Mediterranean flora contains high cryptic biological species diversity, with fieldwork to be carried out in 2015 in Spain and Greece.

The purpose of the PhD fellowship is research training leading to the successful completion of a PhD degree. The fellowship requires admission to the PhD programme at the Faculty of Mathematics and Natural Sciences. Appointment to a PhD research fellowship is conditional upon admission to the Faculty's research training programme. A plan for the research training must be submitted no later than two months after taking up the position, and the admission approved within three months. Compulsory service, duty work, shall represent 25% of the total hours of the PhD fellow's work.

Requirements

We seek a person with strong collaborative skills and motivation and ability to define own research questions.

Applicants must hold a Master's degree or equivalent in relevant fields in biology. She/he needs hands on experience with molecular laboratory work. Applicants should preferably have competence in plant systematics. Skills in computing and bioinformatics will be of advantage.

We offer

a challanging and friendly working environment salary based on salary level 50 - 55 (NOK 429 700 - 466 800 per year) favourable pention arrangement attractive welfare arrangements workout during hours, 1,5 h pr week

Evaluation of the application

In assessing applications, particular emphasis will be placed upon the academic and personal ability of the PhD candidate to complete the project within the given timeframe and write a thesis under supervision.

Interviews with selected candidates will be arranged.

We also refer to the English translation of regulations pertaining to the conditions of employment for PhD research fellowship positions: http://www.uio.no/english/research/doctoral-degree-and-career/phd/application/ https://www.uio.no/english/about/regulations/personnel/academic/regulations-employment-conditions-postdoc.html A good command of English is required:

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OklahomaStateU GrassTilleringGenetics

Research focus: We are seeking a highly motivated student to conduct research on evolutionary and quantitative genetics of branching in grasses, as part of an NSF Plant Genome grant focused on tillering in panicoid grasses (in collaboration with researchers at West Virginia University, Brigham Young University, and the University of California at Berkeley). The primary objective of this research is to use three panicoid grasses, maize, sorghum, and Setaria, to identify components of the gene regulatory network controlling branching. Our lab is focused on Setaria, combining traditional QTL mapping with expression QTL studies, mutant analysis, and modeling to understand the genetic components of branching and their responses to environmental stimuli such as shading. There is considerable flexibility for graduate projects within this broad theme.

Essential qualifications include successfully completed masters degree in genetics and/or molecular biology, experience in molecular lab techniques including working with RNA, experience in growing plants, and excellent writing skills. Desirable qualifications include experience with quantitative and phylogenetic analysis software, next generation sequence library construction and data analysis, and programming in R and/or Python.

Salary: Stipend will be $21,504 per calendar year plus tuition and health benefits. A mixture of TA and RA positions over the course of the Ph.D. will allow you to balance valuable teaching experience with research time.

Application deadline: February 13th, 2015; but applications will be reviewed as they arrive.

Application materials: Please send a brief cover letter, resume, transcripts, GRE scores, and contact information for two references to andrew.doust@okstate.edu by the deadline to be considered for this position.

Andrew Doust Botany Department Oklahoma State University Physical Sciences 301 Stillwater, OK 74078

Phone: 405-744-9559 Email: andrew.doust@okstate.edu

Websites: http://botany.okstate.edu/people_research/Doust/index.html http://tillering.okstate.edu/ http://osubioret.okstate.edu/ andrew.doust@okstate.edu

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OxfordBrookesU 2 EvoDevo

Two fully funded 3 year studentships starting in September 2015 in the McGregor and Nunes labs:

Project 1: The development and evolution of organ size Project 2: Investigating the contribution of genitalia divergence to reproductive isolation and speciation in Drosophila

For informal enquires please contact Alistair McGregor (amcgregor@brookes.ac.uk) or Daniela Santos Nunes (msantos-nunes@brookes.ac.uk).

For more information about the projects and the host labs see: http://mcgregor-evo-devo-lab.net/McGregor_lab/home.html http://bms.brookes.ac.uk/staff/maria-santos-nunes Start Date: 14th September 2015

Closing date for applications: 15th March 2015

Value p.a.: Bursary of £13,863 for 2015/16 and fees

Applicants require a good Honours degree level equivalent to a UK degree BSc (minimum 2.1 or higher).

EU Applicants must provide IELTS certificate minimum score level 6 in each of the four areas of reading, writing, listening and speaking with overall minimum score 7.0 or undergraduate degree awarded by UK university within the last two years. IELTS certificate must not be older than two year.

Please note that only UK/EU applicants can apply

Please download application form at: http://www.hls.brookes.ac.uk/images/research/phd-studentship-application-form-jan-14.doc Applications will only be accepted by email to the Research Administrator at the following address: hlsapplications@brookes.ac.uk

Please additionally submit a CV and if appropriate IELTS test score certificate

As part of the studentship, any successful applicant will be required to undertake up to 6 hours undergraduate teaching per week during the 12 week semesters without further remuneration. This may include supporting the teaching of statistics. You will also be expected to participate in a course to develop your teaching skills.

Dr. Alistair P. McGregor Reader in Biology Evolution of Animal Development and Morphology Department of Biological and Medical Sciences Oxford Brookes University Gipsy Lane Oxford OX3 0BP United Kingdom Tel: +44 (0)1865484191 Fax: +44 (0)1865483242 www.mcgregor-evo-devo-lab.net – Dr. M. Daniela S. Nunes Lecturer in Evolutionary and Developmental Biology Evolution of Animal Development and Morphology Department of Biological and Medical Sciences Faculty of Health and Life Sciences Oxford Brookes University Gipsy Lane Oxford, OX3 0BP UK Tel. +44 (0)1865 482741

Daniela Santos Nunes <msantos-nunes@brookes.ac.uk>

OxfordBrookesU ButterflyEmbryos

A fully funded PhD opportunity is available in the lab of Dr Casper J. Breuker (Oxford Brookes University): "How does a butterfly embryo cope with environmental stress?" (Breuker lab: http://www.researchgate.net/profile/Casper_Breuker) Collaboration with Dr Melanie Gibbs Centre for Ecology and Hydrology (Wallingford)

Relevant Recent blogpost about our butterfly embryo research: http://cehsciencenews.blogspot.co.uk/-2014/10/butterfly-tennis-balls.html For enquiries about the position please email Casper Breuker: cbreuker@brookes.ac.uk

Details: Full details (and how to apply) can be found at: http://www.findaphd.com/search/-ProjectDetails.aspx?PJID=3D61476ronmental stress? at Oxford Brookes University

Funding notes: Competitive three year full time studentship Eligibility: Only(!) UK/EU applicants can apply Closing date for applications: 15th March 2015 Start Date: 14th September 2015Value p.a.: Bursary of £13,863 for 2015/16 & fees

EU ApplicantsRequire IELTS certificate minimum score level 6 in each of the four areas of reading, writing, listening and speaking with overall minimum score 7.0. Or undergraduate degree awarded by UK university both not older than two years. Applicants required a good Honours degree level equivalent to a UK degree BSc (minimum 2.1 or higher)

Please download application form at: http:/-/www.hls.brookes.ac.uk/images/research/phd-studentship-application-form-jan-14.doc Applications will only be accepted by email to the ResearchAdministrator at the following address:hlsapplications@brookes.ac.uk

casper_j_breuker@yahoo.co.uk

Paris6U BioinformaticsMetagenomics

Hello,

Please find below the description of a PhD position to 'Search for unknown environmental sequences of medical/biological interest using large sequence similarity networks'**

Our knowledge on the evolution of important gene families etc. have so far largely relied on the comparative analysis of sequences from cultured microbial organisms and their MGE, both from a medical and from a more fundamental perspective. For example,the drug resistance genes we know, or the DNA and RNA polymerases, or ribosomal subunits we know, were mostly studied in organisms with cultured genomes, which represent a fraction of Life on Earth. The conservation, rate of transfer, mutation or recombination rates, and Ka/Ks ratio of these sequences have notably been investigated, suggesting which gene families are more conserved, and which ones are more evolvable. Importantly, the growing amount of molecular data from environmental samples or single cells (with the current development of single cell metagenomics) is now providing important additional data to test whether genetic diversity in environmental sequences is significantly larger than genetic diversity in the gene families of cultured organisms (and their MGE). A positive answer, indicating a potential greater evolvability of environmental gene families than currently known, would thus challenge much of our current biological inferences, because it would show to which extent the complexity of genes and genomes evolutionary history had been underestimated.

Sequence similarity networks offer a promising complementary approach to phylogenetics to analyze metagenomic and genomic data and to investigate highly divergent gene forms and relationships of distant homology. These graphs allow for mathematical analyses of genetic diversity and similarities over dozens of millions of sequences, providing a powerful framework to address the evolution of composite genes and genomes.

Our lab is now looking for a PhD student in evolutionary bio-informatics, who will be funded for three years by an ERC grant (for a salary of 35,000 euros/year; approximately 1753 euros/ month after taxes). The candidate will take advantage of graph properties and algorithms from the graph theory, inspired from the study of social, regulatory, and interaction networks, and apply them on publically available and original environmental data toaddress questions such as:

- Can we detect new forms of polymerases/restriction enzymes in temperate or cold environments ?

- Can we detect highly divergent drug resistance genes in the environment?

- Can we identify divergent environmental homologs of usually strongly conserved gene families in each/all domain(s) of life (such as ribosomal protein coding genes)? The observation of conserved divergent groups of environmental sequences may suggest the existence of still undetected deep-branching microbial lineages in nature

He/she will also identify environments rich in divergent gene forms and design original primers to look for microbes with highly unusual genes through single cell genomic studies.

The PhD candidate will work within a consortium of friendly bioinformaticians (Philippe Lopez), evolutionary biologists (Eric Bapteste), and graph theorists (Michel Habib, Laurent Viennot), and be hosted in the

University Pierre and Marie Curie in the center of Paris, France. The current team description and publications can be found at:http://www.evol-net.fr/ The candidate should have a good background in bio-informatics, and/or a strong interest for evolutionary biology.The position will start as soon as possible, ideally as early as June 2015. Applicants are requested to send a detailed resume, a motivation letter, a pdf copy of their masters thesis, and the names of two scientific referees to:

eric.bapteste@snv.jussieu.fr

A first round of applications will be closed by May 15, 2015.

Eventually, a second round of applications will be considered for a start in September/October 2015.

eric.bapteste@snv.jussieu.fr eric.bapteste@snv.jussieu.fr

QueensU 2 SeabirdAdaptation

I am looking for one or two PhD or MSc students or a post-doctoral fellow to join my research team studying adaptation in seabirds. We have two main study systems:

1) Band-rumped storm-petrels represent an exciting case of repeated parallel evolution of sympatric allochronic races (populations separated by breeding time - basically, feathered sticklebacks). Initial studies in my lab documented the pattern of divergence. We are now investigating the mechanisms of parallel adaptation and speciation using genomic methods. The new project will entail combination of molecular data with an existing large data set to estimate heritability of various morphological and life history traits. Other projects within this study system are possible. Field work on barren tropical islands will be required.

2) Thick-billed Murres breed throughout the north Atlantic, Pacific and Arctic Oceans, and are increasingly challenged by climate change. The need, and the potential, for a species to adapt to anthropogenic change depends on the plasticity of key traits such as breeding time and heat tolerance. I am looking for a new student to combine genetic data with an existing large dataset to study the fitness effects and heritabilities of several physiological and life history traits. Field work on a remote arctic island will be required. This student will be co- supervised by Dr. Kyle Elliott (McGill University).

Applicants must have some background in evolutionary genetics. Practical experience with genomics and bioinformatics is an asset. The successful applicant(s) will join a dynamic group of faculty and students studying ecology and evolution at Queen's University. Please send a resume or curriculum vitae, informal transcript, and contact information for two academic references to Dr. Vicki Friesen (address below). Acceptance is conditional on scholarship funding through either Queen's University or an external agency. Positions are not restricted to Canadians. Please contact vlf@queensu.ca for further information.

Dr. Vicki Friesen, Professor Department of Biology, 4443 Biosciences, 116 Barrie Street, Queen's University, Kingston, ON K7L 3N6, Canada Tel: 613-533-6156 Fax: 613-533-6617

Haida Saying: Treat the Earth well: it is not given to us by our parents, it is loaned to us by our children.

Vicki Friesen <vlf@queensu.ca>

Rennes UWuerzburg FishEvolutionSex

Evolution of sex determining regulatory networks

Sex can be determined by a plethora of mechanisms and the different mechanisms do not follow a phylogenetic pattern. Moreover sex determination is highly variable, sometimes even among closely related groups of organisms. The current understanding is that the primary signal, which triggers the genetic sex determination cascade, differs between the various groups of organisms, while the downstream regulatory network remained evolutionarily highly conserved. Our recent results and a detailed re-examination of previous work indicate however, that also downstream of the primary sex determiner a great variety of molecular mechanisms exist. This is in stark contrast to the molecular control of other vertebrate organ systems. So far, no explanation has been offered how such a variety in the molecular pathways of sexual development is possible and why it exists. Teleost fish show a particular wide variety of sex determination mechanisms were even sister species can have totally different modes how the male vs female decision during embryogenesis is made. We use fish of the genus Oryzias (medakas and related species) as models to approach three major questions:

1.) Are different SD mechanisms triggering the same, related or totally specific molecular pathways during the process of the fate differentiation of the gonad anlage?

2.) How stable are SD mechanisms in evolutionary terms?

3.) What is the evolutionary meaning of the high variability of sex determination mechanisms?

The PhD project will focus on the identification of chromosomal sex determination mechanisms in different species of the genus and a comparative molecular characterization of regulatory interactions of a known sex determining genetic network from the medaka Oryzias latipes in related species with similar or divergent sex determining mechanisms. On the methodological level the project will include up to date new sequencing technologies (RAD-tags, RNA-seq, ChIP-seq) and the tool-box for functional analyses in evolutionary developmental biology (in-vivo bioimaging, conventional transgenesis and genome editing by CRISPR/Cas9). The PhD project is embedded in a binational collaboration between the INRA institute for Fish physiology and Genomics in Rennes, France and the Biocenter of the University in Wuerzburg, Germany. The PhD student will be enrolled at the International Graduate School of Wuerzburg and work at both locations according to the experimental plan during the progress of the project.

For more details and practical information, please contact: Dr. Amaury Herpin (aherpin@rennes.inra.fr) at Rennes and Prof. Dr. Manfred Schartl (phch1@biozentrum.uni-wuerzburg.de) at Wuerzburg.

Amaury Herpin <amaury.herpin@rennes.inra.fr>

Sherbrooke SexualSelectionKangaroos

Ph.D.: sexual selection in kangaroos. I am looking for a student interested in exploring the determinants of mating skew and reproductive success in male eastern grey kangaroos. The project will combine two three-months seasons of fieldwork in southern Victoria, Australia, with analysis of an existing 7-year database including ecological and morphological measurements and over 500 identified paternities in two populations. Over 1200 kangaroos have been marked and sampled, they are habituated and easy to observe. Nearly all individuals are recaptured each year, to measure changes in mass and size in this species with indeterminate growth. Applicants should have a M.Sc. degree, strong quantitative skills and experience in fieldwork. Previous experience with DNA analyses and quantitative genetics would be an asset. A scholarship of Can$ 19,000 a year for 3.5 years is available. Holders of or strong candidates for external scholarships will be preferred. The research will be conducted in collaboration with Dany Garant at the Université de Sherbrooke and Graeme Coulson at the University of Melbourne. The Université de Sherbrooke is a francophone institution, therefore either some knowledge of French or an interest in learning it are essential. If you are interested, e-mail me explaining why you want to do this research and why I should be interested in you, with a CV and the e-mails of two people able to evaluate your potential as a researcher. The program could start in May or in September 2015.

Marco Festa-Bianchet m.festa@Usherbrooke.ca See http://marco.recherche.usherbrooke.ca/marco.htm and http://marco.recherche.usherbrooke.ca/advice.htm for more information

m.festa@USherbrooke.ca

SLU Alnarp PlantHerbivore ParasitoidInteractions

A 4-year PhD position is available at SLU on the topic "Plant Resistance Ecology: A new tool to engineer biological control of herbivores"

Several plant traits are important for plants' interactions with herbivores and parasitoids. One very important plant trait is resistance against herbivores. A general question to investigate is how herbivore-parasitoid interactions are affected when resistance in wild plants evolves, and when domestic plants are bred for increased resistance.

Horticultural plants are often dependent on biological control of herbivores provided by parasitoids. This ecosystem service may be affected if resistance increases or declines during plant breeding. Knowledge regarding such plant effects opens up novel opportunities to actively breed for improved biocontrol. Similarly, plant resistance evolution in natural populations may lead to altered trophic interactions which could affect the level of herbivory experienced by the plant.

The aim of this PhD project is to investigate how plant resistance against herbivores affects plant-herbivore-parasitoid interactions in woodland strawberry (Fragaria vesca). The PhD student will have access to a large common garden with 100 wild plant genotypes, that differ in their resistance against herbivores.

The full ad can be downloaded here: http://www.slu.se/sv/om-slu/fristaende-sidor/aktuellt/lediga-tjanster/las-mer/?eng=1&Pid=1701 Johan

Johan A. Stenberg Associate Professor

Sveriges lantbruksuniversitet Swedish University of Agricultural Sciences

Department of Plant Protection Biology PO Box 102, SE-230 53 ALNARP Visiting address: Sundsvägen 14 Mobile: +46 70 622 00 42 johan.stenberg@slu.se, www.slu.se/stenberg Johan A Stenberg <Johan.Stenberg@slu.se>

SwanseaU MicrobialGenomics

PhD studentship in Immunology and Evolutionary Microbial Genomics (Swansea University, UK)

General description: Research will be conducted under the direct supervision of Dr. Thomas Wilkinson and Professor Samuel K. Sheppard, and based in the Department of Medical Microbiology and Infectious Diseases at the College of Medicine of Swansea University (United Kingdom). The successful student will join a team of multi-disciplinary scientists working in the MRC Cloud Infrastructure for Microbial Bioinformatics (CLIMB) Centre and the BBSRC-funded medical mass spectrometry team. More information on the research group can be found on http://www.sheppardlab.com/ . Project details: Early and rapid detection of infection is a major goal of Clinical Microbiology. In particular an ability to differentiate between sepsis and other non-infectious causes of systemic inflammation such as Systemic Inflammatory Response Syndrome (SIRS) is particularly pertinent as it will determine antibiotic administration. Recently, we and others have identified 25-hydroxycholesterol as an important inflammatory mediator regulating the production of pro-inflammatory IL-1 driven responses. To date these studies have linked inflammation with the antiviral interferon response. In this context less is known about 25-hydroxycholesterol and bacterial infection. This project will investigate whether major bacterial pathogens, including Staphylococcus aureus, Campylobacter and Escherichia coli generate unique metabolic signatures of 25-hydroxycholesterol and its degradation products. We will use the whole genome data of over 5,000 bacterial isolates organised in our online databases to select the major disease causing clones for host / pathogen whole blood modelling prior to Mass Spectrometry analysis of isolated sera.

The project will focus on two major areas of host pathogen interactions: i) the cellular response of the organism and host; ii) the population genomics of microbes so that host responses specific to a species or evolutionary conserved lineages of pathogens can be identified.

Requirements: Enthusiasm and practical experience in immunology, microbiology, molecular techniques and computer-based genetic analysis is necessary but training and support will be provided to strengthen these areas. The successful candidate will be highly motivated, creative, independent and have a good degree in immunology, molecular biology, microbiology, bioinformatics, genetics or ecology (BSc or MSc, 2:1 or 1st only). Previous experience in a molecular biology/immunology laboratory or in bioinformatics research is also strongly desirable. Good English writing and oral skills are essential.

Details: - The duration of the studentship is 3 years (2015-2018). - The position is open until filled, but a preferred deadline for application is 31st July 2015, to allow for registration to start in the Fall semester. - The position is fully open for UK and EU students. - Salary will be commensurate with regular UK postgraduate stipends, i.e. £13,863/year (˜ euro 18,425/year), tax-free. - Tuition fees are fully covered by the studentship. - Students will also have opportunities to attend national and international conferences during their candidature and a chance to compete for internal College of Medicine travel bursaries.

Application: Please contact us (sheppardlab@gmail.com) for applications (please attach CV and describe motivation). More details: http://www.sheppardlab.com/ Dr. Guillaume Méric NISCHR Health Research Fellow Medical Microbiology and Infectious Diseases Swansea University, College of Medicine ILS1 Building Room 531 (Floor 5) Singleton Park, Swansea SA2 8PP United Kingdom ˜ E-mail: g.meric@swan.ac.uk Phone: +44(0)1792-606672 ˜ Sheppard Laboratory: http://www.sheppardlab.com/ MRC CLIMB Consortium: http://www.climb.ac.uk/ Guillaume Méric <g.meric@swansea.ac.uk>

TrentU AmphibianPopGenetics

MSc, PhD, and PDF positions available V Amphibian occupancy patterns, population genetics, and disease dynamics

Funded by a Strategic NSERC grant (2014), we are building a team of 4 PhD students, 2 MSc students, and 2 post-doctoral fellows, to work on research related to the detection and monitoring of amphibians and their pathogens (chytrid fungus, ranavirus) in Canada.

Using environmental DNA as a basis for the research, the team will conduct: 1) Habitat occupancy modeling for amphibians and their pathogens; 2) Analysis of the evolutionary dynamics of pathogens and amphibian hosts; 3) Assessment of potential synergistic interactions between pathogens and aquatic contaminants; and 4) Modeling the drivers of amphibian population decline. We may also include a component assessing host and pathogen epigenetics and gene expression.

Students will develop research projects that fit within the context of the broader program, such as: Validation of eDNA for detecting amphibians; Assessment of ranavirus pathogenicity; Chytrid fungus evolutionary dynamics; and Modeling drivers of amphibian occupancy and pathogen-induced gene expression. We are seeking students to initiate their research in Spring or Fall 2015, with the research to be conducted across southern Ontario. At least 2 PhD students are needed by May 1, 2015.

Interested applicants should submit a letter of interest, CV, unofficial transcripts and names of 3 references to: Dennis Murray, Trent University, dennismurray@trentu.ca (www.dennismurray@trentu.ca). Because several positions must be filled urgently, postings will be closed as soon as qualified applicants are found. Therefore, interested applicants should apply early.

Individual research team members also can be contacted and include: Craig Brunetti, Trent University craigbrunetti@trentu.ca (www.brunettilab.com); Chris Kyle, Trent University christopherkyle@trentu.ca (http://kylelab.nrdpfc.ca); David Green, McGill University david.m.green@mcgill.ca (http://redpath-staff.mcgill.ca/green/-David%20Green's%20Home%20Page%20frames.htm); David Lesbarreres, Laurentian University dlesbarreres@laurentian.ca (http://gearg.jimdo.com/-people/head/); Marie-Josee Fortin, University of Toronto mariejosee.fortin@utoronto.ca (//labs.eeb.utoronto.ca/fortin); Chris Wilson, Ontario Ministry of Natural Resources and Forestry chris.wilson@ontario.ca (http://-web.nrdpfc.ca/cwilson.htm); Christine Bishop, Environment Canada cab.bishop@ec.gc.ca (http://-christinebishop.blogspot.ca)

dennis murray <dennismurray@trentu.ca>

TromsoUMuseum Metabarcoding

PhD Candidate in metabarcoding at Tromsø University Museum, Norway Application deadline: 10.03.2015 Ref.no: 2015/399 Tromsø University Museum has a PhD position vacant from 1st of July 2015 for applicants who wish to obtain the degree of Philosophiae Doctor (PhD). The position is attached to the research group in taxonomy and biodiversity. The appointment is for a period of four years.

The PhD position will be connected to two ongoing projects. 1) The Norwegian Barcode of Life project (NorBol, http://www.norbol.org/en/) is a national network of research institutions collaborating on DNA barcoding of organisms in Norway and a regional node in the International Barcode of Life Project (iBOL). For vascular plants, we do low coverage shotgun sequencing of genomic DNA and assemble the whole plastid DNA, nuclear rDNA and large parts of mitochondrial genome. 2) The After Ice DNA Metabarcoding project (http://-en.uit.no/ansatte/inger.g.alsos) explores the occurrence of boreal species at northern latitudes by ancient DNA analyses using the P6 loop of the plastid DNA trnL (UUA) intron. Lake sediments have been collected at key sites for palaeoenvironmental reconstructions in Norway and Svalbard.

The PhD candidate will bridge these projects by developing laboratory and bioinformatic tools to apply shotgun sequencing on the ancient samples. This will provide valuable data which the candidate will use to explore effects of past climate change on e.g. species turnover, dispersal, extinction, and phylogenetic diversity. In both projects, we collaborate with colleges at the University Joseph Fourier in Grenoble, who run similar projects focused on the Alps, and the candidate is expected to spend a 3-6 month research stay there.

See: http://www.jobbnorge.no/ledige-stillinger/-stilling/110289/phd-candidate-in-metabarcoding-attromsoe-university-museum Best wishes, Inger

Prof. Inger Greve Alsos Tromsø University Museum P.O.Box 6050 Langnes NO-9037 Tromsø Norway Telephone: +47 77 62 07 96 Telefax: +47 77 64 51 05 Email: inger.g.alsos@uit.no http://en.uit.no/-ansatte/inger.g.alsos http://svalbardflora.net/ Alsos Inger Greve <inger.g.alsos@uit.no>

UAlaska Fairbanks SedgeGeneticDifferentiation

We have 2 years of funding for an MS or PhD student, beginning this summer or later, to help determine levels of genetic differentiation between two sedge species. The project would involve setting up and caring for common gardens in remote parts of Alaska, carrying out lab work (microsatellites or next-gen sequencing), data analysis and paper writing.

The goal of the research is to determine whether the common circumpolar sedge, Carex subspathacea, and the less common C. ramenskii are genetically distinct. Natural populations of the two taxa are morphologically distinct, with one being tall and the other short. It has been suggested that C. subspathacea and C. ramenskii are actually a single species, and that the short stature of C. subspathacea is maintained by heavy goose grazing. In an experiment excluding geese on the YK Delta where the two species co-occur, C. subspathacea reverted to the tall form resembling C. ramenskii, while C. ramenskii reverted to the short-statured C. subspathacea when grazed, suggesting that the two species are actually grazing morphs of the same species However on the north slope of Alaska, C. ramenskii does not occur, and C. subspathacea maintains its short growth form even when excluded from grazing. This poses the questions as to whether there is genetic differentiation among populations of C. subspathacea at the regional scale, and whether C. subspathacea and C. ramenskii are indeed grazing morphs of the same species.

If interested, please contact Diana Wolf <dewolf@alaska.edu> and/or Roger Ruess <rwruess@alaska.edu>

Diana Wolf phone:(907)474-5538 Associate Professor fax:(907)474-7666 Institute of Arctic Biology Dept. of Biology and Wildlife 311 Irving I 902 N Koyukuk Drive University of Alaska Fairbanks Fairbanks, AK 99775-7000 http://raven.iab.alaska.edu/~dewolf/ dewolf@alaska.edu

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UCologne 3 ArabidopsisAdaptation

The University of Cologne invites applications from motivated and committed candidates for a PhD position in the research group of Prof. Juliette de Meaux in the faculty of Natural Sciences.

Genetic adaptation is often shown to proceed by the appearance of a mutation with a large effect that gets quickly fixed in the population. But these mutations do not explain the whole of adaptation. We believe that a significant part of adaptation occurs by the accumulation of small effect mutations, akin to those postulated by Fisher in his infinitesimal model. Can we understand new aspects of adaptation if we dissect the molecular origin of these mutations? This is the question we are addressing in our laboratory.

In this project, the PhD candidate will decipher the molecular basis of adaptive plastic responses in Arabidopsis lyrata. Physiological responses to environmental stimuli are poorly known in the outcrossing A. lyrata, despite its close relatedness to A. thaliana. Using a quantitative-genetics crossing scheme, the candidate will quantify cis-regulatory and dominance variation in gene expression in environmental conditions reflecting regional climatic differences. This approach will extend F1 hybrid studies pioneered by our lab. It aims at highlighting the polygenic basis of local adaptation in this species. This approach allows drawing the distribution of cis-regulatory mutations throughout the genome. Molecular systems (e.g. GO categories, or clusters of co-expressed genes) regionally enriched in cis-acting mutations are likely target of region-specific selection. These targets can subsequently be validated in the lab, or in the field. With this project, the PhD candidate will acquire skills ranging from genomics to molecular genetics and ecology.

The applicant must hold a Master degree in Biology or Bioinformatics and prove interest in plant molecular, population or ecological genetics. Experience in statistical analysis of quantitative data is welcome. Some background in Evolutionary Biology is a must. This position is open to applicants of all nationalities but the language in the lab is English. Applications or questions regarding the position should be sent by mail to jdemeaux@uni-koeln.de, with the following subject line

Ã euro “ PhD application Polygenic adaptation lyrata Ã euro ” de Meaux lab. A letter of motivation, a CV and the contact to at least 2 independent referees should be provided, all in a single pdf file. Revision of applications will begin on April 7th and continue until the position is filled. Funding is for 3-4 years starting in Summer/Fall 2015. For more information on our lab and research visit our website http://www.botanik.uni-koeln.de/1146.html Interested students currently completing their Master thesis are encouraged to informally contact the PI if they have questions concerning the position.

Cologne is Germany’s vibrant Metropolis on the Rhine. The city is well known for its wild carnival, its famous Kolsch beer, its Cathedral and its vivid contemporary art and musical scene. Cologne is the fourth biggest city in Germany with over a million inhabitants from all over the world and an interesting mix of restored historic buildings and modern post-war architecture. Most importantly, Cologne University is one of the oldest and largest Universities in the Country. Our research group is hosted at the Biological Center of the University of Cologne and associated to the Excellence Research Cluster CEPLAS (http://ceplas.eu/de/), which fosters active interactions between plant scientists of the Universities of Cologne, Dusseldorf and the Max Planck Institute of Plant Breeding Research. In this context, our PhD students are assured to start their scientific career in a world-class scientific environment.

The University of Cologne invites applications from motivated and energetic candidates for a PhD position in the research group of Prof. Juliette de Meaux in the faculty of Natural Sciences. Genetic adaptation is often shown to proceed by the appearance of a mutation with a large effect that gets quickly fixed in the population. But these mutations do not explain the whole of adaptation. We believe that a significant part of adaptation occurs by the accumulation of small effect mutations, akin to those postulated by Fisher in his infinitesimal model. Can we understand new aspects of adaptation of we dissect the molecular origin of these mutations ? This is the question we are addressing in our laboratory.

In this project, the PhD candidate will decipher the molecular basis of adaptive plastic responses in the model species A. thaliana. Using classical Qst/Fst approaches, the candidate will evaluate the importance of several plastic responses for regional adaptation. This approach will be complemented by an analysis of regional cis-regulatory divergence with

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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

UFlorida InsectEvolution

Call for applications: PHD ASSISTANTSHIP AVAILABLE in the Lucky Lab at the University of Florida. Research Focus: Insect systematics, speciation, biodiversity, ecology, population genetics, evolution and/or citizen science. Focus on ants is preferred, but not required.

Qualifications: * Demonstrated ability to complete projects and publish results. * Master’s degree in entomology, ecology and evolutionary biology or relevant biological science. Applicants with intellectual interest in ants and evolutionary processes are especially encouraged to apply. * Demonstrated ability to complete projects and publish results. * Excellent written and oral communication abilities. * Minimum GPA of 3.5 and competitive GRE scores. * Experience with the following is an asset: insect classification, collections management, morphological and molecular systematics, bioinformatics, fieldwork.

Interested candidates should send an email to Dr. Andrea Lucky at alucky@ufl.edu with the subject header PHD POSITION IN ANT BIOLOGY. Please include CV, statement of interest and names and contact information of three references. Applications will be considered on a rolling basis, but the suggested submission deadline is March 6. Start date is Fall 2015.

Dr. Andrea Lucky. University of Florida Entomology/Nematology. Gainesville, FL 32611-0620, USA. Email: alucky@ufl.edu. Website: www.andrealucky.com alucky@ufl.edu

UHawaii Manoa CavefishEvoDevo

UHawaiiManoa.EvoDevo_Neuroscience_Cavefish Two Graduate students positions (EvoDevo and Neuroscience) from 2015 Fall University of Hawaii Manoa, Honolulu, Hawaii

We are looking for two graduate students who will work on the fields of “EvoDevo” or “Neuroscience”.

Our group mainly works on the evolution of behavior and its underlying nervous system in Mexican blind cavefish (Astyanax mexicanus). Besides its regressed traits including eyes and pigments, cavefish evolved multiple enhanced sensory systems to guides itself in the perpetual darkness. However, its genetic/genomic bases and the mechanism to integrate the extra sensory information remain to be unknown. Our group will thus investigate the molecular and genetic mechanism to build constructive traits through evolution. The successful candidates have experiences with standard molecular techniques such as DNA/RNA extraction, PCR etc. Research will require rearing and handling of fish embryos and larvae and the experiences with these will be significantly considered.

Application details are described in http://manoa.hawaii.edu/graduate/content/zoology Application deadline for 2015-2016 has already passed (Jan 15th) but applications will be considered up until Feb 23rd. Please contact the PI, Assistant Prof. Masato Yoshizawa (yoshizaw@hawaii.edu) as soon as possible if you have questions and/or consider this position.

Masato Yoshizawa Ph.D. Assistant Professor Laboratory for Evolutionary Biology in Development and Behavior Department of Biology University of Hawaii Manoa 2538 McCarthy Mall, EDM 216 Honolulu, HI 96822, USA

Tel: 1-808-956-6682 Fax: 1-808-956-4745 email: yoshizaw@hawaii.edu

yoshizaw@hawaii.edu

UHuddersfield 5 EvolutionaryGenetics

THE UNIVERSITY OF HUDDERSFIELD: DEPARTMENT OF BIOLOGICAL SCIENCES, SCHOOL OF APPLIED SCIENCES

The Leverhulme Trust Doctoral Scholarship Centre in Evolutionary Genomics

Supervisors: Professor Martin B. Richards, Dr Maria Pala, Dr Martin Carr, Dr Stefano Vanin

Five PhD Studentships in Evolutionary Genomics

Closing date for applications: March 31st, 2015

Funding availability: Funded PhD projects for UK/EU students

We are seeking the first cohort of five PhD scholars in Evolutionary Genetics for the new Leverhulme Trust Centre at Huddersfield, to begin in October 2015. The scholars will receive training from leading experts in their respective fields and undertake cutting-edge research in archaeogenetics, palaeogenetics, bioinformatics, genomics, next-generation DNA sequencing, phylogenetics, population genetics, human evolution and forensic analysis.

We envision openings this year in the archaeogenetics of Europe, Southeast Asia/ Pacific and Native Americans, working with mitochondrial DNA, Y-chromosome and genome-wide variation (including ancient DNA), and in forensic analysis on molecular insect identification from South American and European archaeological burials. In eukaryotic evolution, research work will include the evolution of fungal genomes and transposable element families.

The students will work in the new molecular biology/ancient DNA facilities at Huddersfield, alongside existing students in all of these areas and two research fellows who will provide day to day guidance, along with the academic staff.

Applicants should hold a good first 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. For the insect-related project, a general knowledge of general entomology/zoology and invertebrate morphology is required. 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 then email your CV, transcripts and two letters of recommendation in support of your application to Professor Richards (email: m.b.richards@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: Archaeogenetics: Professor Richards on +44 (0)1484 471676 (email m.b.richards@hud.ac.uk) or Dr Maria Pala on +44 1484 472273 (m.pala@hud.ac.uk) Eukaryotic evolution: Dr Martin Carr on +44 (0)1484 471608 (m.carr@hud.ac.uk) Forensic entomology/funerary archaeology: Dr Stefano Vanin on +44 (0)1484 473179 (s.vanin@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-university-secures-1m-funding-8557938 University of Huddersfield inspiring tomorrow's professionals. [http://marketing.hud.ac.uk/_HOSTED/EmailSig2014/EmailSigFooter.jpg]

M.B.Richards@hud.ac.uk

UIceland PopGenParallelEvolutionCharr

*Ph.D. Scholarship: Population genomics of parallel evolution in Icelandic Arctic charr *

What are the molecular underpinnings of parallel evolution? Do the same pathways, genes or even alleles contribute to divergence in multiple isolated populations within a species?These and related questions will be addressed by a team of researchers, and a capable Ph.D. student responding to this advertisement. The Ph.D. project utilizes the parallel evolution of a small benthic variety of Arctic charr /(Salvelinus alpinu/s) in Iceland and is designed to investigate the genetics of this recent, rapid and repeated diversification.

Project outline

Many key questions of evolutionary genetics can now be investigated in detail due to theoretical advances and high throughput molecular techniques. The project is built on extensive ecological work on Arctic charr, a cold adapted salmonid that invaded Icelandic freshwaters after the last ice age (about 12,000 years ago). In multiple habitats, especially spring fed streams and lakes, charr have diversified into limnetic and benthic forms, and in some cases they coexist in sympatry. *The principal objective of the research is to identify key genes and pathways that associate with ecological specialization (e.g. morphology, life history characteristics) in Arctic charr.*The Ph.D. projects aims are to: i) Identify SNPs that associate with dwarfism and/or morphotype and assess if and how variation at these loci correlates with ecological specializations across multiple populations. ii) Test whether genes that associate repeatedly with ecological specializations are under positive selection or if they have experienced relaxation of purifying selection.

Ideal candidate and requirements

We are seeking a student with dedication, drive and good theoretical background in population genetics and evolution and an interest in the genetics of divergence. The work involves planning and executing sampling in the field, acquisition and analysis of high-throughput sequencing data and numerical analyses. The position will be at the University of Iceland and the work will take place there.Experts at the University of Guelph, Canada, the University of Aarhus, Denmark, and the Hlar University College, Iceland, will also participate in the project.

Qualifications

The applicant must have completed a M.Sc. degree in Biology or related fields from a University approved by the University of Iceland's Graduate School. Those with an advanced degree including at least a 60 ECTS credits thesis project will be given precedence.

Terms of employment

The PhD study should be completed within four years of full time study. The PhD-student may be involved in teaching, for two semesters maximum.

Application

Applicants should send a letter of intent (maximum two pages) explaining your interest in working on this project, why they want to pursue a Ph.D., what they hope to gain and learn during their PhD studies and what makes them suitable for this project. They should also send a CV, transcripts of university diplomas, courses taken at bachelor and masters level, degree project thesis and names and contact information of two persons that could provide letters of references. Applications should be sent before March 15th, 2015, to sigsnor@hi.is <mailto:sigsnor@hi.is>.

University of Iceland

The student will join the Arctic charr group at the Institute of Life and Environmental Sciences, under the supervision of Sigurdur S. Snorrason, Arnar Palsson and Zophonias O. Jonsson. The Arctic charr group consists of several Ph.D. students and senior personnel, and has collaborators in Iceland, Denmark and Canada. The combined expertise covers population ecology and genetics, molecular biology and bioinformatics. At the institute we have well equipped molecular biology labs, and instruments and computer pipelines for high throughput sequencing, are accessible there or at collaborating centers.

The University of Iceland strives to work against workplace discrimination and to offer equal opportunities to everyone.

For further information contact: Sigurdur S. Snorrason (sigsnor@hi.is <mailto:sigsnor@hi.is>), Arnar Palsson (apalsson@hi.is <mailto:apalsson@hi.is>) or Zophonias O. Jonsson (zjons@hi.is <mailto:zjons@hi.is>).

Further information on Arctic charr group at the University of Iceland: http://luvs.hi.is/en/arctic-charr-development-and-genomics Best regards, Arnar

– Arnar Palsson - Associate Professor in Bioinformatics Faculty of Life and Environmental Sciences University of Iceland Sturlugata 7, 101 Reykjavik, Iceland Tel: +(354) 525 4265 Fax: +(354) 525 4632 E-mail: apalsson@hi.is uni.hi.is/apalsson/en/

Arnar Plsson <apalsson@hi.is>

UKonstanz 2 EvolutionaryEcol

The Ecology lab at the University of Konstanz (the group of Mark van Kleunen) and the lab of Biodiversity Research/Systematic Botany (the group of Jasmin Joshi) at the University of Potsdam are seeking to fill two 3-year PhD positions in a DFG-funded project on the role of epigenetic inheritance in rapid evolutionary adaptation of invasive plants. The PhD students will do common-garden experiments and molecular-marker studies using plants from invasive /Solidago canadensis /and /Solidago gigantea/ populations, and will do reciprocal transplant experiments with multiple invasive and native species. One of the PhD students will be based in Konstanz and the other one in Potsdam

Applicants should have a deep interest in plant invasions, plant evolutionary ecology and evolution and hold a Master degree (or equivalent) in the relevant research fields (e.g. plant ecology, evolution). Applicants are expected to have relevant laboratory experience, and an interest in the design and analysis of ecological experiments. This position requires strong communication skills and strong writing and statistical skills (preferably in R).The salary will be at 65% of scale 13 TV-L. The latest starting date is 1 May 2015.

The University of Konstanz < http://www.uni-konstanz.de/index.php?lang=en > is one of the Universities of Excellence in the Federal Republic of Germany, and is located on a small campus just outside the beautiful university town of Konstanz < http://en.wikipedia.org/wiki/Konstanz >, which is at the shore of Lake Constance. The Ecology group < http://cms.uni-konstanz.de/vkleunen/ > is young and very international, and works on a diverse set of topics, including among others mating system evolution, plant responses to global change and determinants of plant invasiveness.

The University of Potsdam < http://www.uni-potsdam.de/en/university-of-potsdam.html > is a young and dynamic university and an equal opportunity employer. Potsdam is a beautiful and green city close to the German capital of Berlin. The Biodiversiy Research/Systematic Botany group < http://www.uni-potsdam.de/en/ibb/researchgroups/fullprofessors/biodiversity.html > works on a diverse set of topics such as plant adaptation to novel environmental conditions, coexistence mechanisms in plant populations and the relationship between biodiversity and ecosystem functions.

If equally qualified, disabled applicants will be considered preferentially. We aim at increasing the number of female researchers and encourage qualified women to apply. The University of Potsdam and the University of Konstanz make an effort to assist its members in family-related issues. The University of Potsdam has been repeatedly awarded the Total E-quality award, and the University of Konstanz has been certified by the Hertie Foundation to be a family-friendly institution.

If you are interested in one of these positions, please, send a letter of motivation (also indicate whether you would prefer the position in Konstanz or the one in Potsdam or do not have a preference), a CV, a writing sample (for example part of your MSc or Bachelor thesis or a paper), and the contact details of two references to marc.stift@uni-konstanz.de. Please, merge all these documents into *a single PDF* file, and include your name in the file name. The *application deadline *is *15 March 2015*.

Mark van Kleunen

Mark van Kleunen <mark.vankleunen@uni-konstanz.de>

UMontreal EvolutionaryPhysiology

*MSc/PhD Position in evolutionary physiology in Montreal**

An opportunity is available for an MSc or PhD position in the research group of Dr Sophie Breton at the Universite de Montreal, to work on the only animal group that diverges from the Strict Maternal Inheritance (SMI) of mtDNA rule, i.e. bivalves with their radically different Doubly Uniparental Inheritance (DUI) system.

Project: DUI is a mother-to-daughter & son and father-to-son mtDNA inheritance system where females transmit their mtDNA to all offspring, and males transmit their highly divergent mtDNA to only their sons (M vs. F DNA divergence >40%). However, the mechanisms underlying DUI are still unknown and the cause of deviation from the "SMI rule" in bivalves remains an open question. This FRQNT-funded project aims to test the hypothesis that has been proposed to explain the function of the M genome in bivalves, i.e. that it could increase the fitness of sperm. Therefore, the successful applicant should have experience or a strong interest in evolutionary biology and physiology.

Qualifications: MSc or PhD applicants should have (or expect to complete) a BSc or MSc degree, respectively. PhD applicants should have publications in PubMed-listed journals. Applicants will be expected to apply for scholarship funding support if selected for the position.

Full funding is available to support the successful candidate for two or three years in addition to a limited travel budget. Expected start date is between June and September 2015. The Universit de Montral is a French language institution where graduate work may be undertaken in English or French.

Interested students should contact s.breton@umontreal.ca *before March 6* and attach a CV, academic transcript, contact details of two academic referees, and a brief description of their research interests.

Please note that only those selected for an interview (Skype or telephone) will be contacted. Preference will be given to Canadian citizens and permanent residents.

– Sophie Breton Professeure adjointe Universit de Montral Pavillon Marie-Victorin, Facult des Arts et des Sciences CP 6128, Succursale Centre-Ville Montral QC H3C 3J7 514-343-7460 (tel)

sophie breton <breton.sophie@gmail.com>

UNevada Reno 2 Biodiversity

Two motivated PhD student applicants are sought to work on projects related to a recently funded, highly collaborative, NSF Dimensions of Biodiversity project at the University of Nevada Reno. The research is focused on a well-studied, tropical system involving plants in the genus Piper (Piperaceae), associated herbivores, and parasitoid wasps and flies. Research will utilize transformative and innovative approaches to quantifying biodiversity that will allow us to link measures of interaction diversity at an ecologically relevant scale to genetic diversity, population genetic structure, and plant chemical diversity. The research includes work in genomics, physiology, and phytochemistry laboratories, as well as field experiments and sampling in Mexico, Costa Rica, Ecuador, Peru, Argentina, and Brazil. We are looking for students broadly interested in evolutionary biology and ecology, with specific interests in the evolution of tri-trophic interactions, population genomics, and the ecological and evolutionary consequences of phytochemical variation. We are an interdisciplinary group of ecologists, evolutionary biologists, and chemists; more information about representative research activities can be found at webpages for the various faculty participants (Dyer, Forister, Jeffrey, Parchman, Richards, Smilanich; http://www.unr.edu/eecb/people).

UNR has a strong interdisciplinary PhD program in Ecology, Evolution, and Conservation Biology (http://environment.unr.edu/eecb/). Graduate students accepted into the EECB program are guaranteed financial support through Teaching Assistantships (TAs) which includes health insurance and an out-of-state tuition waiver. In addition, funds associated with this project are available for summer support, Research Assistantships (RAs), and for field work and data collection associated with specific doctoral dissertation projects.

University of Nevada, Reno (UNR) is a Tier I research university located in a spectacular environment at the confluence of the Great Basin and the Sierra Nevada Mountains. The faculty and graduate students at UNR are highly interactive and include an internationally known group of evolutionary biologists and ecologists. We are equipped with cutting edge molecular and computational resources for modern genome sequence analysis, and a state of the art facility for phytochemical and metabalomic research. In addition to the tropical research, we are also located in an ideal setting for field-based science in the Great Basin and Sierra Nevada regions, allowing enviable access to spectacular montane and desert ecosystems. Reno is 45 minutes from Lake Tahoe, offers a high quality of living, an excellent climate, and is a large enough city to offer diverse activities and amenities. World class rock climbing, skiing, and mountain biking opportunities are in extremely close proximity.

Those interested should contact us via email (tparchman@unr.edu, nolaclimber@gmail.com, mforister@unr.edu, etc.) with a description of your interests, qualifications and preliminary application materials (CV, GRE scores, names and contact information for three references).

Thomas L. Parchman Assistant Professor Department of Biology, MS 314 University of Nevada, Reno Max Fleishman Agriculture Building 1664 N. Virginia Street Reno, NV 89557-0314 tparchman@unr.edu

Thomas L Parchman <tparchman@unr.edu>

UOttawa 2 FungalGenomics

Two Graduate Student Positions (MSc or PhD) in Comparative and Population Genomics of Symbiotic and Pathogenic Fungi - Corradi Lab

The Corradi Lab is currently seeking two talented graduate students (MSc or PhD level). Students will be supervised by Dr. Nicolas Corradi within a CIFAR (Canadian Institute for Advanced Research) - affiliated laboratory located in the Department of Biology of the University of Ottawa, Canada. Lab Website: http://mysite.science.uottawa.ca/ncorradi/index.html The candidates are expected to contribute to some of the ongoing large-scale projects that focus on the Comparative and Population Genomics of two evolutionary unrelated groups of fungi: the Arbuscular Mycorrhizal Fungi (AMF) and the Microsporidia. Enquiries about specific projects can be sent to Dr. Nicolas Corradi (ncorradi@uottawa.ca).

Applicants are expected to have some background in comparative genomics or populations genetics/genomics. Prior experience in either Population Genetics, Environmental Genomics, Metagenomics, genome annotation, Environmental Sampling and Strain cultivation (AMF spores), Fungal taxonomy and programming will be seen as an asset for the final selection of the candidate. Basic knowledge of Linux is desired. The lab is bilingual (English and French). For international applicants, fluency in French is considered as an asset, but is not required.

A complete application package includes 1) a CV, 2) a short description of past research accomplishments and future goals, and 3) the names and e-mail addresses of at least 2 references. Evaluation of applications starts immediately and suitable candidates are expected to join the lab before September of 2015.

The University of Ottawa is a large, research-intensive university, hosting over 40.000 students and located in the downtown core area of Canada's capital city (http://www.science.uottawa.ca/fac/welcome.html). Ottawa is a vibrant, multicultural city with a very high quality of life (http://www.ottawatourism.ca/fr/)

Applications can be sent to Dr. Nicolas Corradi (ncorradi@uottawa.ca).

Representative publications:

- Parisot N. *, Pelin A. * et al. 2014.. Microsporidian genomes harbour a diverse array of transposable elements that demonstrate an ancestry of horizontal exchange with metazoa. Genome Biology and Evolution. 6 (9): 2289-2300. *Contributed equally.

- Riley R. et al. 2014. Extreme Diversification of the MATA-HMG Gene Family in the Plant - Associated Arbuscular Mycorrhizal Fungi. New Phytologist. 201: 254-268

- James T.Y et al. 2013. Shared signatures of parasitism and phylogenomics unite the Cryptomycota and Microsporidia. Current Biology. 23 (16), 1548-1553

- Tisserant E. et al. The arbuscular mycorrhizal Glomus genome provides insights into the evolution of the oldest plant symbiosis. Proceedings of the National Academy of Sciences - USA. 110 (50), 20117-20122R576-R577

- Pombert J.F. *, Selman M.* et al. 2012. Gain and loss of multiple functionally- related horizontally transferred genes in the reduced genomes of two microsporidian parasites. Proceedings of the National Academy of Sciences - USA 109(31):12638-43

- Selman M. et al. 2011. Acquisition of an animal gene by two microsporidia. 2011. Current Biology 21: R576-R577

Nicolas Corradi Professeur Agrégé / Associate Professor Boursier de l'Institut canadien en recherches avancées / Fellow of the Canadian Institute for Advanced Research Université d'Ottawa / University of Ottawa Département de biologie / Department of Biology Pavillon Gendron / Gendron Hall Bureau 257 / Room 257 30 Marie Curie Priv. Ottawa ON Canada K1N 6N5 Tel. +1 (613) 5625800 # 6563 Website:http://mysite.science.uottawa.ca/ncorradi/index.html Nicolas Corradi <ncorradi@uottawa.ca>

UPretoria FlyLongevity

PHD PROJECT AVAILABLE: AGEING, NUTRITION AND OXIDATIVE DAMAGE

Funding is available to test the prediction that longevity in flies is associated with patterns of reproductive effort, and that these patterns are linked to evolutionary history and the cellular processes that may underpin ageing.

Key to the project are selection lines that we have already established. We select for age of reproduction by permitting female marula flies, Ceratitis cosyra, to lay eggs into artificial oviposition substrates at different ages: 5, 15 and 25 days after adult emergence. Selection will continue for at least 20 generations before testing for differences in nutrient intake and ageing mechanisms, but longevity and reproductive effort is determined intermittently as the selection regime progresses.

An opportunity is available for an enthusiastic and motivated student to become involved with this project on the evolution of ageing and work towards the degree of Doctor of Philosophy. The PhD candidate will determine how selection for age of reproduction affects nutritional intake targets, accumulation of oxidative damage and antioxidant capacity in the marula fruit fly, Ceratitis cosyra. This work will involve maintenance of replicate selection lines, the setting up and maintenance of food intake assays coupled with records of fecundity and survival, assays of oxidative damage to proteins (protein carbonyl group formation) and total antioxidant protection, and assays of body composition (body water, total carbohydrates, glycogen, lipids, protein).

Minimum requirements - Completed tertiary studies equivalent to an MSc degree in Biochemistry, Biological Sciences, Entomology, Genetics, Physiology, or Zoology - Commitment to accuracy and ethical research behaviour - Highly-developed skills in the use of SPSS, Statistica or R, and interpretation of their output - Excellent written and oral communication skills in academic English - South African citizen or permanent resident, or a meritorious International applicant

All interested persons that meet the minimum requirements are encouraged to apply.

The successful applicant will receive a tax-free stipend of R80000/year for three years. The project also includes funds for the PhD student to attend at least one international scientific meeting, as well as meetings in South Africa.

Applications must include an application letter that provides evidence for the minimum requirements for the position, a CV including the names and contact details of two academic referees including the MSc supervisor, and copies of academic transcripts that indicate eligibility for the award of an MSc degree.

The project will be based in the Department of Zoology and Entomology on the Hatfield Campus of the University of Pretoria, and supervised by Dr. Chris Weldon, Dr Ruth Archer (Max Planck Institute for Demographic Research, Rostock, Germany) and Prof. Sue Nicolson. The University of Pretoria is a research-intensive university with campuses in Pretoria, its surrounds, and in the country's economic hub, Johannesburg. Pretoria is the administrative capital of South Africa and as such is home to many international embassies. It is also located centrally to large natural areas including the Kruger National Park and several UNESCO World Heritage sites.

Queries and written applications should be directed by email to Dr. Chris Weldon (cwweldon@zoology.up.ac.za).

Applications close: 2 March 2015

Dr. Chris Weldon Senior Lecturer - Entomology

FliES | Flies of Economic Significance Research Group Department of Zoology and Entomology University of Pretoria Private Bag X20 Hatfield 0083 South Africa

http://www.up.ac.za/zoology/?q=user/156/research http://sites.google.com/site/cwweldon/ Chris Weldon <cwweldon@zoology.up.ac.za>

UPuertoRico GenomicsBioinformatics

Joint MS/PHD program in Evolutionary Genomics and Bioinformatics at the University of Puerto Rico at Mayaguez and Penn State University

The Caribbean Genome Center at the University of Puerto Rico at Mayaguez (UPRM) in collaboration with MCIBS Graduate Program Option in Bioinformatics and Genomics < http://www.huck.psu.edu/education/-bioinformatics-and-genomics > of the The Huck Institutes of the Life Sciences < http://www.huck.psu.edu/ > at the Pennsylvania State University (Penn State) announces a new joint graduate program track in Genomics and Bioinformatics.

Successful candidates will in this program will first be admitted to the Masters of Science program in Biology degree at UPR-M with the preferential placement in the Bioinformatics and Genomics at Penn State conditional after the successful completion of MS requirements defense of the thesis at UPR-M. Graduate student support will be available at both institutions (TA and RA).

Our joint graduate program promotes an interdisciplinary training in the biological sciences, that takes advantage of our diverse faculty between the two institutions, joint laboratory, sequencing and computational infrastructure, and a beautiful Caribbean location for your research.

We are looking for enthusiastic, dynamic, and independent students broadly interested in studying the interface between genomics, molecular biology, evolution and bioinformatics. Candidates should ideally have a B.S. degree in Biology or related discipline from an university in Puerto Rico or the United States, and must be proficient in English with a good knowledge of Spanish. Candidates with computer science and/or bioinformatics skills are encouraged to apply. Participants are required to have good communication skills, and the ability collaborate as part of a team to serve as a link between faculties at both institutions. Potential research projects will combine elements of molecular biology, biochemistry, next generation sequencing, bioinformatics, physiology, and molecular evolution with an emphasis on the Caribbean region.

More information on the research at the Caribbean Genome Center research is available at the CGC website (http://www.oleksyk.com), and the Huck Institute for Life Sciences (http://www.huck.psu.edu/-content/research). Potential candidates will be required to first apply directly to the Graduate Program in the Department of Biology at UPR-M (https://app.applyyourself.com/AYApplicantLogin/-fl_ApplicantLogin.asp?id=UPR-GMAYA). At the same time, please apply directly to the program at http://-www.oleksyk.com/apply/ to be considered for the joint program. Please provide a brief description of your background, your research interests, and your reasons for considering the Caribbean Genome Center at UPRM for graduate training.

The application deadline for the 2015-2016 academic year is February 15, 2015.

Please email your questions to Taras Oleksyk (UPR-M) and Cooduvalli Shashikant (PSU)

Dr. Taras K Oleksyk

Associate Professor of Biology

Director of the Caribbean Genome Center

Unievristy of Puerto Rico at Mayaguez

Mayaguez, PR 00680

Dna.lab@upr.edu

Dr. Cooduvalli S Shashikant Associate Professor of Molecular and Developmental Biology Department of Animal Science, College of Agricultural Sciences Program Director, CBIOS Predoctoral Training Program < http://www.huck.psu.edu/content/graduate-programs/-computation-bioinformatics-statistics > Co-Director, MCIBS Graduate Program Option in Bioinformatics and Genomics < http://www.huck.psu.edu/education/-bioinformatics-and-genomics > The Huck Institutes of the Life Sciences < http://www.huck.psu.edu/ > The Pennsylvania State University

css13@psu.edu

Taras K Oleksyk <taras.oleksyk@upr.edu>

UQueensland Australia AlgalGenomicsBioinformatics

A PhD studentship opportunity is available with Professor Mark Ragan and Dr Cheong Xin Chan in the Australian Research Council funded project "Symbiodinium: the evolutionary transition to coral reef symbiont", at The University of Queensland's Institute for Molecular Bioscience. Enthusiastic, qualified Masters or Honours graduates are encouraged to apply.

The successful candidate is likely to have advanced skills in molecular or evolutionary bioscience, bioinformatics and/or computational biology. Knowledge and interest in coral reef biology would be an advantage.

This position is created within a Discovery Projects grant funded by the Australian Research Council to understand the evolutionary transition of the dinoflagellate algae Symbiodinium to coral reef symbiont. Coral reefs are sustained by symbiosis between Symbiodinium and the coral host, and breakdown of this symbiosis under environmental stress results in coral bleaching and eventual death. Through genome sequencing of eight Symbiodinium isolates from reef corals plus two free-living relatives, the Project aims to identify genes that have been gained, lost or shared, or are under adaptive selection, along the trajectory from free-living forms to symbionts.

The University of Queensland's Institute for Molecular Bioscience is a leading global research institute. IMB was established in 2000 as UQ's first research institute and is the cornerstone of one of the largest bioscience research precincts in Australia.

Acceptance is contingent on the candidate (a) being exempt from registration fees, or securing a full fee waiver from the University of Queensland; and (b) securing at least 50% scholarship support for living stipend.

Please email enquiry to: Professor Mark Ragan (m.ragan@uq.edu.au) The University of Queensland Institute for Molecular Bioscience

More info about Ragan group: http://imb.uq.edu.au/-mark-ragan More info about postgraduate studies at the IMB: http://postgraduate.imb.uq.edu.au/-index.php?id=1 c.chan1@uq.edu.au

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USaskatchewan RedSquirrelPhenology

I am currently advertising one Ph.D. student opening in my lab in the Department of Biology at the University of Saskatchewan (www.lanelab.ca) to begin September, 2015. Funding will be provided through a departmental or university-level teaching assistantship or scholarship. Competition for these funding sources is approaching quickly (one scholarship deadline is March 2 and another is a couple of weeks later). If you are interested in this position, therefore, please apply ASAP.

The Project: Reproductive phenology of North American red squirrels (Ph.D.) The Kluane Red Squirrel Project (KRSP) was initiated in the late 1980s and now represents one of the longest running and most-comprehensive studies of a wild mammal in the world. Researchers from multiple universities are involved and exciting collaborations have produced many important, interdisciplinary findings. A clear strength of this project stems from our ability to quantify the primary food resource for individual red squirrels (white spruce seed, cached as cones). This project will investigate the causes and consequences of phenological variation of individual red squirrels. Phenological shifts are now the most often cited ecological responses to climate change and can have substantial consequences for individual fitness and population viability. Quantitative genetics analyses will be used to estimate heritabilities and genetic correlations (i.e., evolutionary potential) in phenological traits and opportunities are available to collaborate with other researchers in energetic physiology, population ecology, endocrinology and animal behaviour. All fieldwork will occur in the spectacular southwest Yukon Territory at KRSPs field camp.

Relevant literature: Lane, J.E., L.E.B. Kruuk, A. Charmantier, J.O. Murie and F.S. Dobson. 2012. Delayed phenology and reduced fitness associated with climate change in a wild hibernator. Nature 489: 554-557.

Williams, C.T., J.E. Lane, M.M. Humphries, A.G. McAdam and S. Boutin. 2013. Reproductive phenology of a food-hoarding mast-seed consumer: resource- and density dependent benefits of early breeding in red squirrels. Oecologia 174: 777-788.

Boutin, S. and J.E. Lane. 2014. Climate change and mammals: evolutionary versus plastic responses. Evolutionary Applications 7: 29-41.

Graduate student funding at the UofS is quite competitive so the successful applicant will have a GPA >80% (converted to the UofS 1-100 scale) over the past two years of schooling and a degree in a relevant discipline (i.e., Ecology, Evolutionary Biology, Physiology, Environmental Biology). Of note, while I certainly appreciate the hard work that is put into obtaining a degree in Biotechnology, I do not view this as relevant experience for these positions. In addition, a passion for fieldwork (in a beautiful, but remote, place), strong scientific communication skills (both written and oral) and statistical proficiency (or a willingness to gain it) is necessary. Evidence of scientific productivity (manuscripts published or in preparation, conference attendance and presentation) is also expected.

If you are interested in applying for this position, please submit a cv (including names and contact details of references), a short (1 pg) description of research interests and an unofficial copy of your transcripts to jeffrey.lane@usask.ca. Applications will be accepted up to May 31, 2015, but will be evaluated as theyre received. To ensure full consideration of your application, therefore, please submit asap. Any questions can be directed to Jeff Lane (email above).

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

USaskatchewan WildHorses

Ph.D. applications to work with the wild (feral) horses of Sable Island, Nova Scotia: focus on ecology and evolution and/or conservation.

Location: University of Saskatchewan, Saskatoon, Saskatchewan, Canada

Closing: Will need to contact me as soon as possible to put together an application for internal scholarship, due Thursday, March 5, 2015. Start date is negotiable, but ideally students would be available July 1 or August 1 for immediate field work. Application for the scholarship will require an application to the U of S College of Graduate Studies and Research (online) well ahead of time, and to meet the deadline for the scholarship applications should be submitted asap (small online fee), i.,e., by early February. Students must have a record of publication in mainstream peer-reviewed journals and GPA of 3.8 or higher (to be competitive for this scholarship opportunity).

Apply: Email me a CV and pdf copies of both undergrad and graduate transcripts. Email to philip.mcloughlin@usask.ca. Please write Island PhD as the subject line.

Description: We are developing a long-term, collaborative individual-based program of research into the ecology and evolution of the feral horses living on Sable Island, Nova Scotia. As part of this initiative, I am looking to recruit a Ph.D. student to ask fundamental questions of the population ecology, life history, behaviour, conservation, and/or evolution of the feral horse population. I am particularly looking for a mature M.Sc. student that is interested in developing a Ph.D. program that will contribute to and make use of the long-term dataset my lab is collecting on the life histories of the horses on the island, and collaborate with geneticists aligned with our program. This summer was the seventh year of data collection, which includes summer censusing and identification of all individuals on the island using digital photography, and documentation of individual life histories with the goal of constructing whole-island pedigrees. Sample sizes are large, with 552 horses alive on the island in Aug 2014. Ph.D. students with 2V3 years of further data collection will be in a position to ask interesting questions regarding the populations mating system, landscape and conservation genetics, individual-based dynamics, band dynamics and dispersal, behaviour and dominance, habitat selection, social networks, sex ratios and sexual selection, and questions involving traits such as intestinal parasite communities, body size and coloration patterns. Trends in the above will likely be related to a very strong and interesting gradient in habitat quality along the length of Sable Island from west to east, associated with availability of preferred forage and access to fresh water (horse density drops by half from west to east). We are also very interested in students with a background in conservation biology as we are currently developing a research theme examining the risks inherent to small populations like that on Sable, including inbreeding depression and demographic stochasticity.

Field work on Sable Island is a team effort, and all students must be prepared to contribute to common aspects of field work and assist others with their projects in addition to working on their own research program. The former will include daily walking censuses and photography of horses, identifying individuals from digital photographs, database management, and collection of samples. All projects on the island flow from the individual- based study of the horse population, and contributing to the overall success of each field season is a requirement. For this particular application we are looking for a field team leader, and a demonstrated ability to fill such a role will be considered an asset. The successful student must work well in teams, deal well with life in a remote research station, be able to travel for field work for up to 2 months per summer by small airplane, fishing trawler, helicopter, or frigate; accept the limited diet available in remote field camps (with communal cooking), and be reasonably fit (as walking censuses require lots of hiking). Courses on first aid and driving All Terrain Vehicles will be provided prior to field work. Field work will occur principally in late summer on Sable Island; further information on this field site can be found at my lab website, http://mcloughlinlab.ca/lab/ It is important for applicants to be mature enough to develop their own insightful questions. That said, our lab is following several lines of research that potential students may want to build on. Current students are studying or have studied spatial heterogeneity in horse population growth on the island, stress as it relates to band structure and dynamics from cortisol (from hair), parasites, dispersal, body size, condition, patterns in vegetation and successional dynamics, and

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UZurich ExperimentalBiodemography

Subject: PhD position in Experimental Biodemography at University of Zurich (March 23rd deadline)

We are looking for an enthusiastic PhD student with quantitative skills to work in experimental biodemography at University of Zurich. Details of the position can be found at http://www.popecol.org/phd-position/ Potential candidates can get in touch with me for more information. The application deadline is March 23rd.

Arpat Ozgul

Assistant Professor of Population Ecology

Institute of Evolutionary Biology and Environmental Studies | University of Zurich Office: 34-J-24 | +41 (0)44 63 *54746* | arpat.ozgul@ieu.uzh.ch | www.popecol.org Arpat Ozgul <arpat.ozgul@ieu.uzh.ch>

UZurich Macroevolution

Graduate position in macro-evolution / systematics / macro-ecology in Zurich.

The Cape flora of South Africa is arguably the most species-rich temperate flora, and this richness is expressed at both local (alpha-diversity) and regional (gamma-diversity) level. Much of this diversity was generated in a small number of radiations, consequently many closely related species co-exist. We will explore the traits that allow such co-existence. This research involves, inter alia, phylogeny reconstructions (in order to explore phylogenetic community assembly and phylogenetic beta-diversity), anatomical-morphological research (to compare the traits of co-existing species), eco-physiological experimentation, and field work. The work will be supervised by Peter Linder (peter.linder@systbot.uzh.c), and will be based in the Institute of Systematic Botany of the University of Zurich (http://www.systbot.uzh.ch/index_en.html). These projects are part of a research program using the Cape flora as test case to investigate the evolution of plant diversity.

Successful candidates will have a Masters degree in botany / plant sciences and a valid drivers licence. Interested candidates should send Peter Linder their CV's, the names of three potential referees, and a motivativion letter detailing why you are interested in this research.

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

Email: peter.linder@systbot.uzh.ch

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

Vienna PlantGenomics

A PhD student position funded by the Austrian Science Fund (FWF) is available in the group of Plant Ecological Genomics (http://plantgenomics.univie.ac.at) at the University of Vienna, Austria within the project "Understanding evolution through recurrent allopolyploidization". The fellow will be investigating the impact of polyploidization on adaptation in wild European orchid allopolyploids (see www.botanik.univie.ac.at/-systematik/projects/dactylorhiza/). We will combine the most recent genomic and transcriptomic technologies with field experiments to investigate the nature and adaptive value of the molecular diversity produced by iterative allopolyploidizations to result in rapid ecological diversification. The research will also involve working with environmental data, both climatic data and metagenomic biotic data. Field work across large European areas will be undertaken by the team yearly.

We are looking for a highly motivated candidate with an excellent academic track record. A MSc degree (or equivalent) in a related discipline (e.g., molecular ecology, genetics, bioinformatics, evolution) is desirable. The successful candidate is expected to be able to demonstrate some previous experience with evolutionary or ecological studies. Experience with next generation sequencing methodology and/or knowledge of R are a plus, but excellent organization and communication skills are a must.

The position offers a competitive salary (of ca. euro 28,000 per year before tax according to FWF regulations, including social and health security), the opportunity to attend two workshops/summer schools and two international conferences, and to shortly visit a collaborating lab abroad. According to performance, the fellow may become associated with the Vienna Graduate School of Population Genetcs (http://www.popgen-vienna.at/), with additional benefits.

The working language in our laboratory is English; however, German skills will be helpful for everyday life in Vienna. Vienna is a highly attractive city in beautiful surroundings, with a multinational population, and many educational and recreational opportunities. The presence of several outstanding research groups (see www.univie.ac.at/evolvienna/) make Vienna a hot spot of evolutionary research and offers ample opportunities for interactions with peers.

To be considered please send your application per email to ovidiu.paun@univie.ac.at including your CV, a two pages letter of intent describing why are you personally interested in this position and why is polyploidy important for plant evolution, and the names and contacts of three academic referees. Incomplete applications will be disregarded. Screening of applications will begin immediately and will continue until the position is filled. The latest preferred start date is April 1st, 2015.

Dr Ovidiu Paun Department for Botany and Biodiversity Research University of Vienna Rennweg 14, A - 1030 Vienna http://plantgenomics.univie.ac.at ovidiu.paun@univie.ac.at

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Vienna PopulationGenetics

PhD positions in Population Genetics

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

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

Topics include:

— Characterizing piRNA content in D. melanogaster and D. simulans — Population history and adaptation in natural Arabidopsis populations — Population trees and polymorphism-aware phylogenetic models — Episodic selection histories and co-evolution — Wolbachia infection dynamics in evolving Drosophila populations — Functional characterization of beneficial alleles in Drosophila — Genomic signature of migration between populations adapted to different environments — Identification and characterization of naturally occurring variation affecting reproductive diapause in D. melanogaster — Modified evolve and re-sequence design — Convergent and adaptive evolution during ecotype formation in Arabidopsis arenosa — Convergent and adaptive evolution during high-alpine ecotype formation in Heliosperma (Cariophylaceae — The role of epistasis for the invasion, establishment, and survival of locally beneficial mutations

Only complete applications (application form, CV, motivation letter, university certificates, indication of the two preferred topics in a single pdf) received by May 03, 2015 will be considered. Two letters of recommendation need to be sent directly by the referees.

All information about the about available topics, the training program and the application procedure can be found at www.popgen-vienna.at Regards, Julia

– Dr. Julia Hosp Vienna Graduate School of Population Genetics Coordinator www.popgen-vienna.at c/o Institut für Populationsgenetik Vetmeduni

Vienna Veterinärplatz 1 A-1210 Vienna http://www.vetmeduni.ac.at/en/population-genetics/ Tel: +43 1 25077 4338 Fax: +43 1 25077 4390 SMBE 2015 in Vienna http://smbe2015.at julia.hosp@gmail.com

Jobs

Africa WildlifeProjectCoordinator

Job Title African Wildlife forensics: project coordinator.

Salary Up to 35,000 GBP per annum

Start date: April / May 2015

Role A two-year full-time post is available for a project coordinator to help deliver wildlife forensic capacity to Southern and Southwestern Africa. The project, funded under the UK Illegal Wildlife Trade Challenge Fund, aims to coordinate the development of a regional wildlife DNA forensics network with hubs in Botswana and Gabon. The successful applicant will have experience of forensic science, evolutionary genetics and project management, and ideally experience of working in developing countries. The post will involve extensive independent travel, principally in Africa but also worldwide; fluent written and spoken English is essential and

French language ability is desirable.

TRACE Wildlife Forensics Network is a UK based specialist NGO working primarily in Southeast Asia and Africa to build capacity for the application of forensic science to wildlife law enforcement. This project will be undertaken in collaboration with the United Nations Office on Drugs and Crime.

For further information please contact: Dr. Rob Ogden, Programme Director, TRACE Wildlife Forensics Network. Email: rob.ogden@tracenetwork.org;

Applicants should email a C.V. and letter of application as word documents or pdfs to info@tracenetwork.org

Closing date: 21st of February 2015.

Ross McEwing <ross.mcewing@tracenetwork.org>

AMNH NewYork CuratorComparativeBiology

Senior Search: Curator, Professor, and Director of Comparative Biology Initiative, American Museum of Natural History

The American Museum of Natural History (AMNH) in New York invites applications and nominations for an outstanding scholar at the Full Curator & Full Professor level with internationally-recognized research and leadership credentials, and demonstrated, ongoing high-impact research productivity and grantsmanship, to provide innovative leadership for a new museum-wide initiative in comparative biology. This initiative will incorporate the work of multiple investigators at the Museum and at collaborating institutions in genomics (including eukaryotic [including microbial] genomics, metagenomics, phylogenomics, transcriptomics, etc.), phenomics (large-scale phenotypic analysis) and bioinformatics/computational biology, aimed at understanding the evolution and relationships of organisms in ways that clarify and illuminate the architecture of life. The successful candidate for this position should show experience and interest in managing large-scale, interdisciplinary, collaborative, multi-institutional projects and is expected to qualify for and be appointed as a tenured full curator in either the Division of Invertebrate Zoology or Vertebrate Zoology, and as a full professor in the Richard Gilder Graduate School at the AMNH. We seek a creative, active, broad-based researcher and dynamic academic leader who interacts well with others and who will utilize the extensive resources the Museum has to offer in the way of collections, research instrumentation and laboratories, interactions with Museum colleagues and collaborations with area organizations (including the New York Genome Center, area universities, New York Botanical Garden, and others), teaching and mentoring, exhibition, and public education.

We particularly seek applications from, or nominations of, candidates with a compelling vision for the future trajectory of their science, and for comparative biology in general, and whose research addresses fundamental, cross-disciplinary questions. In addition to the above-noted expectations for high productivity and grantsmanship, the successful candidate will have outstanding communication skills in engaging diverse communities and demonstrated capabilities in management of collaborative projects and decision-making. Experience in interacting with governmental and non-governmental agencies and in fundraising are highly desirable, as are collection-based, field-based and/or computational research. Other responsibilities or opportunities include advising graduate students and postdoctoral fellows, offering courses in the Comparative Biology Ph.D. Program of the Museum's Richard Gilder Graduate School, institutional service, development activities, and participating in Museum-sponsored exhibits and educational programs.

In addition to applications, we invite recommendations or nominations of potential candidates, and request that these include a resume and contact information for the nominee. Nominations or applications can be submitted to seniorcuratorsearch@amnh.org. Applicants should submit the following materials electronically, preferably as PDF files, via a single email message to seniorcuratorsearch@amnh.org (Subject line: 2015 Senior Curator IZ-VZ Search Committee: your name): 1) a cover letter in which you indicate your interest, experience, and qualifications for the position; 2) a curriculum vitae; 3) PDF files of up to five recent publications; and 4) names and contact information for five referees who can comment on leadership, scientific and other skills and accomplishments noted above (to be contacted by the Museum only at the time of arranging an interview or for the process of tenure review in the case of a potential appointment). Inquires should be directed to John Flynn, Chair of the Search Committee and Dean of the Richard Gilder Graduate School: dean-rggs@amnh.org. Applications or nominations should be received by April 2, 2015.

Employer Information: The American Museum of Natural History is one of the world's preeminent scientific and cultural institutions. Since its founding in 1869, the Museum has advanced its global mission to discover, interpret and disseminate information about human cultures, the natural world and the universe through a wide-ranging program of scientific research, education and exhibition. The Museum's research collections include more than 33 million natural history and cultural objects, and AMNH scientists undertake more than 100 expeditions annually. Science at the Museum includes five academic divisions, the Richard Gilder Graduate School, Sackler Institute of Comparative Genomics, 1 million specimen-capacity Ambrose Monell Cryo Collection, Center for Biodiversity and Conservation, high performance computational facilities, Microscopy and Imaging Facility, Southwest Research Station, the largest independent natural

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CheetahConservationFund Namibia LabTech ConsGenetics

Genetics Laboratory Technician or Manager Cheetah Conservation Fund, Namibia

The Cheetah Conservation Fund (CCF), Namibia, is currently looking for a highly motivated individual to join its genetics laboratory staff in the position of Laboratory Technician or Manager.

The specific title and remuneration are dependent on the applicant's level of experience. The successful applicant is expected to start in early March 2015. Applicants should send their CV, letter of motivation, and transcripts to genetics@cheetah.org.

The successful candidate should have a strong background in best laboratory practices in molecular biology, and have excellent organizational and communication skills. His/her main responsibilities will include maintenance and operation of our genetic analysers and supervision of interns and students, ensuring that good laboratory practices and protocols are followed. Other responsibilities will be curation of databases, development of laboratory services, writing of permit applications and reports, and keeping the laboratory adequately stocked at all times. Prior experience in these particular tasks is not required; however, willingness to learn and attention to detail are essential. This position will also provide opportunities for direct participation in research projects as time permits.

The genetics laboratory is located at the CCF research centre, about 40 km east of Otjiwarongo, Namibia. Staff members live on CCF property and housing is provided. Meals are prepared by CCF kitchen staff and are eaten communally. Further information regarding CCF and its mission to conserve cheetahs in the wild may be found at www.cheetah.org . Anne Schmidt-Küntzel, DMV, PhD Assistant Director for Animal Health and Research Life Technologies Conservation GeneticsLaboratory Email: genetics@cheetah.org Tel: +264 67 306 225 Fax: +264 67 306 247 Cheetah Conservation Fund (CCF) www.cheetah.org

genetics@cheetah.org

ChineseU HongKong ResAssociate

Post: CUHK Research Associate/Assistant in animal microRNA evolution

Description: We are inviting applications for one to two vacancies of Research Assistant/Research Associate in animal microRNA evolution.

For Research Associate, applicants should have a PhD, or Master's degree plus four years' relevant post-qualification experience. For Research Assistant, applicants should have a Bachelor's degree in Life Science or relevant discipline. Work experience in either molecular biology or bioinformatics is preferred.

Appointments will be made on contract basis for one year commencing as soon as March or April 2015, and renewable subject to mutual agreement.

Interested candidates can contact Dr. Jerome Hui (jeromehui@cuhk.edu.hk).

Jerome Hui <hui.jerome@gmail.com>

ColoradoStateU GuppyBehavior SummerREU

The Guppy Group in the Dept. of Biology at Colorado State University is seeking applicants for an NSF Research Experience for Undergraduates (REU) position in summer 2015 to study the effects of gene flow on guppy behavior. The successful applicant will work closely with Drs. Lisa Angeloni and Chris Funk and PhD students John Kronenberger and Dale Broder to develop an independent research project centered around our ongoing gene flow experiment. The primary objective will be to assess how our experimental treatments differentially affect behavior and how this, in turn, impacts fitness. This REU will provide invaluable experience in study design, behavioral assays, molecular genetic techniques, data analysis, and dissemination of results, and will thereby prepare the student for graduate school and/or a career in inquiry-based scientific research.

This position lasts for 12 weeks (beginning mid- to late-May) and allows for two weeks off if the student so desires. A stipend of $2,000/month will be provided to cover housing and other expenses, and additional funds are available for travel to a scientific conference. The student must be a U.S. citizen or permanent resident and should be enrolled as an undergraduate in Fall 2015. Applications from women, underrepresented minorities, and persons with disabilities are especially encouraged.

To apply, please email the following application materials as PDFs to John Kronenberger (john.kronenberger@colostate.edu) by Friday, March 20th: 1) A cover letter including the following: - Why you are interested in this position? - What previous experience do you have that is relevant for this position? - When are you available to start and end this position? - What are your future plans?

2) A resume including contact information for at least two references

3) A transcript (unofficial is acceptable)

For more information about the experiment referred to above, please visit: http://johnkronenberger.weebly.com/ John A. Kronenberger PhD Student Graduate Degree Program in Ecology Department of Biology Colorado State University 770-355-1855 Check out my website! < http://johnkronenberger.weebly.com/ >

j.kro365@gmail.com

CornellU FieldAssist PlantPollinatorEvolution

The Geber lab at Cornell University seeks a highly motivated, detail-oriented assistant for summer 2015 field research in the Southern Sierra Nevada (May-July) and lab work in Ithaca, NY (July-August). We are studying four species of annual plants in the genus Clarkia and their specialist bee pollinators. Our current fieldwork focuses on how pollinators may impact plant species coexistence.

Our research sites are located in Kern County, California. The lab rents a house on a property where other labs working in this system are also based in the summer. This field assistant would have a private bedroom, access to a shared bathroom and a communal kitchen, and wireless internet access. Frequent trips are made into town (Lake Isabella and Kernville) for groceries and other supplies.

Successful applicants are expected to assist in data collection, data entry, and flower, seed, and bee collection in the field; work in Ithaca will consist of sample processing and data analysis. The assistant will work a 39 hour work week. Weather conditions in the Sierras can be very hot and dry (100+ degrees F) in the summer, so assistants should be prepared to work in hot conditions. Applicants must be able to hike up and steep hills for up to 1 mile at a time, stoop or kneel for extended periods of time, and work in proximity to bees and snakes. The work can be very physically demanding and tiring, and the research team typically collects data 7 days a week. A good sense of humor and a positive attitude are essential.

Qualifications: 1) some undergraduate education in biology, ecology, or related field, or equivalent experience; 2) experience hiking and working outdoors and or previous field research experience; 3) ability to perform repetitive tasks with a cheerful attitude and with attention to detail; 4) willingness to live and work in close quarters with other researchers in a house. Previous experience working with plants, bees, or insects is preferable but not required. Applicants must be available from early May through late August although exact start/end dates are flexible.

Compensation: transportation to and from California, a private room with internet access in the field house, and salary will be provided. Applicants will be responsible for securing their own housing in Ithaca for July and August.

The deadline for applications is March 20. Applicants should submit: 1) a short (1 page maximum) cover letter describing their qualifications as well as future academic/professional goals; 2) a resume or CV outlining previous work experience, relevant courses (completed or in progress), extracurricular activities; and 3) contact information for two references.

Email to: Monica Geber, Professor of Ecology and Evolutionary Biology mag9@cornell.edu

kee39@cornell.edu

GoetheU Frankfurt Bioinformatics

Evolutionary Bioinformatics A position in evolutionary bioinformatics is available in the lab of Prof. Imke Schmitt at the Senckenberg Biodiversity and Climate Research Centre and Goethe University Frankfurt. The successful candidate will support ongoing projects on the evolution and adaptation of lichen-forming fungi and fungal communities by assisting with next generation sequencing data analysis. Depending on the candidate's preferences, he/she can also develop his/her own projects. We are looking for applicants with a Bachelor (or similar degree) in biology or computational biology, and expertise in de novo genome assembly, genome annotation, or metabarcoding. Experiences with python, perl, bash, or R are necessary; knowledge of unix, parallelization on clusters and massive RAM computers is advantageous. Additional tasks will be supporting the lab members in computer administration, data archiving, and data organization. The ideal candidate works well in a team, is highly motivated to work independently, communicates well, and speaks fluent English. My lab and the entire institute provide a very supportive atmosphere. The broader research environment at Senckenberg and Goethe University offers chances for collaboration with experts in fields ranging from molecular ecology and evolution, phylogenetics, to macroecology and climate change biology (modeling and statistics). Attractive computing infrastructure is available (high-RAM computers, clouds, and clusters). Frankfurt, a vibrant city in the center of Germany, provides ample cultural and recreational opportunities and excellent infrastructure for travel. Salary will be TV-H E11, according to the German public service pay scale. We offer full benefits, and training opportunities. The position is available from April 1st 2015, with a flexible start date. The initial contract will be for two years, but it can be extended indefinitely. To apply, please send a cover letter detailing research interests and experience, a C.V., a copy of your bachelor certificate, and a list of two professional references. Please email your application to Prof. Dr. Katrin Böhning-Gaese, c/o Senckenberg Gesellschaft für Naturforschung, Senckenberganlage 25, 60325 Frankfurt am Main, recruiting@senckenberg.de, indicating reference number #8.2 before February 28.2015. Informal inquiries to Imke Schmitt (imke.schmitt@senckenberg.de), before the application are welcome.

Dr. Imke Schmitt Goethe University Frankfurt and Biodiversity and Climate Research Centre BiK-F Senckenberganlage 25 60325 Frankfurt am Main Germany

Tel.: +49 6975421855 email: imke.schmitt@senckenberg.de website: www.bik-f.de/root/index.php?page_idC4 office: Mertonstr. 17-21, Jügelhaus 421C

Imke Schmitt <Imke.Schmitt@senckenberg.de>

HarvardMedSchool 2 LabTech ancientDNA

Research Technician I

Harvard Medical School, Boston, Massachusetts / Howard Hughes Medical Institute

Reports To: David Reich, PhD

A web-based version of this job advertisement can be found a http://www.hhmi.org/careers/2333

We offer an opportunity to support a cutting edge ancient DNA laboratory at Harvard Medical School (http://genetics.med.harvard.edu/reich/-Reich_Lab/Welcome.html) that is studying the impact of human history on biology and disease.

The successful candidate will assume a research technician position and will work closely with scientists studying DNA from human remains dating back over the last 20,000 years.

Principal Responsibilities:

Conduct experiments in support of critical core ancient DNA project in the laboratory

Carry out protocols and propose method options with goal of facilitating successful completion of research aims

Receive samples of ancient teeth and bones and ensure that they are handled and stored in a way that minimizes contamination

Clean and drill artifacts in clean room environment to prepare for release of DNA

Extract DNA and prepare for next generation sequencing in clean room environment

Perform PCR, DNA purification and quantification, solution hybrid capture, and sequencing

Analyze data to identify best samples for further analysis

Maintain meticulous records of experiments and analyses in both lab notebook and tracking databases

Return unused samples to collaborators

Provide laboratory-specific training for incoming research fellows, technicians, graduate students and interns

Order laboratory supplies on timely basis and receive/place all supplies in proper location

Maintain laboratory equipment and oversee repairs

Maintain cleanliness and orderliness in the laboratories

Communicate experimental results in weekly meetings

Preferred Qualifications:

B.A./B.S. in the life sciences with hands-on research experience in basic laboratory techniques and understanding of molecular biology principles

Familiarity with genetics, PCR and, ideally, NGS library preparation/sequencing

Training in sterile laboratory techniques

Strong communication and computer skills, including demonstrated proficiency with Microsoft Word, Excel and, ideally, UNIX.

Strong organizational skills and ability to employ good judgment in prioritizing tasks

Experience in ancient DNA and/or sterile techniques is a great advantage

Additional Information:

Please submit a cover letter and three references with your resume. Please include “008-200 Research Technician” in the subject line of your email.

To Apply:

To apply for this position, please email your resume to:

Nadin Rohland Boston, Massachusetts 02115 Email: nrohland@genetics.med.harvard.edu

Application Deadline: Open Until Filled

David Reich <reich@genetics.med.harvard.edu>

HarvardU Herbaria BiodiversityInformatics

oEB HR at Harvard University

Business Title: Biodiversity Informatics Manager

The Harvard University Herbaria (HUH), with more than five million specimens, comprise the world’s largest University herbarium. Research at HUH in evolution, biodiversity, and conservation revolves around the scientific collections and libraries. In recent years, several ambitious projects to digitize the entire HUH holdings have been initiated. At present, 10% of the collections are digitized.

The HUH is seeking to hire a Biodiversity Informatics Manager that will provide leadership, management, and stewardship of the informatics collections and initiatives. The successful candidate will be responsible for addressing the needs of the academic and scientific community engaged with HUH collections, and the natural history collections more broadly. To meet these needs, the candidate will work with the HUH Director and staff, including a three member biodiversity informatics team, to set priorities and develop plans and initiatives. This may additionally involve interacting with FAS Science Division Research Computing to develop and implement technical solutions.

The Biodiversity Informatics Manager will oversee the development, maintenance, and enhancement of the databases that document the collections and support HUH activities, including library related goals. The candidate will supervise and manage HUH’s digitization activities and oversee the management and sharing of the resulting digital assets. With database and informatics support from Research Computing, the successful candidate will initiate, develop, implement, and manage scientific and academic applications and informatics projects and initiatives to ensure access to and sharing of biodiversity data with the world. Tasks include, but are not limited to: collecting, organizing, and analyzing natural history specimens, spatial modeling, and databasing. The candidate will work with the Director and HUH staff to develop grant proposals for the funding of informatics projects by external agencies, including the National Science Foundation. The person in this position will also act as a liaison to organizations and projects internally, nationally and internationally, including the Harvard Museums of Science & Culture, in which acquisition and delivery of biodiversity information is central.

The basic qualifications for this position are as follows: Masters Degree in botany or a related discipline and five or more years experience in planning, development, and implementation of biodiversity informatics projects. Fluency in at least one programming language is a requirement. Previous experience with highly technical and collaborative projects, including digitization of biological collections and digital media access to collections via databases, digital tools, and websites. Familiarity with at least some of the following: UNIX, HTML, XML, CSS, PHP, SQL, MySQL, ArcGIS, Mac OS X, Windows 7/8, Microsoft Office, Adobe Photoshop, WordPress.

The ideal candidate will also have these additional qualifications: Proven ability to lead, manage, and engage a broad constituency is required. Demonstrated knowledge of museum collections and biodiversity informatics preferred. Superior communications skills required. Must be able to work with people with varying degrees of IT expertise. In order to be considered for this position, all candidates must apply through the Harvard University employment website at employment.harvard.edu. Please reference position requisition number: 34999BR. When applying for this position please submit your resume and cover letter in our preferred format as one combined document (resume followed by cover letter).

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

"Lee, Morgan" <morganlee@fas.harvard.edu>

ImperialCollege London ResAssoc EvolutionaryGenomics

Imperial College London

Department of Life Sciences

Faculty of Natural Sciences

Research Associate in Evolutionary Genomics

Salary: £33,410 - £42,380 per annum (maximum starting salary £33,410)

This is an exciting opportunity for a Research Associate with an interest in Speciation Biology, Plant Biology and Evolution. The successful candidate will carry out cutting edge research in evolutionary genomics, largely analysing existing data and writing up publications. You will have a solid background in population genetics and genomics, statistics and modelling with a strong interest in evolutionary biology. The aim of the project is to determine the relative contribution of pre- versus post-zygotic isolation in the evolution of sympatric Howea palms and to identify those loci underlying speciation.

The post is funded by the Natural Environment Research Council, and will be based at the Silwood Park Campus. The successful candidates will work closely with Professor Vincent Savolainen and his research group. Further details of the research group can be obtained from the research group website: http://www3.imperial.ac.uk/-people/v.savolainen . You must have a PhD or equivalent qualification in evolution, ecology, genetics or a closely related discipline. The successful candidate will have expertise in population genomics, proficiency in statistics and knowledge of and in depth experience of working in evolutionary biology. Experience of management and analysis of complex genetic data and excellence in working in a multi-disciplinary environment are essential.

You must have experience of working in a team, be able to develop and apply new concepts and have a creative approach to problem-solving. You must also have excellent verbal and written communication skills and be able to write clearly and succinctly for publication.

This is a full-time, fixed term appointment available for up to 3 years.

Our preferred method of application is online via our website http://www.imperial.ac.uk/job-applicants/

(please select "Job Search" then enter the job title or vacancy reference number including spaces - NS 2015 038 JT into "Keywords"). Please complete and upload an application form as directed.

Alternatively, if you are unable to apply online, please contact Mrs Christine Short on 020 7594 2276 or email c.j.short@imperial.ac.uk to request an application form.

Closing date: 26 March 2015 (midnight GMT)

Committed to equality and valuing diversity. We are also an Athena SWAN Silver Award winner, a Stonewall Diversity Champion, a Two Ticks Employer and are working in partnership with GIRES to promote respect for trans people.

"Thomas, Jenny" <j.thomas@imperial.ac.uk>

ImperialCollege London ResAssoc EvolutionaryGenomics 2

Imperial College London

Department of Life Sciences

Faculty of Natural Sciences

Research Associate in Evolutionary Genomics

Salary: £33,410 - £42,380 per annum (maximum starting salary £37,070 per annum)

This is an exciting opportunity for a Research Associate with an interest in Speciation Biology, Plant Biology and Evolution. The successful candidate will carry out cutting edge research in evolutionary genomics, largely analysing existing data and writing up publications. You will have a solid background in population genetics and genomics, statistics and modelling with a strong interest in evolutionary biology. The aim of the project is to micropropagate red-stemmed mutant Howea palms from the wild that stably and consistently display the red characteristic, and are therefore fit for plant breeder rights/patenting and commercialisation.

The post is funded by the European Research Council Proof of Concept Scheme, and will be based at the Silwood Park Campus. The successful candidate will work closely with Professor Vincent Savolainen and his research group. Further details of the research group can be obtained from the research group website: http://www3.imperial.ac.uk/people/v.savolainen . You must have a PhD or equivalent qualification in evolution, ecology, genetics or a closely related discipline. The successful candidate will have expertise in population genomics, proficiency in statistics and knowledge of and in depth experience of working in evolutionary biology. Experience of management and analysis of complex genetic data and excellence in working in a multi-disciplinary environment are essential.

You must have experience of working in a team, be able to develop and apply new concepts and have a creative approach to problem-solving. You must also have excellent verbal and written communication skills and be able to write clearly and succinctly for publication.

This is a full-time, fixed term appointment available for up to one year.

Our preferred method of application is online via our website http://www.imperial.ac.uk/job-applicants/ (please select "Job Search" then enter the job title or vacancy reference number including spaces - NS 2015 040 JT into "Keywords"). Please complete and upload an application form as directed.

Alternatively, if you are unable to apply online, please contact Mrs Christine Short on 020 7594 2276 or email c.j.short@imperial.ac.uk to request an application form.

Closing date: 30 March 2015 (midnight BST)

Committed to equality and valuing diversity. We are also an Athena SWAN Silver Award winner, a Stonewall Diversity Champion, a Two Ticks Employer and are working in partnership with GIRES to promote respect for trans people.

"Thomas, Jenny" <j.thomas@imperial.ac.uk>

INRA France 30 EvolutionaryBiol

Ranked the number one agricultural institute in Europe and number two in the world, INRA (National Institute for Agricultural Research - France) carries out mission-oriented research for high-quality and healthy foods, competitive and sustainable agriculture and a preserved and valorised environment.

Every year, INRA seeks researchers from all disciplines to reinforce laboratory and fieldwork teams. Researchers will be heavily involved in scientific networks and tackle environmental, economic and social issues. They are expected to strive for excellence and come up with useful, concrete applications for the real world. Individual research projects will go hand in hand with group efforts in a bid to further knowledge and innovation, in order to produce sustainably, preserve the environment, and improve human nutrition.

INRA is recruiting 30 Research Scientists (PhD or equivalent) through open competitions and offering permanent positions.

Positions are open in a wide range of scientific disciplines such as animal quantitative genetics, quantitative genetics and plant development, agrifood sciences and techniques, metabolism and physiology, genetic mechanisms of adaptation, physico-chemistry of interfaces and biological processes for the environment, functional ecology and modelling, evolutionary ecology and modelling, ecology, genetics, pathogens, veterinary and agrifood sciences (microbiology, molecular protozoology and immunology), applied mathematics and informatics, compromise and uncertainty in the evaluation and management of ecosystem services, economics and many more.

Applications are available until to March 2, 2015.

All useful information to apply is available on: http://jobs.inra.fr/eng/offers/emploi_perm/open-competitions/cr2/?campagne=23129&intitule=-open+competitions&concours=24348 For further details: concours_chercheurs@paris.inra.fr

[INRA] < http://www.inra.fr/ >

Corinne NICOLAS

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Kunming ResAssist EvolutionCooperation

Assistant Researcher

Behaviour and Evolution of Cooperation

Kunming Institute of Zoology, China

http://english.kiz.cas.cn/ An assistant will be employed from March 2015 at the Kunming Institute of Zoology, China. The position is for a few months and will be funded by a National Science Foundation of China (NSFC) research grant to Dr. Riccardo Pansini and Prof. Rui-Wu Wang (Kunming Institute of Zoology), and Prof. Lei Shi (Yunnan University of Finance and Economics, Kunming). The post-holder will join a research team working on the evolutionary roots of cooperation empirically on humans as model species.

The work will involve the modelling of cooperative behaviour and evolutionary game theory.

Ideal candidates will have a Master in Evolutionary biology, Anthropology or related disciplines. The candidate should have excellent skills in the implementation of the scientific method, have a keen interest in behaviour, and have acquired previous experience in statistical modelling (R and SPSS).

The candidates should have excellent English language skills and very good Chinese ones.

The salary will be up to 5,000 RMB per month including allowances for when travelling outside town.

If required, housing, visa and work permit enabling the successful candidate to live and work in China will be arranged by our institute.

Depending on the successful completion of the assistantship, the position will be upgraded to a paid PhD (working on the same or different model species) in the following academic year.

Interested candidates shall send by the end of February a full English CV including the contact details of two referees, and a few lines explaining why they want the position, to Riccardo Pansini r.pansini@gmail.com

Experimental and Theoretical Ecology Group

Kunming Institute of Zoology

Chinese Academy of Sciences

Jiaochang Donglu East road 32, 650223 Kunming - China

http://rpansini.altervista.org/ http://159.226.149.45/-demo/ Riccardo Pansini <r.pansini@gmail.com>

MaxPlanckInst Ornithology FieldAssist BlueTits

The Department of Behavioral Ecology and Evolutionary Genetics at the Max Planck Institute for Ornithology in Seewiesen, Germany, is seeking a field assistant to work from 1st April to 31st May 2015. The assistant will participate in a study on the reproductive biology of a blue tit population in a protected forest site in Southern Germany. Specifically, the assistant will help carrying out an experiment in which provisioning effort by one parent will be manipulated (by exposing it to begging playbacks) in order to examine its effects on provisioning behavior of the other parent. The work will primarily consist of recording nest visits from a hide and controlling the playback device. This will include long days (up to 8 hours) in a hide and thus require a lot of patience and endurance. In addition, the assistant will help with preparations of the experiment, as well as with maintaining the long term data on breeding behavior of the blue tits through regular nest checks.

Successful candidate must have experience with field work, with working long hours under all weather conditions and with collecting detailed observational data. Applicants should be highly motivated, dependable, well organized and have the ability to collect data accurately. Field work hours will be long and tiring, and applicants must be prepared to work at any time (including weekends and holidays), with no days off during the peak experimental period.

The working language at the Institute is English, so good knowledge of the language is required. Applicants should be aware that Lyme disease spread by ticks is common in the area, and should inform themselves about the disease in advance.

The payment would be in accordance with the collective agreement for public employees up to pay group 6 TVöD.

The Max Planck Institute for Ornithology employs a dynamic, dedicated, and international group of researchers who are focused on exploring the fields of evolution, ecology, genetics, and neurobiology.

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

For inquiries, please contact Dr. Santema, Tel.: 08157 932-234, E-Mail: petersantema1@gmail.com

Review of applications will start immediately until the position is filled. If you are interested in applying for the field assistant position as described above, please apply (including your CV) by latest 13st February 2015 by E-Mail to:

cdobus@orn.mpg.de

Peter Santema <petersantema1@gmail.com>

MountainLakeBiologicalStation UndergradSummer

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Summer 2015 REU Opportunities Mountain Lake Biological Station www.MLBS.org **

Dear Colleagues and Friends,

Mountain Lake Biological Station (University of Virginia) announces its 2015 summer *NSF REU undergraduate research internship program*,**now in its 23^th year.**

**

REU participants are recruited from around the country for a unique 10-week learning and living research experience in the southern Appalachian Mountains. Students conduct independent research in field ecology, evolution, behavior and physiology under the supervision of station scientists. REUs are paid internships that include all station costs, travel, and a *$5,250 stipend*.

Application deadline February 20.

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2015 REU Internships:http://mlbs.org/reuprogram Please forward this information to colleagues or students you think might be interested.

Thanks for your help!

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*/**** Learn all about Mountain Lake opportunities at www.MLBS.org ****/*

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Eric Nagy, Associate Director and REU Coordinator

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Eric S. Nagy, Ph.D. Associate Director Mountain Lake Biological Station & Department of Biology University of Virginia P.O. Box 400327 Charlottesville, VA 22904-4327 ofc: 434-243-4989 | 540-626-5227 cel: 434-906-3122 eml: enagy@virginia.edu web: virginia.edu/biology/faculty/nagy.htm | mlbs.org

Eric Nagy <enagy@virginia.edu>

NCMuseum Raleigh EvolutionaryBiol

Position: Natural Science Research Curator III Working Title: Director, Evolutionary Biology Research Laboratory Vacancy Number: 65010170 Salary Range: $48,195-$125,000 Hiring Range: $48,195-$125,000 Department: NC Department of Environment and Natural Resources Division: NC Museum of Natural Sciences Type of Appointment: Permanent Full-Time Location: Raleigh Posting Date: 2/23/2015 Closing Date: 3/23/2015

Division Information: This position is located in Raleigh, North Carolina at the NC Museum of Natural Sciences, an award-winning major institution with a prominent State-wide, national and international profile. This key position works in the Evolutionary Biology Research Laboratory, a unit within the Museum's Research & Collections section. This position is a joint-appointment between the NC Museum of Natural Sciences and the UNC system (specifically, with the North Carolina State University College of Sciences). The employee will have non-tenure track faculty status and associated teaching and service requirements as a Research Professor with the College of Sciences, Department of Biological Sciences.

Description of Work: The NC Museum of Natural Sciences and the Department of Biological Sciences in the College of Sciences at North Carolina State University jointly announce a search to recruit an evolutionary biologist with experience in and a commitment to engaging the public in the study of evolution. The position is jointly split between the NC Museum of Natural Sciences (55%) and the Department of Biological Sciences at NC State (45%). This position includes research, outreach, teaching and service responsibilities at both institutions. Given existing strengths in NC's Triangle area (including museum/university partnerships in public science, the launch of a new center in evolutionary medicine: TriCEM, https://tricemdotorg.wordpress.com/about/, and the land-grant mission of NC State University), candidates with experience in or interest in applied evolution are particularly encouraged.

The successful candidate will have an outstanding record of scholarly publications, research support and engagement. This position has several areas of responsibility, including:

1. Development of an original scientific research program in some aspect of evolutionary biology; research programs may have local, regional, and/or international focus and will include pursuit of external research funding, data generation and analyses, and publication/dissemination of results. Some aspects of this research should be suitable for display in the NC Museum of Natural Sciences' Evolutionary Biology Research Laboratory (a glass-walled laboratory 'on-exhibit' in the Nature Research Center wing of the Museum); 2. Operational management and administration of the Evolutionary Biology Research Laboratory, including supervision of laboratory with oversight of equipment, budgets, personnel, research programs, and volunteer programs; 3. Teaching, at NCSU's Department of Biological Sciences, one class per year related to evolution; 4. Training/mentoring undergraduate and graduate students and/or postdoctoral researchers, with a particular focus on training that bridges museum/university goals; 5. Engaging the public in understanding the study of evolution and participation in science communication initiatives, including active participation in Museum education and outreach programs, participation in Museum special events, interaction with Museum visitors, serving as a role model for students and citizen scientists, and creating programmatic themes that raise the science literacy of visitors;

Knowledge, Skills, and Abilities: **To receive credit for your work history and credentials, you must list the information on the application form. Any information omitted from the application form, listed under the text resume section, or on an attachment will not be considered for qualifying credit** A successful candidate will have the following knowledge, skills and abilities:

(1) Considerable knowledge of many aspects of evolutionary biology (2) Experience applying principles and practices of research, with special expertise in some aspect of evolutionary biology (3) A demonstrated mastery of materials, equipment, and techniques used in

laboratory practices and in fieldwork (4) Experience in teaching undergraduate and/or graduate courses in evolution or related subjects (5) A demonstrated track record of effective and creative science communication to diverse public audiences (6) Experience writing and/or administering grants to fund biological research

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NHM Oslo PlantSpeciation

Natural History Museum Researcher in Evolutionary Biology (Plant Speciation)

One 3-year position is available at the Natural History Museum (NHM), University of Oslo, as Researcher (SKO 1109).

The Natural History Museum, University of Oslo, is the largest of its kind in Norway and has approximately 150 employees engaged in research, teaching, curating of collections and public outreach in botany, mycology, zoology, paleontology and geology. The museum is located in the beautiful Botanical Garden close to the city centre of Oslo.

Job description

The position is connected to the project SpArc (High speciation rates in Arctic plants: genomic mechanisms and relevance to the latitudinal diversity gradient), funded by the Research Council of Norway for four years from 2015. The successful applicant will be part of a strong project team including researchers at the University of Oslo and international collaborators with long relevant experience. The NHM has already hired one 4-year postdoctoral fellow who will work full-time on this project together with a PhD fellow to be hired, and together with the researcher announced here. The successful applicant is expected to carry out part of the research in the laboratory of one of our international collaborators.

The SpArc project follows up recent discoveries in arctic diploid plants, showing that there are many cryptic biological (i.e. reproductively isolated) species within what has traditionally been recognized as well-defined, single taxonomic species. In this project, we will identify the genomic mechanisms of postzygotic reproductive isolation in two arctic systems, and test whether more southern floras contain similarly high, but hitherto undetected, cryptic biological species diversity. Based on crossing experiments and high-throughput DNA sequencing we will address whether selfers contain more cryptic species than outcrossers when controlled for lineage age, and whether polyploid formation from a diverse pool of recently diverged, cryptic diploid species can help explain why the Arctic harbours one of the most polyploid-rich floras on Earth. The project will provide new and potentially ground-breaking insights into both the dynamics of the latitudinal diversity gradient and the fundamental process of species divergence.

The researcher will participate in work to identify the genetic mechanisms resulting in frequent reproductive isolation using genome sequencing and high-throughput QTL mapping approaches. A main focus will be to test the hypothesis that diploid cryptic biological species have contributed to the high diversity of arctic polyploid species using high-throughput sequencing.

Requirements

We seek a person with strong collaborative skills and motivation and ability to define own research questions. The candidate should be an active scientist with a PhD in a relevant field in evolutionary biology and have hands-on experience with high-throughput DNA sequencing. In addition, she/he should preferably have competence in speciation genetics, bioinformatics and genome assembly.

We offer

Salary based on salary level 57 - 65 (NOK 482 800 - 559 600 per year depending on qualifications) A challenging, supportive and friendly working environment. Membership in the Norwegian Public Service Pension Fund. Attractive welfare benefits.

Evaluation of the application

In assessing applications, emphasis will be placed upon academic track record as well as personal ability.

Interviews with selected candidates will be arranged.

A good command of English is required: http://www.mn.uio.no/english/research/doctoral-degree-and-career/regulations/proficiency-requirements.html The application must include:

Application letter CV (summarizing education, positions and academic work, scientific publications and other relevant activities) Copies of educational certificates and letters of recommendation Copies of scientific publications and academic work that the applicant wishes to be considered by the evaluating committee A two- to three-page description of previous research, future research plans and research interests Names and contact details of 2-3 referees (name, relation to candidate, e-mail address and telephone number)

The application with attachments is to be delivered in our electronic recruiting system EasyCruit. Foreign applicants are advised to attach an explanation of their University's grading system. Please remember that all documents should be in English or a Scandinavian language.

The University of Oslo has an agreement regarding acquisition of rights to work results for all employees, with the aim to secure rights to research results, etc.

The University of Oslo has a goal of recruiting more women in academic

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Rennes ResAssist PopulationModeling

Permanent assistant engineer at the French National Institute for Agricultural Research; Position based at the Institute of Genetics, Environment and Plant Protection (IGEPP) in Rennes, France, starting summer 2015. Salary: 1700 â¬$permonthdependingonexperience, plusextrasalarybenefitsandcomputingbonus.Applicationbeforethe19thMarch$2015.

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Application developer in population modeling and geomatics

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General proposal

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Mathematical and algorithmic models developed at the Institute of Genetics, Environment and Plant Protection (IGEPP) contribute to understand, infer and predict the evolutionary and ecological dynamics of plant species, bioaggressors and their natural enemies and competitors in agro-ecosystems. We also use our models with experimental data to indirectly characterize biodiversity and to infer ecological and evolutionary processes driving species. The numerical solution of our spatiotemporal demogenetic models in explicit landscapes are finally used to infer new cultural practices and guide possible actions to limit the impacts of crop pests. The successful candidate will join the Modeling Group (˜ ten people) in our institute. Based on the projects and models formalized by the Group, the candidate will be in charge of the rapid prototyping, code optimization and routine operations of model predictions. To parameterize models and to validate the predictions, he (she) will also automate the handling of geomatics and temporal data from agro-ecosystems studies. The recruited assistant engineer (Level 6, European Qualifications Framework Ë "Bachelor" or "Licence-applied Master" level) will contribute to the modeling scientific programs in IGEPP and participate in advancing knowledge in ecology and evolution of populations and communities linked to agro-ecosystems. He (she) will work with researchers using common mathematical and algorithmic objects on various scientific topics ranging from population genetics to ecology of communities. To do this, he (she) will manage and use a bunch of computing servers and software licenses, suitable for intensive numerical computation.

Job standard summary —— The application developer realizes the code development required by scientific programs and ensures the maintenance of computer applications components in compliance with current standards.

Tasks ——— - Ensure coding, numerical computation and testing of a subset of a software application based on a mathematical formalization or an algorithmic scheme - Perform and automate management operating procedures and make user interfaces - Develop test cases - Support all or part of the operational implementation of the application - Write technical documentation for developed computer codes - Maintain the software, diagnose and correct malfunctions

Official requirements —— Minimum Bachelor or Licence in Computer Sciences or Mathematics. - Thorough knowledge of programming methodology; Good knowledge of algorithms, numerical computations and how to apply a programming methodology; Good knowledge in applied mathematics, or the will to acquire a mathematical training - General knowledge of an operating system, of object programming, of computer security rules - General knowledge of the application domain (population genetics and dynamics, agroecology) and of mathematics (dynamic systems, discrete and continuous mathematics, probabilities) - Knows at least a compiled language (typically C++ / C), a scripting language (Python, Shell) and a domain specific language suited to mathematical/statistical modeling (R, Scilab, MATLAB) - Capable of developing portable applications for Linux and Windows, and communicate with users - Minimum level B2 in written and spoken English and

French - Appreciate team work and development, able to organize work and account for progresses of his/her work, to participate in the technical support of trainees and to watch on technological developments and tools for numerical computation - Basic knowledge in ecology and / or biological evolution would be an asset; Experience in the treatment of geomatic data would be appreciated.

Contacts —— Nicolas PARISEY, +33(0)2 23 48 51 52, nicolas.parisey@rennes.inra.fr Sylvain POGGI, +33(0)2 23 48 51 52, sylvain.poggi@rennes.inra http://www6.rennes.inra.fr/igepp_eng/ Call for applications —— http://jobs.inra.fr/eng/offers/emploi_perm/open-competitions/ce-it/?campagne#129&intitule=open+competitions&concours5069

Job description (French language as to be mastered at level B2 minimum, see http://www.coe.int/t/dg4/linguistic/Cadre1_en.asp) ——

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RoyalBCMuseum VictoriaCanada EntomologyCurator

ENTOMOLOGY CURATOR - ROYAL BRITISH COLUMBIA MUSEUM - DEADLINE MARCH 24

The Royal British Columbia Museum, in Victoria, BC, is hiring a new entomology curator. For detailed information about the position and how to apply, please go to: http://royalbcmuseum.bc.ca/assets/Posting3.pdf The Entomology Collection is among the most active and growing collections in the Royal BC Museum holdings: containing approximately 600,000 specimens and specimen lots. It is estimated that there are 35,000 insect species in British Columbia, yet fewer than half have been recorded. The ideal candidate will have a minimum of 4 years' museum experience (or similar) proven experience conducting original research in entomological systematics. Knowledge of exhibition development methodology and knowledge of museum practices, including documentation standards, is required. Excellent communication skills and comfort delivering presentations and providing information, identifications and expertise relating to Entomology across a wide diversity of audiences is necessary. Must be Canadian and/or have landed immigrant status in Canada.

stevep@uvic.ca

Sacramento California Bioinformatics

Bioinformatics Scientist II YOUR TASKS AND RESPONSIBILITIES

* To provide scientific and computational support to multiple functional groups within Biologics and provide transcriptomics, comparative genomics, and potentially other omics solutions for controlling pests and diseases in plant and promoting plant health using microbes;

* Proactively identifying and incorporating new algorithms and technology to automate the analysis of microbial genomes and plant- microbe interactions;

* Managing next-generation sequencing (NGS) data and NGS analyses using custom scripts and open source tools;

* Working with other bioinformatics team members to understand their roles and to serve as backups as needed;

* To analyze NGS data including performing comparative genomics, transcriptomics, metagenomics analyses for controlling pests and diseases in plant and promoting plant health using microbes.

* Generate custom scripts to handle NGS data analysis in Python or Perl and work on a high performance cluster;

* To conduct statistical analysis that integrates genomic analyses with phenotypic data, as well as provide statistical support to different functional groups;

* Communicating effectively through listening, documentations and presentations, especially using compelling visualization tools to share analysis and interpretation of data;

* Proactively identifying and incorporating new algorithms and technology to automate the analysis of microbial genomes and to extend the features of existing analysis pipeline;

Reference Code

0000112165

WHO YOU ARE

The candidate is required to possess the following:

* M.S. and 5+ years of experience, or a Ph.D. in Genomics, Microbiology, Computational Biology, Bioinformatics or Ecology and Evolutionary Genetics, with 3+ years of postgraduate experience;

* Ability to handle a large data set efficiently using scripts, particularly in the analysis of NGS data;

* Genome assembly of microbial genomes;

* In-depth familiarity with various public genomic databases;

* Familiar with commercial and open-source bioinformatics tools;

* Experiences working in the biotech sector focusing on plant health and crop protection;

* Knowledge of statistical software tools and packages;

* Fluent in Python, Perl or other scripting languages;

* Familiar with SQL and some knowledge of using relational databases such as PostgreSQL;

* In-depth knowledge of secondary metabolite production in microbes;

* Knowledge of bacterial and plant genetics is preferred.

* Working with high performance computing clusters.

Dilara Ally Senior Bioinformatics Scientist Biologics

Bayer CropScience LP 890 Embarcadero Drive., Sacramento, CA. 95605, U.S.A. Direct: +1 (916) 661-3332 Mobile: +1 (619) 481-8726 Email: dilara.ally@bayer.com www.bayercropscience.us Dilara Ally <dilara.ally@bayer.com>

Sweden 6 Bioinformatics

Call for interest: Six (6) permanent positions providing advanced bioinformatics support, located at SciLifeLab Bioinformatics Platform nodes across Sweden.

The bioinformatics platform at SciLifeLab (www.scilifelab.se) is a national infrastructure in rapid growth and development, now looking for 6 permanent staff members to join the Bioinformatics Long-term Support team, preferably placed at bioinformatics nodes in Umeå, Linköping, Gothenburg, or Lund. Together with other national bioinformatics staff, the new recruits will aid the build-up of the national platform by establishing local platform nodes. The successful candidates have a PhD or similar relevant working experience from advanced studies within bioinformatics. We are looking for candidates experienced in providing analyses, software solutions, database design and/or user interfaces in areas like whole genome variant discovery, statistical genetics, population genetics, transcriptomics, proteomics, metabolomics, systems biology and integrative bioinformatics.

Note that the formal recruit process at the respective university will be started once this call for interest has been evaluated. The deadline for this call is February 27th 2015. More info about the positions http://www.scilifelab.se/vacancies/ Contact: Thomas Svensson, thomas.svensson@scilifelab.se Björn Nystedt, bjorn.nystedt@scilifelab.se Managers, SciLifeLab Bioinformatics Long-term Support

bjorn.nystedt@scilifelab.se

Taipei EvolutionaryBiologist

Evolutionary Biologist

The Biodiversity Research Center, Academia Sinica (BRCAS, homepage: http://biodiv.sinica.edu.tw/), Taipei, Taiwan, invites applications for a tenure track position in Evolutionary Biology. The rank is open, though junior scientists are preferred. Candidates with a research interest in evolutionary biology are encouraged to apply. Candidates who use molecular and genomic approaches and have a good postdoctoral research experience are preferred.

BRCAS is still in an expansion mode. The center provides each PI with some internal support and a good start-up. BRCAS is strong in marine biodiversity and molecular and genomic evolution. It is in charge of a sequencing core with two HiSeq2500s, one MiSeq and one 454, and Academia Sinica is well equipped with modern research facilities. The position will be open until filled; however, the first review will be conducted in mid March 2015. An applicant should submit the names and e-mail addresses of three references along with CV (including a list of publications), 3 representative papers (pdf files), and a statement of past achievements and future research interests to Ms. Miao-Suey Lin (zomslin@gate.sinica.edu.tw). Please indicate the rank to which you want to apply: our 'assistant research fellow' is equivalent to 'assistant professor'

Wen-Hsiung Li

Wen-Hsiung Li <wli@uchicago.edu>

Taipei PlantBiodiversity

Plant Biodiversity Researcher

The Biodiversity Research Center, Academia Sinica (BRCAS, http://biodiv.sinica.edu.tw/), Taipei, Taiwan invites applications for a scientist whose research is field collection-based, addressing fundamental questions in vascular plant systematics, taxonomy, phylogenetics, biogeography, and/or related fields. Qualified candidates must have a strong postdoctoral research track record. While we anticipate the appointment at the tenure-track Assistant Research Fellow level (equivalent to an Assistant Professor), extraordinary candidates at higher levels may be considered.

BRCAS provides each PI with annual internal funding and good start-up for new PIs. Faculty members have opportunities to mentor graduate students through Academia Sinica's "Taiwan International Graduate Program" (TIGP). The successful candidate is expected 1) to conduct fundamental research; 2) to curate and to grow our research museum collection (about 140,000 botanical and 45,000 zoological specimens); and 3) to support museum outreach. Candidates are expected to establish an internationally recognized program. We encourage applicants with at least part of the research focused in Taiwan and the Asia Pacific region.

Deadline for application is March 15, 2015. The applicant should submit names and e-mail addresses of three references along with CV (including a list of publications), 3 representative papers (pdf files), and a statement of past achievements and future research interests to Ms. Miao-Suey Lin (zomslin@gate.sinica.edu.tw).

Wen-Hsiung Li <wli@uchicago.edu>

TulaneU 2 ResAssist Hawaii

The Blum Lab in the Department of Ecology & Evolutionary Biology at Tulane University invites applications for 2 full-time research associate positions to start in Spring 2015. We are looking for enthusiastic, conscientious and highly self-motivated individuals to work on a project investigating the consequences of aquatic invasive species (AIS) removal for native Hawaiian stream fishes.

Both incumbents, who will be based on Oahu in Hawaii, will participate in field surveys and related work to support genes-to-ecosystem assessments of at-risk species responses to AIS removal. Incumbents also will contribute to data analysis for project reports and peer-review publications.

Prior experience participating in or leading field research is desired. Successful applicants will be expected to work independently and collaboratively as an active member of a large research group. Incumbents must be able to conduct stream-based field work, such as snorkel surveys, in sometimes remote locations and in variable weather conditions. Incumbents also must be able to perform detailed data analyses with a high level of precision.

We are particularly interested in applicants that have experience with Hawaiian stream ecosystems, including but not limited to AIS and native amphidromous fauna. Strong written, verbal and analytical skills are essential. A Bachelor's degree or higher in ecology or a related field is also desired.

We highly encourage Hawaiian residents and Pacific Islanders to apply. An initial appointment will be for one year, with continuation dependent upon performance and funding. Salary will be commensurate with experience and qualifications.

A PDF-format application package including (1) a letter of interest; (2) a curriculum vitae detailing past research experience and educational training; and (3) contact information for three professional references should be submitted via e-mail to Ms. Shelley Meaux (cbr@tulane.edu). Please write "Hawaii research associate position" in the subject line. For earliest consideration, apply by 15 March 2015. Applications will be accepted until the position is filled.

Tulane University is an Affirmative Action/Equal Employment Opportunity/ADA Employer. Women and minorities are encouraged to apply.

Michael J. Blum

Associate Professor, Dept of Ecology & Evolutionary Biology Eugenie Schwartz Professor of River & Coastal Studies Director, Tulane-Xavier Center for Bioenvironmental Research Tulane University New Orleans, LA 70118 504-862-8295 (phone) 504-862-8706 (fax) www.tulane.edu/~mjblum cbr.tulane.edu

< http://www.tulane.edu/%7Emjblum >

"Blum, Michael J" <mjblum@tulane.edu>

UAlabama Director MuseumResearch Collections

Director of Museum Research and Collections at the University of Alabama

Note to Applicants: Submit a letter of interest, resume, and names, addresses and phone numbers of at least three references when applying.

Job Summary: The Director of Museum Research and Collections is responsible for facilitating and promoting the pursuit, discovery and dissemination of knowledge through museum-based research conducted by University faculty, curators, and students as well as outside researchers. The Director will provide oversight for the acquisition of objects for the UA Museums collections and for the management of the collections, including necessary and appropriate documentation, conservation, preservation, protection, preparation, research, exhibition, and interpretation of collections objects belonging to or in the temporary custody of UA Museums.

Additional Department Summary: The Director will facilitate the activities of the UA Museums Council of Curators as the Chief Curator and will encourage collaborative research efforts and interdisciplinary grant proposals by Museum Curators. The Director is expected to develop and conduct research in his/her own academic discipline and secure external grant funds. Results of research/scholarly work should be published, disseminated in peer-reviewed journals, and/or presented at conferences or symposiums. The Director will serve as a Curator in a museum-related discipline such as paleontology, biology, geology, or archaeology.

The Director will supervise staff in carrying out collections care and management. The Director is expected to remain current with regard to developments in the field including relevant state and federal statutes and professional ethical standards.

Required Minimum Qualifications: Doctorate in Biology, Geology, Anthropology, Archaeology, or related field and extensive experience in collections-based research and museum collections management.

Additional Required Department Qualifications: Valid U.S. driver's license. Must be at least 21 years of age and have an acceptable motor vehicle report as determined by the insurance carrier.

Skills and Knowledge: Must have strong record of scholarly research and publication in high-quality peer-reviewed academic journals. Must have knowledge and skills in collections management policies and procedures and collections database management. Must have good organizational skills to maintain collections data, loans, general inventory, condition reports, and conservation needs. Ability to organize and direct the work of others and train staff for program specific requirements.

Background Investigation Statement: Prior to hiring, the final candidate(s) must successfully pass a pre-employment background investigation. A prior conviction reported as a result of the background investigation DOES NOT automatically disqualify a candidate from consideration for this position. A candidate with a prior conviction will receive an individualized review of the prior conviction before a hiring decision is made.

Equal Employment Opportunity: The University of Alabama is an Equal Employment/Equal Educational Opportunity Institution. All qualified applicants will receive consideration for employment without regard to race, color, religion, national origin, sex, sexual orientation, age, genetic information, disability, or protected veteran status, and will not be discriminated against because of their protected status. Applicants to and employees of this institution are protected under Federal law from discrimination on several bases. Follow the link below to find out more. "EEO is the Law" Poster

For complete details and to apply go to http://staffjobs.ua.edu/? jobI8895

jpfriel@bama.ua.edu

UCLondon Independent Fellowships

Excellence Fellowships in Evolution and Ecology

University College London

UCL's Department of Genetics, Evolution and Environment (GEE) is looking to recruit promising early-career researchers. GEE is a world class Department with a broad research portfolio. We are aiming to strengthen research in the general areas of evolution and ecology and are particularly encouraging applicants in the following broad areas: - Biodiversity and ecology (Prof Georgina Mace) - Statistical and computational genetics (Prof Nick Luscombe) - Ecological genetics of disease (Prof François Balloux) - Origins of eukaryotic complexity (Dr Nick Lane) - Deep-time evolutionary analysis

(Prof Max Telford and Dr Anjali Goswami)

Recruitment opportunities are available through the UCL Excellence Fellowship scheme run by the School of Life and Medical Sciences (deadline 13 May 2015) and through externally funded Fellowship schemes (ERC, Royal Society, NERC, BBSRC, Wellcome Trust). The UCL Excellence Fellowship offers salary and research funding, as well as generous funding supplements for individuals bringing externally funded fellowships to UCL http://www.ucl.ac.uk/slms/research/excellence-fellowship/ Candidates are required to identify a sponsor in GEE. They should get in touch with any of the contacts listed above for informal discussions as soon as possible (CV and cover letter). Alternatively contact Dr Max Reuter (m.reuter@ucl.ac.uk) who is in charge of fellowship support or Prof Andrew Pomiankowski (ucbhpom@ucl.ac.uk) the Head of Department.

The Department has a track record of supporting fellowship applicants from initial application to securing subsequent permanent employment within the department. You can find more information about the department at http://www.ucl.ac.uk/gee . A note for non-UK applicants: Fellowships are an integral part of the UK academic system. Externally funded grants covering salary and research expenses are open to non-UK applicants from a range of funding agencies. These awards allow early- and mid-career scientists to concentrate on their work unhindered by teaching and administrative loads.

Max Reuter

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

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

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

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UHawaii Hilo EvolutionBiol

Dear EvolDir community, The University of Hawaii Hilo is looking to fill an open position of Assistant Professor of Biology. Women and individuals from groups under-represented in the sciences are especially encouraged to apply. Aloha, Elizabeth

—–

*Assistant Professor (Biology), *position number 82322, UH Hilo, College of Arts & Sciences, tenure-track, full-time, general funds, nine-month appointment to begin approximately August 2015, pending position clearance and availability of funding.

Duties: Teach undergraduate courses in Genetics and Cell and Molecular Biology. Develop an independent research program in area of expertise that is supported by extramural funding; advise students; participate in departmental governance and related University and community service. The University of Hawai'i at Hilo also offers the opportunity for participation in graduate programs.

Minimum Qualifications: Ph.D. from an accredited college or university in a biological science discipline appropriate to the position, teaching experience in biological sciences, research experience in area of expertise in Genetics, and demonstrated ability to work with students from diverse cultural backgrounds.

Desirable Qualifications: Demonstrated teaching experience at the college or university level in undergraduate courses in areas related to Genetics, Genomics, Cell Biology, and Molecular Biology. Demonstrated record of student advising and training; a successfully funded research program in area of expertise in genetics, and the ability to develop a research program in the Hawaiian or Pacific region that complements existing department strengths in plant biology and evolution, with the potential to obtain extramural funding.

Salary Information: Commensurate with qualifications and experience.

To Apply: Submit a cover letter indicating the position title and position number and how you satisfy the minimum and desirable qualifications, a curriculum vitae, academic transcripts, and statements of research and teaching interests. Please note that copies of transcripts are acceptable for application; however, original documents issued by a university registrar are required upon hire. Provide contact information for three (3) references. Electronic submissions are preferred.

Mail Application To: Dr. Elizabeth Stacy, Biology Department, University of Hawai'i at Hilo, 200 W. KÄwili St., Hilo, Hawai'i, or electronically to estacy@hawaii.edu. Please refer to position number 82322.

Inquiries: Dr. Elizabeth Stacy, Biology Department, University of Hawai'i at Hilo, 200 W. KÄwili St., Hilo, Hawai'i. estacy@hawaii.edu <awayaj@hawaii.edu>

Closing Date: March 15, 2015

UH Hilo is an EEO/AA Employer

M/W/Disability/Veterans.

– Elizabeth Stacy Associate Professor of Biology and TCBES University of Hawaii Hilo 200 West Kawili Street Hilo, HI 96720 Phone: 808-932-7715 Fax: 808-932-7295

estacy@hawaii.edu

UKent Tech BlastocystisAdaptation

Part-time (50%) Laboratory Techinician: Revealing the anaerobic adaptations of the mitochondrion-related organelles of Blastocystis.

We are seeking to appoint a Laboratory Technician for a fixed term period of 3 years and Part-time. The main purpose of this position is to assist and support the various science activities associated with the on-going work in the Laboratory of Molecular and Evolutionary Parasitology (PI: Dr. Anastasios Tsaousis) at the School of Biosciences. The primary aim of this BBSRC project is to investigate the anaerobic adaptations of the mitochondrion-related organelles of Blastocystis.

Project: Blastocystis is a human intestinal parasite, recently considered to be a stramenopile, with a controversial pathogenicity, mainly because of lack of knowledge around its life cycle and function of its organelles. Since Blastocystis is a strict anaerobe, it was thought that lacked of canonical mitochondria, and instead it had hydrogenosomes, anaerobic organelles related to mitochondria. Recent genomic and transcriptomic data generated from Blastocystis demonstrated the presence of 700 putative mitochondrial and hydrogenosomal proteins. Amongst these only a few so far have been shown to localise into the organelles. The organelles are predicted to have additional mitochondrial characteristics, including pathways for amino acid metabolism, pyruvate metabolism and an incomplete tricarboxylic acid cycle. The Blastocystis mitochondrion-related organelles (MROs) have metabolic properties that are found in aerobic and anaerobic mitochondria but also in hydrogenosomes. The purpose of this project is to understand the evolutionary adaptations of Blastocystis and especially its mitochondrion-related organelles (MROs) under different environmental conditions. This work will identify the significance of the evolutionary important of mitochondrion-related organelles for the organism, but in addition will discover novel functions that can potentially be used in systems biology, or targeting parasitic and even mitochondrial diseases. The project will involve purifying the MROs under different environmental conditions, followed by proteomic and biochemical analyses of the different novel pathways.

The candidate will be responsible for specific duties involved in the day-to-day running of the project in Dr. Tsaousis' laboratory, as well as providing practical help for other lab members including undergraduate students. He/she will work under the supervision of Dr. Anastasios Tsaousis and the PDRA working on the project, and may help in technical, non-academic aspects of supporting other lab members.

Closing date for applications is February 22, 2015.

For any questions or clarifications, please contact Dr. Anastasios Tsaousis at: a.tsaousis@kent.ac.uk

Further information about the post and the application procedure can be found at: https://jobs.kent.ac.uk/-fe/tpl_kent01.asp?s=3D4A515F4E5A565B1A&jobid=-3D39022,2386213498&key=42771961&c=-255856466547&pagestamp=secipgmlphnaydengd
Kind regards,

Anastasios Tsaousis

Dr. Anastasios D. Tsaousis (PhD) Lecturer in Biosciences University of Kent, School of Biosciences, Room: Ingram 220 Canterbury, CT2 7NJ, UK tel: +44 (0) 1227 827007

email: tsaousis.anastasios@gmail.com A.Tsaousis@kent.ac.uk

Webpage: http://www.kent.ac.uk/bio/profiles/staff/-tsaousis.html Personal webpage: www.adtsaousis.com A.Tsaousis@kent.ac.uk

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ULondon Bioinformatics

Hi all,

We're recruiting a Lecturer* or Senior Lecturer* in Bioinformatics

http://www.jobs.qmul.ac.uk/5436 (will include some teaching in china)

The ad is worded broadly for a number of reasons - don't be scared of applying.

We're based in the best part of London; would love to interact with someone with strengths in evolutionary or behavioural genomics.

I am happy to answer informal questions by mail or skype/Hangouts - I am not directly on the recruitment panel.

Kind regards,

Yannick

* UK equivalent to assistant prof; these are "permanent" jobs; generally 3 years probation.

Yannick Wurm - http://wurmlab.github.io Ants, Genomes & Evolution â y.wurm@qmul.ac.uk â skype:yannickwurm 5.03A Fogg â School of Biological & Chemical Sciences â Queen Mary, University of London â Mile End Road â E1 4NS London â UK

Yannick Wurm <y.wurm@qmul.ac.uk>

UMainz EvolutionaryGenomics

Reminder! Deadline closing soon!

Job announcement

In the Faculty 10 Biology, Zoological Institute, Department of Evolutionary Biology at the University of Mainz is looking for an

Assistant Professor / Junior group leader

(Akademischer Rat at a University / Bes.Gr. A 13 BBesG)

Field: Evolutionary Genomics / Behavioral Genomics

from April 15st 2015 on.

The contract is initially for 3 years with the possibility of extension to up to a total of nine years depending on previous employment at German universities (12-year rule). In case the prerequisites of civil service law are not fulfilled, an engagement as a Scientific Assistant (EG 13 TV-L) is possible. More information on potential contract length and position can be given on an individual basis.

We invite applications for an Assistant Professor (Akademischer Rat / A 13) position in the Department of Evolutionary (Prof. Dr. Susanne Foitzik) at the Institute of Zoology at Johannes Gutenberg University of Mainz, Germany. This young international research team focusses on the evolution, behavior, genetics, chemical ecology of social insects (http://www.bio.uni-mainz.de/zoo/evobio/index_ENG.php). Collaboration with other groups of in the department of Evolutionary Biology are desirable. Excellent research conditions are available at the newly renovated and well-equipped genetic and chemical laboratories in Mainz. Furthermore, new climate chambers are available for animal maintenance. A NextGen sequencing facility is available on campus. For further information, please contact foitzik@uni-mainz.de.

We are seeking a highly motivated young researcher with a strong background in evolutionary genomics or behavioral genomics to establish a junior research group within Department of Evolutionary Biology. Candidates must hold a Ph.D. and postdoctoral experience is necessary. The successful candidate should address evolutionary or behavioral questions in social insects or other arthropods and should preferentially apply the newest genomic methods including the necessary bioinformatics (e.g. next-gen sequencing and transcriptomics).

The successful candidate should have an excellent publication record. Experience with grant acquisition and teaching is advantageous. The candidate should setup an independent, competitive research group and is encouraged to apply for grants in Germany or the EU (e.g., DFG, ERC). The position comes with a teaching requirement of 4 h per week during the semester in the Master and Bachelor programme. Some basic zoology classes are preferably taught in German. Consequently, a willingness to learn German is required. The candidate has the option to acquire a "Habilitation". The working language of the lab is English.

Requirements of appointment:

- University degree and a PhD in biology (or related field) - a full-time employment of at least two years and six month after Master or PhD

The Johannes Gutenberg-University Mainz is interested in increasing the number of women in science. Applications from female scientists are strongly encouraged. Similarly, qualified candidates with disabilities will be preferred.

The University of Mainz hosts many excellent scientific institutions (http://www.uni-mainz.de/eng/) and Mainz is a historic city located on the Rhine River with many students and a rich social and cultural life (http://www.mainz.de/WGAPublisher/online/html/default/hpkr-5nkek8.en.html).

Interested candidates should send an application (as a single e-mail pdf attachment) containing a CV, a list of publications (including reprints of the three most important publications), research and teaching statements, and contact information for two potential referees to:

Prof. Dr. Susanne Foitzik Evolutionary Biology

Institute of Zoology Johannes-v.- Müller-Weg 6 55099 Mainz

Germany foitzik@uni-mainz.de

Closing date for the application is February 28th, 2015

Starting date for the position is negotiable, earliest possible date is April 15st 2015

Prof. Dr. Susanne Foitzik Evolutionsbiologie Institut für Zoologie Johannes Gutenberg Universität Mainz Johannes von Müller Weg 6 55099 Mainz

Tel: +49 (0) 6131 39 27 840 Fax: +49 (0)6131 39 27 850 Email: foitzik@uni-mainz.de

"Foitzik, Susanne" <foitzik@uni-mainz.de>

UMinnesota PlantEvolGenetics SummerREU

Ruth Shaw's Research Group in the Dept. of Ecology, Evolution & Behavior at the University of Minnesota is seeking applicants for an NSF Research Experience for Undergraduates (REU) position in summer 2015 to study the process of ongoing adaptation in experimental populations of partridge pea (*Chamaecrista fasciculata*) in prairie habitat. The student will work closely with Dr. Ruth Shaw and Dr. Seema Sheth to develop an independent project in the area of plant evolutionary genetics, with possibilities ranging from estimating heritability and phenotypic selection on various plant traits to conducting studies of pollination ecology. The student will gain invaluable experience in performing field work and in conducting an independent research project, from hypothesis formulation through oral and written dissemination of results, thereby preparing the student for a career in inquiry-based scientific research. The student must be a U.S. citizen or permanent resident and should be enrolled as an undergraduate in Fall 2015. The ideal candidate should enjoy working outdoors and have an interest in learning about the evolution and ecology of plants in the Midwest prairies, and candidates planning to pursue a graduate career in evolution, ecology, or conservation biology are particularly well-suited for this position. The REU intern will receive a stipend of $5,000 and room and board in the Twin Cities (with occasional overnight travel to field sites). Costs of travel to and from the Twin Cities will also be provided. The deadline to apply for this position is March 9, 2015, and the 10-week internship will begin on Monday, June 8 and end on Friday, August 14. Please contact Seema Sheth (snsheth@umn.edu) for more information. The University of Minnesota provides equal access to and opportunity in its programs, facilities, and employment without regard to race, color, creed, religion, national origin, gender, age, marital status, disability, public assistance status, veteran status, sexual orientation, gender identity, or gender expression. Individuals of underrepresented groups are especially encouraged to apply. Please spread the word to any interested and qualified undergraduates.

To apply, please e-mail the following application materials to Seema Sheth (snsheth@umn.edu) with the subject line "REU" no later than March 9, 2015:

1) a statement explaining the following:

- Why you are interested in this position?

- What previous experience do you have that is relevant for this position?

- What are your future plans?

- What dates are you available to start and end this position?

- confirm eligibility for the REU program

- the name of the person who will serve as your reference

- your e-mail address and phone number

2) resume

3) transcript (unofficial is acceptable)

4) 1 letter of recommendation (sent by your reference)

For more information about Ruth Shaw's research group, visit: ruthgshaw.wordpress.com

Seema N. Sheth

Postdoctoral Associate Dept. of Ecology, Evolution and Behavior University of Minnesota E-mail: snsheth@umn.edu Phone: (612) 625-5709 seemasheth.weebly.com

Seema Sheth <snsheth@umn.edu>

UOregon ResAssist AgingBiology

RESEARCH ASSISTANT. A full-time research position conducting drug screens leading to extended lifespan is available in the Phillips Lab at the University of Oregon, Eugene. Candidates having a B.A, B.S. or M.S. are invited to apply. We seek a highly motivated and responsible individual who enjoys participating in an interactive intellectual environment to join us in our studies of genetics and genomics using the nematode

Caenorhabditis elegans and its relatives as model systems. The candidate will be responsible for working with a team conducting large scale longevity and fitness assays, as well as performing general laboratory tasks. Previous experience with basic molecular techniques and/or the genetics of model organisms is preferred. Further details regarding ongoing research is available at http://www.uoregon.edu/~pphil. Salary is commensurate with education and experience. Please send CV and names of three references to: Patrick Phillips, Ph.D., via ie2jobs@uoregon.edu or c/o Search # 15045AB, Institute of Ecology and Evolution, 5289 University of Oregon, Eugene, OR 97403-5289.

The successful candidate will support and enhance a diverse learning and working environment. To ensure consideration, please submit applications by February 16, 2015, but position will remain open until filled.

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.

Patrick C. Phillips, Ph.D. Professor of Biology Institute of Ecology and Evolution Email: pphil@uoregon.edu Phone: (541) 346-0916 | FAX (541) 346-2364 Address: 5289 University of Oregon Eugene, OR 97403-5289 USA Web: Lab http://www.uoregon.edu/~pphil IEE http://evolution.uoregon.edu

pphil@uoregon.edu

UReading EvolBiol

Eight academic jobs in the School of Biological Sciences, University of Reading including four (one Associate Professor and three lecturer positions) within the "Ecology & Evolutionary Biology" section of the school (EEB). Follow http://www.jobs.ac.uk/enhanced/linking/university-of-reading/biological-sciences/ for the particulars. The School values inclusivity and encourages applications from women and other under-represented groups.

"Julie A. Hawkins" <j.a.hawkins@reading.ac.uk>

USussex EvolutionaryBiol

The University of Sussex is looking to appoint an outstanding biologist at the level of lecturer/senior lecturer working on topics in evolution, behaviour or conservation biology to join its Evolution, Behaviour and Environment (EBE) subject group within the School of Life Sciences. The position forms part of a programme of recruitment in Evolution, Behaviour and Environment. The successful candidate will join ~15 other staff who work in EBE, and will also benefit from the School's strengths in Neuroscience and Genome Biology, and its support for cross-disciplinary research. An overview of research within the EBE theme can be found at http://www.sussex.ac.uk/lifesci/ebe/research . The successful candidate will be a scientist who is outstanding at the level applied for, with an established or developing international research profile. We will consider all outstanding candidates, and particularly encourage those who use plant or vertebrate study systems. The individual will also have a track record of delivering high quality teaching. The key quality for appointment will be research and teaching excellence. Applicants for Senior Lecturer must have a demonstrable ability to attract appropriate research funding. Potential candidates are strongly encouraged to make informal contact with the Subject Chair for Evolution, Behaviour and Environment (Professor Jeremy Field), or the Head of the School of Life Sciences (Professor Laurence Pearl), before applying.

Applications should be accompanied by a full CV, a statement of research interests and aspirations (not more than 4 pages), and the names of three academic referees.

Closing date for applications: 1 March 2015

For full details and how to apply see www.sussex.ac.uk/jobs a.c.eyre-walker@sussex.ac.uk

Vienna ComputationalBiol

Independent Group Leader Computational Biosciences 6-8 years, 1.6 Mio Euros.

The position (see below) should fit perfectly for a theoretical evolutionist at advanced postdoc stage. Application is highly competitive.

More information: www.wwtf.at/programmes/ls/-index.php?lang=EN#c4567h Vienna is a great place for evolution, and in particular theory. Evolutionists in Vienna: see www.evolvienna.at Interested candidates should not hesitate to get in tough with one of us.

Joachim Hermisson.

– Joachim Hermisson Professor for Mathematics and Biosciences University of Vienna Department for Mathematics Oskar-Morgenstern-Platz 1, 1090 Vienna, Austria and Max F.Perutz Laboratories Dr.-Bohrgasse 9, 1030 Vienna, Austria phone: +43 (0) 1 4277 50648 email: joachim.hermisson@univie.ac.at www.mabs.at Vienna Research Groups for Young Investigators Call 2015 (currently open)

Computational Biosciences

This call is issued for one to two positions as part of WWTFs Life Sciences funding programme. It addresses Vienna-based research institutions that intend to hire an excellent young researcher from abroad for the set-up and management of an independent research group. WWTF takes unconventional research careers into consideration. WWTF in total grants up to 1.6 Mio. æ per research group for six to eight years. Full proposal have to be submitted by 15 July 2015, 2pm. Decisions are planned for December 2015. Hearings of selected candidates will take place in Vienna 9th or 10th of December.

A Vienna Research Group is an assembly of researchers that launches individuals in their post-doc phase onto their next career step. Typically it is the first genuine± group led by such a young researcher who undertakes leadership responsibility for several group members. Vienna Research Group leaders usually are two to eight years after PhD; care duties may extend this period by up to four years. WWTF intentionally aims this initiative at very young researchers.

Vienna Research Groups operate for six to eight years. Key milestones are: (i) an interim evaluation after three to four years; and (ii) the end of the first± phase, chiefly financed by WWTF, after five years. The second phase will depend on the framework and opportunities available at the home institutions and will run for one to three years. Funding by WWTF is supplemented, particularly in the second phase (i.e. years 6, 6-7 or 6-8), by a significant rise in financing by the host institution. Vienna Research Group leaders are to be independent in designing their research work and recruiting their staff.

joachim.hermisson@univie.ac.at

Other

ABI 3130sequencer PC answers

Thank you to everybody who answered my query relating to buying a replacement PC for an ABI 3130 sequencer. We have managed to successfully replace our old ABI PC with a similar computer. The following instructions describe how we managed to do this.

Thanks

Robert

robert.donnelly@plymouth.ac.uk<mailto:robert.donnelly@plymouth.ac.uk>

1. A second-hand computer was purchased that met the minimum computer requirements specified by ABI:

- Hardware: PentiumÂ IV Processor,

2.00 GHz Processor

- Operating System: Windows XPÂ

Professional Edition

- Installed RAM: 1 GB

- Hard Disk Storage: Dual 36 GB hard

drives

- Peripheral: CD/RW

2. A network card was added to the PC (3Com 3C905CX TX M 10 100 PCI Ethernet Network Interface Card)

3. The computer was booted from the original Windows XP CD-Rom. At this stage both hard-drives were partitioned. This created a total of four partitions.

4. After installation of Windows XP, the partitions were formatted in Disk Manager.

5. Network card drivers were then installed.

6. The network card was connected to the Sequencer via an Ethernet cable.

7. A new network connection was created using the IP address 192.168.0.1 and Subnet Mask 255.255.255.0

8. After the sequencer successfully connected to the PC, the data collection software was installed. This required a configuration file to be supplied.

9. With the data collection software installed and running, both the Genemapper and Gene sequencing software was installed

Robert Donnelly <robert.donnelly@plymouth.ac.uk>

AGA awards deadline Apr15

The American Genetic Association grants awards each year for support of special events that advance the mission of AGA, particularly to support students to attend the event. Eligible events include specialized workshops and short courses in topical areas of organismal genetics and genomics, but any event relevant to AGA's purpose will be considered.

Events that could lead to an article in the AGA's Journal of Heredity will receive special consideration. Awards are usually between $5,000-$20,000.

Please visit the AGA website, www.theaga.org, or contact Anjanette Baker (agajoh@oregonstate.edu) for application forms and further details.

Anjanette Bakerâ Managing Editor, Journal of Heredity http://jhered.oxfordjournals.org/ Manager,â American Genetic Association http://www.theaga.org/ 2030 SE Marine Science Dr Newport, OR 97366 https://www.facebook.com/AmericanGeneticAssociation AGAJOH@oregonstate.edu

Alberta VolFieldAssist GroundSquirrel

Field Assistants Required-Columbian ground squirrels Kananaskis, Alberta, Canada

We are looking for 2 volunteers to assist with fieldwork for the period of April 10 to Aug 31, 2015. The project investigates the ecology of Columbian ground squirrels. As a member of the study, assistants will be involved with monitoring the phenology (when animals emerge from hibernation), reproduction and survival of individuals. Fieldwork will involve live-trapping and handling of animals, radio-telemetry, behavioural observation and assistance with the measurement of physiological (metabolism) traits on free-ranging animals. This is an excellent opportunity to gain experience working with a collaborative research team on a long-term study of a wild mammal.

All fieldwork is carried out in the spectacular Rocky Mountains of southwestern Alberta, Canada, home to some of the most majestic wildlife in North America. We will be staying at the University of Calgarys R.B. Miller and Barrier Lake research stations in Kananaskis, Alberta (http://bgs.ucalgary.ca/facilities/facilities). You will interact with other researchers working with ground squirrels on a diversity of projects in behavioural and population ecology. Additionally, the field stations are home to a number of other researchers working on a variety of projects, ranging from insects to large mammals.

Food and accommodation are provided. Volunteers are required to provide for their own travel to either Calgary, Alberta or Saskatoon, Saskatchewan. Travel between the field station and Calgary or Saskatoon is provided. Training will be provided and specific experience is not necessary, but candidates should have an interest in a number of the following (the more the better!): ecology, evolutionary biology, wildlife, field biology, and animal behaviour. Periods of time will be spent camping and, as such, successful applicants need to enjoy the outdoors, be up-beat, positive, responsible and work well as a member of a team.

If you wish to apply for one of these posts then please send a CV with a cover letter and contact details for three references (with e-mail addresses), by email to Jeff Lane (contact info below). Applications will be accepted until by Mar 9, 2015, but will be evaluated as they are received. To ensure full consideration for one of these positions, therefore, it is best to apply ASAP.

Contact: Dr. Jeff Lane Department of Biology University of Saskatchewan u.columbianus@hotmail.com

“Lane, Jeffrey” <jeffrey.lane@usask.ca>

Bedtime PictureBook About Evolution

Hi there,

I just published a bedtime picture about evolution. This story is meant to be a small introduction to the very simple requirements of evolution. The reader (small kids, their parents, everyone else) follows the life of Hopfs and encounters variation, heritability and selection. The book is available for free* in different digital formats (iBook, pdf, online) and languages (English, Spanish, German and Portuguese) on the project website: http://www.heuschele.com/worldofhopfs/ This project would not have been possible without the support of the European Society for Evolutionary Biology (eseb).

I hope you like it, and if you do please share it with your friends and colleagues.

Best wishes, Jan Heuschele

*but also in a “support the author version” in case you want to see more books like this.

janheuschele@gmail.com

ChicagoBotanicGarden UndergradResearchExperience

Information at www.cbgreu.org

The Chicago Botanic Garden, with colleagues from partner institutions, hosts a ten-week summer research experience. This program offers undergraduate participants an opportunity to explore a diverse array of scientific fields related to plant biology and conservation. Travel, room and board, and research costs are covered by the program. Participants also receive a $5,000 stipend.

Now accepting applications. The deadline has been extended through to February 8th, 2015.

The Summer program will run from Monday 8th June to Friday 14th Aug (There is some flexiblity with start dates)

For more information please visit our website www.cbgreu.org Jeremie Fant and Dan Larkin Chicago Botanic Garden Glencoe Il 60022

Lab@chicagobotanic.org

CostaRica VolFieldAssist StreamBiotaEvolution

Stream Biomonitoring Intern Position Available

Asociacion ANAI, an award-winning Costa Rican NGO working in the La Amistad area of Costa Rica and Panama, has a volunteer intern position available immediately (due to a last minute cancellation) in our innovative Stream Biomonitoring Program.

The opportunity is to participate in a program, linked to ANAI's other work best encapsulated in our slogan "protecting biodiversity on a full stomach". The urgent need is during our main field monitoring season of mid-February to mid-May. The work involves assisting (6 days a week) with monitoring fish and benthic macroinvertebrate assemblages and instream habitat. The fish work includes both sampling using electrofishers and visual censusing with mask and snorkel in the river systems draining the huge binational La Amistad World Heritage Site.

Much of the field time will be spent in remote indigenous and campesino communities working with and training local parataxonomists to help them deal with regional environmental isses, including proposed hydro dams. The volunteer will also be expected to assist in office and maintenance work, including data management and preparation for courses and meetings.

In addition to being available for the season, applicants should: - Be prepared to endure difficult conditions including long hikes, wading in swift flowing rivers, extreme weather (heat, rain, mud) and biting insects. - Have an interest in biology and conservation issues. - Be in good physical health - Know how to swim. - Have at least moderate capability in spoken Spanish. - Driver's license and ability to drive standard transmission is desirable.

The volunteer will be expected to pay his or her own way to Costa Rica plus basic food costs. We will cover all transportation within Costa Rica and Panama, housing in San Jose and at our field office in Hone Creek, lunch during field work days, food and lodging expenses on overnight or longer expeditions to remote sites, and all necessary equipment.

Our facilities in Hone Creek include dormitory style housing, with separate bath (cold water), kitchen and laundry facilities and 24 hour security. There are 2 grocery stores and 2 modest restaurants within walking distance. The situation varies from year to year, but there is often the opportunity to economize by collaborating in meal preparation at the office.

If interested, or with further questions, reply to my personal email billmclarney@gmail.com, or either of my colleagues, Maribel Mafla (mmafla@anaicr.org) and Ana Maria Arias (anamaria@anaicr.org).

Bill McLarney Director, ANAI Stream Biomonitoring Program

billmclarney@gmail.com

DiseaseEvolution exchanges

Dear colleagues,

We invite applications for research exchanges as part of an NSF-funded Research Coordination Network (http://ideas.princeton.edu). Our research exchanges are intended to allow researchers the opportunity to spend ~3 weeks working intensively away from their home institution, within a group with complementary expertise, to investigate the evolutionary biology of infectious diseases.

Two examples of possible research exchanges: 1) a theoretician visiting an empiricist's lab to learn more about how data are collected, integrate that knowledge into models they have already developed, run in silico experiments to test competing hypotheses, and jointly design the next experiment to be undertaken by the empiricist. 2) two empiricists bringing new datasets from different systems to a theoretician's lab to provide a reality check for models, jointly test the fit between model and data and answer new questions about biology across systems.

We request a concise application to include: your proposed research, with whom you propose collaboration and why, where the work will take place and an estimated budget (travel/subsistence).

Eligibility: Anyone is eligible, however exchanges will be awarded preferentially to meritorious PhD students and postdocs. International participants are welcome, though the host institution must then be in the US.

Quarterly application deadlines for 2015: 15 March, 15 June, 15 Sept and 15 Dec

Where to submit an application: Please visit our website in order to submit an application electronically or for further information: http://ideas.princeton.edu/-research-exchanges/ Thanks and all best wishes, Andrea

algraham@princeton.edu

ESEB outreach fund deadline

ESEB Outreach Fund

The European Society for Evolutionary Biology (ESEB) welcomes applications to the ESEB Outreach Fund for projects that promote evolution-related activities. The goal of this initiative is to improve public knowledge about evolution globally.

Applications for funding will be accepted for educational initiatives that promote evolution, development of evolutionary material (books, films, web sites) intended for a general audience, public outreach seminars, public exhibitions, etc. While most projects will be financed for a sum between 1000-1500 Euros, exceptions can be made if a strong argument is provided for additional funds.

The application form can be found on www.eseb.org (click on the "Outreach Fund" link). Applications will be accepted twice yearly (deadlines March 15, September 15) and should be submitted by email to Ute Friedrich (office@eseb.org; Subject: Outreach).

< http://www.eseb.org >

Dr. Ute Friedrich ESEB Office Manager Email: office@eseb.org European Society for Evolutionary Biology - www.eseb.org

office@eseb.org

Ethanol replacement query

Dear All

We have recently identified a need to rationalise the amount/volume of ethanol preserved specimens in the laboratory. In addition to regular housekeeping, rationalisation and outsourcing, one solution could be draining the existing ethanol, air drying and then replacing with either a DMSO (EDTA, NaCl), or RNAlater style solutions. Therefore, I would be really keen to find out from the community if any laboratories had been through this process and road tested the samples long term following the downstream preservation approaches. Alternatively, if anyone could identify the molecular biological reasons why this would not be a good idea, it would be good to find out. As always, I will collate and repost emerging solutions for the benefit of the community.

Many thanks to EvolDir and hope to hear from you regarding identifying solutions to what could be a developing issue for many of us.

Cheers and best wishes

Si

Simon Creer Senior Lecturer Molecular Ecology and Fisheries Genetics Lab Environment Centre Wales Building School of Biological Sciences Bangor University Bangor Gwynedd LL57 2UW UK

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

Ethanol replacement query answers

Dear All

Many thanks to all who responded and apologies if I did not get back to everyone (some mails bounced), but here is a summary of the soundbites I received from the community.

Briefly, at least one very reputable lab had replaced EtOH with RNA later or similar non-branded product and the genetic material was/is fine for subsequent analysis. There were many other queries and suggestions, of which drying was a popular choice, especially for tissues such as fish fin clips. I think that the comments provide really interesting reading and thanks to everyone who responded. Certainly food for thought for future strategies. Please see below.

Cheers and best

Si Creer

my experience the RNAlater solutions are fantastic for both RNA and DNA preservation at RT and lower temperatures. Tissue tend to become "rubbery" or "hard" in ethanol. My yields and quality of DNA was also much higher compared to ethanol storage. Dry storage also worked acceptably.

kinds of tissues are you trying to preserve and what are your downstream plans for them? DNA-based work only? Beware that because of its EDTA content and low pH, RNAlater will dissolve some mineralized tissues and may form crystals around small, soft-bodied specimens (I work on marine worms) or small tissue samples.

Invertebrate Systematics, 2013, 27, 81V86 http://dx.doi.org/10.1071/IS12067 DNA preservation: a test of commonly used preservatives for insects Corrie S. Moreau A,D, Brian D. Wray A, Jesse E. Czekanski-Moir A,C and Benjamin E. R. Rubin A,B

preferred method of preserving the samples and DNA is air drying. Briefly, we take a small fin clip (this can be done non-lethally) and place between a small piece of filter paper to absorb the moisture. The samples are then put into a desiccator (or warm dry area) for 3-5 days or until completely dry. We have found that the key to preserving high quality DNA is to begin the drying process immediately after the tissue is removed from the fish. Once fully dry, the samples can be stored for years at room temperature. As a bonus, this is a highly space-efficient method, and we can store a large number of samples in a small area, no reagents required.

also handle some ethanol-preserved tissue. When possible, we transfer ethanol samples to a dried state for long-term storage. This process involves blotting as much excess ethanol as possible with a lab wipe or blotter paper, overnight evaporation in a fume hood, and then ~3 days in a desiccator.

have recently extracted DNA from samples that have been stored at room temp on our sample shelf for about 10 years, and got good microsatellite and SNP genotype data from them. In my experience, the majority of the DNA degradation takes place in the first few hours following: 1) removal of the fin clip from the fish, 2) thawing of frozen samples, or 3) death of the animal, as with carcass samples from stream surveys. Once the tissue has dried, enzymatic activity ceases, so the quicker you can get the sample dry, the better. Most of the data-poor samples that I deal with are from salmon carcasses, and there seems to be a strong negative correlation between data quality and amount of time the carcass has been decomposing on the stream bank!

should mention that each tissue sample gets its own envelope, on which all the relevant sample info is written (and later entered into an electronic database). We use small coin envelopes that are about 9 x 5.5 cm. I buy "#1 coin brown" envelopes from envelopes.com in the US, but I'm sure there is a similar retailer in the UK. The blotter paper is Whatman 1 filter/blotter paper 46 x 57 cm, which we cut into ~2.5cm squares.

RNA later for ethanol is fine for fin clips

Simon Creer Senior Lecturer Molecular Ecology and Fisheries Genetics Laboratory School of Biological Sciences Environment Centre Wales Bangor University Gwynedd LL57 2UW Tel: +44(0)1248 382302 Fax: +44(0)1248 382569 web: http://mefgl.bangor.ac.uk/si.php Skype: spideycreer Twitter: @spideycreer

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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

EvoDevo UndergraduateSummerInternship

Dear Colleague,

This email is to remind you that the upcoming deadline for UNDERGRADUATE SUMMER INTERNSHIP funding from the Evo-Devo-Eco Network (EDEN) is March 11, 2015. EDEN is a program funded by the National Science Foundation of the USA. The goal of this program is to train undergraduates in the field of Evo-Devo-Eco, with an emphasis on emerging model systems.

Eligible students should be undergraduates of any nationality at any college or university, including liberal arts colleges, community colleges, and universities, both within and outside of the U.S.. Eligible host labs should be conducting research using new and emerging model organism and must be at a U.S.-based institution. If the proposed host lab is working on a well-established model organism, your application must explain how the techniques or skills that you learn in the host lab will be applied to work on new or emerging model organisms at your home institution.

Students may apply to work in a lab that is at their home institution, as long as the proposed research involves new and emerging model organisms. However, in cases where all other aspects of applications are considered to be equally competitive, preference will be given to applicants who propose to travel to a lab that is not at their home institution.

Please visit http://edenrcn.com/funding/ugrad_internships.html for complete program details.

For examples of previous undergraduate projects supported by EDEN, please visit http://edenrcn.com/ree/undergrad.html . Please note that the updated eligibility for EDEN funding is as follows:

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

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

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

Best wishes,

Cassandra Extavour

"Perlo, Barbara" <perlo@fas.harvard.edu>

Evolution videos answers

I received about 30, really useful responses to my query about good videos for a 2nd year evolution course. Many people wanted to hear what I heard back, so I have pasted the responses below. 'Thank you' to everyone who took the time to share their insights.

Dr. Vicki Friesen, Professor Department of Biology, 4443 Biosciences, 116 Barrie Street, Queen's University, Kingston, ON K7L 3N6, Canada Tel: 613-533-6156 Fax: 613-533-6617

Haida Saying: Treat the Earth well: it is not given to us by our parents, it is loaned to us by our children.

The "Stated Clearly" animations are short but very good.

Cheers,

Julia

Dr Julia D Sigwart

This youtube video is extremely lucid and well produced & comes with a simulator associated.

https://www.youtube.com/watch?v=SeTssvexa9s ps Part II goes into quite advanced issues on mutational load.

Richard Nichols

I hope this is useful

http://www.torontopubliclibrary.ca/detail.jsp?Entt=RDM2702731&R=2702731 Pedro

–

Pedro Fernandes

This site, while focused on ecology, had several good ones for evolution.

https://dynamicecology.wordpress.com/2013/10/08/videos-for-teaching-ecology/ Best wishes,

Sam [Zeheloff]

I am teaching an Evolutionary genetics/populations genomics course at Master level, and I am always starting with a course on the scientific theory of evolution based on J Coyne great 2009 book, it might be too general but I think it really gives a great overview of ideas and context for any evolution course, so I make my students watch J Coyne video on Youtube: https://www.youtube.com/watch?v=hqGX08Og4CE that you may know, but just in case

all the best Pauline [Garnier-Gere]

This is not a movie - rather a computer dynamic illustration a bit in the game category - but it might be of help.

http://www.cals.ncsu.edu/gn/ex/mit-eve.html Best wishes, –henry [Schaffer]

I use short (<10min) clips from the following documentaries

1st choice:

What Darwin didn't know (BBC Documetary) Armand Marie Leroi This is a DVD that you can borrow/buy. Currently not available on you tube, removed for copyright issues. Occasionally shows-up in YouTube, for a while.

http://www.imdb.com/name/nm2001160/ http://eweb.furman.edu/ ˜ jfoltz/Courses/BIO102/lect/Videos/WDDK_transcript.pdf Not really as good... in my opinion:

Evolution - What Darwin Never Knew - NOVA PBS Documentary https://www.youtube.com/watch?v=AYBRbCLI4zU Best,

Pedro

–

Pedro Fernandes

I saw your Evoldir note. I have a series of videos, based on the style of the Khan Academy (http://www.khanacademy.org/), that could possible serve your needs. Khan has pioneered the reverse classroom approach, where the students first watch a short video then come to class to discuss it. My videos are aimed at high school and early college students. There are 54 short (15 min) videos, and a growing series of circa 1 hour lectures on a variety of topics (http://post.queensu.ca/˜forsdyke/videolectures.htm). Kingston, of course, has much to do with the development of evolutionary ideas, Darwin's research associate, George Romanes, being born here in 1848! My attempts to get the new medical school building south of Earl Hall named Romanes Hall have so far been unsuccessful. Should the students be interested, more can be found in my textbook (Evolutionary Bioinformatics, 2nd edition 2011), and there are my earlier historical works (The Origin of Species Revisited, McGill Queen's Press 2001, and a biography of William Bateson 2008).

Don [Forsdyke]

The HHMI BioInteractive Evolution series is absolutely wonderful. I use almost all of them in my teaching 2nd/3rd year Evolution students. In particular, the series of short films in The Making of the Fittest series are great (see link below). There are also interactive activities that go along with the videos, although I have never used those.

Best of luck, Jannice

http://www.hhmi.org/biointeractive/making-fittest
http://www.hhmi.org/biointeractive/explore-evolution
Jannice Friedman

The american public broadcasting company (PBS; equiv to BBC) did a series several years ago called 'Evolution' (as part of their NOVA

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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

GCWilliams Prize EvolMedPublHealth

The International Society for Evolution, Medicine and Public Health is proud to announce the launch of the George C. Williams Prize. The $5,000 Prize will be awarded to the first author of the most significant article published in 2015 in the Society's flagship journal, *Evolution, Medicine and Public Health*. Oxford University Press publishes the journal open access. Stephen Stearns is the editor. Author's fees are waived for 2015. All articles published in 2015 will be automatically considered for the Prize.

The Prize recognizes the contributions of George C Williams to evolutionary medicine, and aims to encourage and highlight important research in this growing field. In a seminal 1957 paper, Williams initiated work on several problems central to medicine, including an evolutionary theory of aging and life history traits including menopause. He did important work on the problem of why sex exists. Perhaps his most lasting contribution is his 1966 book Adaptation and Natural Selection, a critique of group selection that transformed how biologists think about the evolution of sociality. In the 1990's he collaborated with Randolph Nesse on a series of papers and a book that inspired much ongoing work on how evolutionary biology can help us understand disease and improve human health.

The Society's Publications Committee, chaired by Andrew Read, will appoint the Prize Committee. The Prize Committee will interpret the criterion of 'most significant article' with attention to the focus on major unanswered questions that characterized the work of George Williams. Articles by members of the Prize Committee and their students and close colleagues are not eligible for the prize. Members of the Publications Committee and their students and close colleagues are eligible with special restrictions.

For full information see http://evolutionarymedicine.org or http://emph.oxfordjournals.com .For information about the Society's inaugural meeting March 19-21 see http://evmedmeeting.org Randolph Nesse <nesse@asu.edu>

GraduateUndergrad Funding PlantEvoDevo

Cross-Disciplinary Visits and Training Grant

The microMORPH RCN promotes and fosters cross-disciplinary training and interaction through a series of small grants that allow graduate students, post-doctoral researchers, and early career faculty to visit labs and botanical gardens. Being listed on the microMORPH community web page is required of all successful applicants (and encouraged for everyone else!).

Award Amount: Each Year, microMORPH is able to fund five graduate student, post-doctoral, or early career faculty cross-training research opportunities for up to $3,500 to cover travel, lodging, and pier diem.

Submission Deadline: The next microMORPH Cross Disciplinary Training Grant deadline is 11:30 pm March 1st, 2015.

Eligibility: To be eligible for a microMORPH training grant you must fulfill one or more of the following requirements: 1) you must be a U.S. citizen or, 2) you must be affiliated with a U.S. university or institution (in a graduate program or working as a post-doc or faculty member), or 3) the lab you plan to visit for your training experience must be at a U.S. university of institution.

How to Apply: For full application instructions (including list of required documents) and to submit applications, please visit the microMORPH website(http://projects.iq.harvard.edu/micromorph).

Proposal Evaluation: Two members of the steering committee (one organismic and one molecular) and a third individual from outside the core participants (chosen by the steering committee) are charged with evaluating applications.

Questions or Comments?: Contact Becky Povilus at RCNmicromorph@gmail.com

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Undergraduate Summer Internships/Training Grants

The microMORPH RCN promotes and fosters cross-disciplinary training and interaction through a series of small grants that allow undergraduates to visit labs and botanical gardens as well as gain invaluable laboratory experience while contributing to scientific discovery.

Award Amount: Each year, microMORPH is able to fund ten 10-week research internships/training grants for undergraduates. $5,000 is available per grant, which can be used for travel and housing for the period of the internship.

Submission Deadline: Undergraduate training grant proposals are due on 11:30 pm on March 1st, 2015

Eligibility: To be eligible for a microMORPH undergraduate training grant you must fulfill one or more of the following requirements: 1) you must be a U.S. citizen or, 2) you must be affiliated with a U.S. college, university, or institution (in an undergraduate program), or 3) the lab you plan to visit for your training experience must be at a U.S. university of institution.

How to Apply: For full application instructions (including list of required documents) and to submit applications, please visit the microMORPH website(http://projects.iq.harvard.edu/micromorph).

Proposal Evaluation: Two members of the steering committee (one organismic and one molecular) and a third individual from outside the core participants (chosen by the steering committee) are charged with evaluating applications.

Questions or Comments?: Contact Becky Povilus at RCNmicromorph@gmail.com

Pamela Diggle

Professor Department of Ecology and Evolutionary Biology University of Connecticut

860-486-4788

"Diggle, Pamela" <pamela.diggle@uconn.edu>

Italy VolFieldAssist BeetleConservation

FIELD ASSISTANTS for monitoring SAPROXYLIC PROTECTED BEETLES in the LIFE-MIPP Project. Website: www.lifemipp.eu . Reference Institutions: CFS, National Forest Service (project coordinator); CRA ABP, Council for Agricultural Research and Economics Research Center for Agrobiology and Pedology.

The field assistants will help in fieldwork for the monitoring of 5 species of saproxylic beetles (*Cerambyx cerdo*, *Rosalia alpina*, *Morimus asper/funereus*, *Osmoderma eremita* and *Lucanus cervus*) in five protected areas in Central and Northern Italy (Appennines and Alps). The sampling seasons will be from May to August 2015 (field assistants are expected to join the project for at least 2 weeks). The aim of the research is to develop standard monitoring protocols for the saproxylic beetles listed in the Habitats Directive, as required by the European Community. The field assistants will work with a team consisting of master students, PhD, post-docs and researchers. The work will consist in not-invasive methods as the count of animals in transects, capture/mark/recapture, photographic identification, interception traps, collection of remains. Moreover, the project also benefits from an innovative technique by the use of a sniffer dog. Duties will include insects handling (marking, measuring), data entry and data management. The fieldwork will be demanding and will be organized in 4-5 day sessions.

Qualifications/Experience Candidates must have experience with fieldwork in general and interest in insect. Field work hours will be long and tiring and applicants should be prepared to work at any time including weekends and holidays.

No financial compensation will be provided but accommodation and meals will be covered by the project.

Candidates should have at least a BSc in Biology or in Natural Science or a related field. Ideal candidates are highly motivated, well organized and able to work independently, while at the same time able to work in a group.

Applications Review of the applications will begin Mid-February and continue until the positions are available. To apply, please send (1) a statement of relevant experience and motivation, (2) a very short resume or CV to both Dr. Alessandro Campanaro (ale.naro@gmail.com) and Dr. Fabio Mosconi (fabio.mosconi@gmail.com).

Best regards, Alessandro Campanaro and Fabio Mosconi

alessandro.campanaro@uniroma1.it

LandscapeGenomics call

“The least cost path from landscape genetics to landscape genomics: challenges and opportunities to explore NGS data in a spatially explicit context” is the title of a Research Topic for Frontiers in Ecology and Evolution to explore a number of critical challenges and opportunities for the transition from landscape genetics to landscape genomics.

We invite the submission of papers (original research, general commentary, opinion article, etc.**) related to the transition from landscape genetics to landscape genomics. The papers may include : a) data and analysis of spatial analysis of empirical NGS data to identify markers under selection and quantify effects of environmental factors and heterogeneity on gene flow and selection; b) simulation and modeling to explore the application of spatially explicit, individual-based modeling in a NGS context; c) experimental genomics in common garden and gene-line selection experiments to discuss the challenges and opportunities of integrating experimental genetics with emerging genomic data;

See the full text of the call for papers here: http://-journal.frontiersin.org/ResearchTopic/3790 Deadline for abstract: March 27, 2015 (declaration of intent, not compulsory) *Deadline for submission: September 25, 2015*

The topic editors,

Samuel Cushman, Andrew Shirk, Glenn Howe, Melanie Murphy, Rodney Dyer, Stéphane Joost

**More information on Frontiers Research Topics: http://www.frontiersin.org/about/RTGuidelines
stephane.joost@epfl.ch

MountainLake EarlyCareer Fellowships

The University of Virginia's Mountain Lake Biological Station (MLBS) in the southern Appalachians is excited to offer a limited number of fellowships to support station and residency costs for researchers to explore new projects or collect preliminary data. This is a rare opportunity to make an extended stay of up to 2 months at one of North America's premier field stations at no cost to the researcher. Preference will be given to individuals and projects with the potential to develop into long-term research activities at the Station. We especially encourage applications from individuals in the postdoctoral or early faculty phases of their careers, but will not exclude other individuals from consideration.

For more information about the fellowship program, research opportunities or Mountain Lake Biological Station (mlbs.org), please contact the Director Butch Brodie (bbrodie@virginia.edu).

Interested individuals should submit a single pdf file including CV and a 2-3 pp proposal outlining the proposed research and planned dates of residence (or duration of stay) to MLBS@virginia.edu. Review of proposals will begin March 20, 2015.

bbrodie@virginia.edu

NESCent 2015 VideoContest

NESCent 2015 Evolution Film Festival/Video Contest

Scientists and science educators of all stripes - students, postdocs, faculty, and full- or part-time science communicators - are invited to enter the Fifth Annual Evolution Video Competition, sponsored by the National Evolutionary Synthesis Center (NESCent) and the Society for the Study of Evolution (SSE). 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 2015 Evolution meeting in Guarujá, Brazil. (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 SUNDAY, MAY 31st, 2015 (11:00 PM, EST).

For more information (and to see entries from previous years) please visit filmfestival.nescent.org or contact Jory Weintraub (jory@nescent.org).

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

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

NewPhytologist EvolutionMycorrhizas

I wanted to make you aware of the online publication of a Special Issue of New Phytologist on the Ecology and evolution of mycorrhizas. The Editorial by Dickie et al. 'Evolving insights to understanding mycorrhizas' introduces the special issue and can be read for free here: http://onlinelibrary.wiley.com/doi/10.1111/nph.13290/full The special issue's full table of contents can be found here: http://onlinelibrary.wiley.com/doi/10.1111/nph.2015.205.issue-4/issuetoc and in summary below:

Forum Editorial

Evolving insights to understanding mycorrhizas (pages 1369-1374) Ian A. Dickie, Ian Alexander, Sarah Lennon, Maarja Ãpik, Marc-André Selosse, Marcel G. A. van der Heijden and Francis M. Martin

Commentary

Priorities for research on priority effects (pages 1375-1377) David Johnson

Moving beyond the black-box: fungal traits, community structure, and carbon sequestration in forest soils (pages 1378-1380) Christopher W. Fernandez and Peter G. Kennedy

Letters

How harmonious are arbuscular mycorrhizal symbioses? Inconsistent concepts reflect different mindsets as well as results (pages 1381-1384) F. Andrew Smith and Sally E. Smith

Plant root and mycorrhizal fungal traits for understanding soil aggregation (pages 1385-1388) Matthias C. Rillig, Carlos A. Aguilar-Trigueros, Joana Bergmann, Erik Verbruggen, Stavros D. Veresoglou and Anika Lehmann

Parsing ecological signal from noise in next generation amplicon sequencing (pages 1389-1393) Nhu H. Nguyen, Dylan Smith, Kabir Peay and Peter Kennedy

Fungal associations of basal vascular plants: reopening a closed book? (pages 1394-1398) William R. Rimington, Silvia Pressel, Jeffrey G. Duckett and Martin I. Bidartondo

The fungal perspective of arbuscular mycorrhizal colonization in 'nonmycorrhizal' plants (pages 1399-1403) Ylva Lekberg, SÃren Rosendahl and PÃl Axel Olsson

Profile

Francis M. Martin (pages 1404-1405)

Review Tansley reviews

Mycorrhizal ecology and evolution: the past, the present, and the future (pages 1406-1423) Marcel G. A. van der Heijden, Francis M. Martin, Marc-André Selosse and Ian R. Sanders

Tansley insights

Towards a holistic understanding of the beneficial interactions across the Populus microbiome (pages 1424-1430) Stéphane Hacquard and Christopher W. Schadt

Phytohormones as integrators of environmental signals in the regulation of mycorrhizal symbioses (pages 1431-1436) María J. Pozo, Juan A. López-Ráez, Concepción Azcón-Aguilar and José M. García-Garrido

Partner selection in the mycorrhizal mutualism (pages 1437-1442) Gijsbert D. A. Werner and E. Toby Kiers

Ectomycorrhizal fungi - potential organic matter decomposers, yet not saprotrophs (pages 1443-1447) Björn D. Lindahl and Anders Tunlid

Interplant signalling through hyphal networks (pages 1448-1453) David Johnson and Lucy Gilbert

Research reviews

Local-scale biogeography and spatiotemporal variability in communities of mycorrhizal fungi (pages 1454-1463) Mohammad Bahram, Kabir G. Peay and Leho Tedersoo

Research Rapid reports

Endogone, one of the oldest plant-associated fungi, host unique Mollicutes-related endobacteria (pages 1464-1472) Alessandro DesirÃ², Antonella Faccio, Andres Kaech, Martin I. Bidartondo and Paola Bonfante

Full papers

Mycorrhizal phenotypes and the Law of the Minimum (pages 1473-1484) Nancy Collins Johnson, Gail W. T. Wilson, Jacqueline A. Wilson, R. Michael Miller and Matthew A. Bowker

Host diversity affects the abundance of the extraradical arbuscular mycorrhizal network (pages 1485-1491) Daniel J. P. Engelmoer and E. Toby Kiers

From mycoheterotrophy to mutualism: mycorrhizal specificity and functioning in Ophioglossum vulgatum sporophytes (pages 1492-1502) Katie J. Field, Jonathan R. Leake, Stefanie Tille, Kate E. Allinson, William R. Rimington, Martin I. Bidartondo, David J. Beerling and Duncan D. Cameron

Preferential allocation, physio-evolutionary feedbacks, and the stability and environmental patterns of mutualism between plants and their root symbionts (pages 1503-1514) James D. Bever

Order of arrival structures arbuscular mycorrhizal colonization of plants (pages 1515-1524) Gijsbert D. A. Werner and E. Toby Kiers See also the Commentary by David Johnson

Carbon sequestration is related to mycorrhizal fungal community shifts during long-term succession in boreal forests (pages 1525-1536) Karina E. Clemmensen, Roger D. Finlay, Anders Dahlberg, Jan Stenlid, David A. Wardle and Björn D. Lindahl See also the Commentary by Christopher W. Fernandez and Peter G. Kennedy

Exploring the transfer of recent plant photosynthates to soil microbes: mycorrhizal pathway vs direct root exudation (pages 1537-1551) Christina Kaiser, Matt R. Kilburn, Peta L. Clode, Lucia Fuchslueger, Marianne

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PeerJ CompSci

PeerJ aims to speed up the pace and openness of Computer Science publishing with launch of new journal PeerJ Computer Science

San Francisco, CA and London, UK Tuesday February 3rd 2015

Award winning open access publisher PeerJ today announces the launch of PeerJ Computer Science, a cross-disciplinary open access journal publishing articles across all fields of computer science. PeerJ PrePrints will start accepting computer science preprints on Tuesday February 3rd and the peer-reviewed journal will open for submissions on Thursday February 12th, which is also PeerJ's two-year anniversary of publishing in the biological and medical sciences.

From February 3rd interested authors can visit https://peerj.com/computer-science to find out more about the journal, and its 322 strong Editorial and Advisory Board (which includes a number of high profile computer scientists including Vint Cerf, Wendy Hall, David Patterson and Mary Shaw for example). PeerJ is offering free publication to all those who register their email at this page, and also to their colleagues simply by providing their email details.

Jason Hoyt, Co-founder and CEO of PeerJ said "We've received a constant stream of requests to bring our unique lifetime publishing model and user design philosophy to other disciplines ever since we launched PeerJ two years ago for the life sciences. We feel now is the right time to build upon our success by offering PeerJ's services to the computer science community, who have been looking for a modern and improved publishing experience.

Tim O'Reilly, founder of O'Reilly Media and a member of the PeerJ Board, added "Open source software has transformed the practice of software development. So it is about time for an open access computer science journal to bring computer science research publishing into the 21st century. It's great to be part of helping make that happen." PeerJ's existing connections with Tim O'Reilly places PeerJ well to build deeper connections within the computer science community and to understand how best to serve their needs.

The landscape for academic publishing within computer science is ripe for change. There are very few open access journals currently serving the computer science community, and authors in this field are mainly publishing their work either at academic conferences or in subscription journals. The traditional journal route can be very slow for authors in this field with lengthy review processes, which is one of the reasons why authors often find that disseminating their work at a conference is a much faster route to obtaining a decision. The current system for publishing in computer science is in need of some fresh innovation, and by opening up submissions for computer scientists PeerJ is aiming to bring a 21st century publishing platform to computer scientists.

PeerJ Computer Science will operate in exactly the same way as PeerJ articles will be published through CC BY licensing ensuring that the content is freely accessible to the world. The business model also remains the same with authors paying a low cost fee to publish their article, starting at $99 for lifetime publication. Although it remains to be seen how fast the new journal will be, PeerJ's life science and medicine authors currently receive a first decision in a median time of 22 days, which would help to address the need for quick turnaround times for computer scientists. By publishing cross-disciplinary research across the full spectrum of computer science, PeerJ Computer Science hopes to engender more cross-fertilisation between fields and to become a hub for the computer science community as a whole to interact. PeerJ intends to work closely with the computer science community from the outset to help shape the journal as it grows.

Peter Binfield, Co-founder and Publisher of PeerJ added We built PeerJ with the scientific community in mind, and our technologies enable better ways to publish articles. We want our Authors, Reviewers and Editorial Board to help us shape the journal as it grows, so we'll be listening intently and taking on board their suggestions and recommendations. We know computer scientists want a better way to publish their research, and we will aim to provide that by shaping the platform to meet their requirements. We're excited to see how we can move publishing in computer science forward and better serve the needs of this community.

Full list of Advisory Board Members for PeerJ Computer Science

Chieko Asakawa, IBM Japan Grady Booch, IBM Francine Berman, Rensselaer Polytechnic Institute Christine Borgman, UCLA Vint Cerf, Google Krishnendu Chakrabarty, Duke University Jennifer Chayes, Microsoft Research Lynn Conway, University of Michigan Peter Denning, Naval Postgraduate School Ian Foster, University of Chicago Martin Fowler, Thought-

Works Wendy Hall, University of Southampton Jim Hendler, Rensselaer Polytechnic Institute

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Pruning phylogeneetic trees

Dear Colleagues,

Microbial epidemiologists often need to determine how new isolates of pathogens are related to known isolates. Today that means constructing phylogenetic trees based on whole genome sequences. The practice has been to use all the available genome sequences plus new isolates as the data set. New genome sequences are being added to the data bases at an astonishing rate, and a sample of new genomes of interest can be obtained so quickly that there are often 50-100 new genomes to consider. That means that the sizes of data sets are exploding, sometimes beyond the capacity of the software to handle. We are no faced with so much of a good thing that analyzing the data is becoming increasingly difficult.

In fact, we dont REALLY need to know where each new isolate fits in with every previously known strain in one tree. It would be quite sufficient to be able to assign new isolates to major clades, and then in a second pass to use only the members of that clade to make a tree of those isolates that fir into that clade, using all known members of that clade for the second pass.

In effect, what we want to be able to do is to prune a large (200-300 genomes) phylogenetic tree so that every important clade is represented and a representative set of members of each is included. If a set of 150 genomes could be trimmed down to a representative 30-50 genomes for the first pass that would be ideal.

The problem is how to rationally prune a tree. We want every important node represented, but how to choose the important nodes? How many representative genomes of each clade? How to ensure that they adequately represent the phylogenetic diversity within that clade?

Are you aware of software designed for such tree pruning? Can you point me to useful papers on the subject?

Thanks for taking the time to read this plea for help, and thank you in advance for any advice or suggestions you might have.

Barry

Barry G. Hall Director, Bellingham Research Institute Je suis Charlie

"Barry G. Hall" <barryghall@gmail.com>

Pyrenees VolFieldAssist EvolBiol

Field assistants summer 2015: Volunteer positions in evolutionary biology

Nick Barton's group at the Institute of Science and Technology (IST) Austria requires volunteers to assist with field work on plant speciation in the Pyrenees (Spain) this coming summer (June - August).

The project: We are studying the evolutionary dynamics underlying species diversification in the genus Antirrhinum (snapdragons). A major focus of this research involves field work on natural hybrid zones between two subspecies with different flower colours. Most of the field work is contributing to a long-term pedigree project aimed at establishing a direct link from genotype to phenotype to fitness. With 14,000 samples collected over five generations (so far), this provides an exciting and powerful system to examine many outstanding questions in speciation and quantitative genetics in wild populations. We are seeking volunteers to assist with the field work, which involves working in teams mapping the location of individual plants (GPS), tagging and sampling them for leaves and flowers, measuring quantitative traits, phenotyping them for flower pigmentation and processing material for later DNA extraction. There may also be opportunities to be involved in other projects we are doing on plant-pollinator interactions, pollen fertility and community ecology surveys. Most of the work is outdoors, however we do spend some time indoors processing samples. The work is highly team orientated, typically in groups of 2-3 in the field and larger groups processing samples back at the research station. This is a great opportunity for anybody looking to obtain experience in field work relating to evolutionary biology, plant ecology and plant-animal interactions. You will also be part of a large multidisciplinary team including researchers from IST Austria (Vienna), John Innes Centre (Norwich, UK) and the University of Toulouse.

The field site is located near Ripoll in a beautiful part of the Pyrenees of North Eastern Spain (Catalonia). We stay in comfortable apartments overlooking a picturesque valley, with close access to hiking trails and small villages. All food, accommodation and travel (within Europe) are covered. However, we cannot offer any further stipend.

For these positions we are looking for hard working and enthusiastic biology students with a strong interest in working outdoors with plants. You must be meticulous with recording data and also be comfortable working as part of a team. Experience with field-based projects and plants is preferred but not essential.

We require assistance between early June and the end of July. Depending on the year and the plants, we may extend our time into August. Length of stay is flexible but a minimum stay of 3 weeks is required.

Please send any questions to the email address below. How to apply? By the closing date of March 31st, please send a statement of your background, CV, why you are interested and the length of time you would be available via email to:

david.field@ist.ac.at

Dr. David Field

Postdoctoral Fellow

Barton Group

IST Austria

AMCampus 1

Klosterneuburg3400

Phone: +432243 9000 3008

Web: http://ist.ac.at/research-groups-pages/-barton-group/team/david-field/ Web: https://-sites.google.com/site/davidfieldresearch/home David Field <david.field@ist.ac.at>

Sample Management Software 2 answers

Hi again,

After my return of answers to my initial question (see below) I received a few more answer, which I share in my updated answers. I number the new answers starting with 12, because 1-11 are printed beow for your records.

Thanks again, community!

Cheers, Robert

12. If you do use an SQL set up, you might be interested in using the firefox add-on to access the database (https://addons.mozilla.org/en-us/firefox/-addon/sqlite-manager/). There is also a good introductory tutorial on sql here: http://software-carpentry.org/-v5/novice/sql/index.html 13. We curate a sample collection of 15 000 tissue samples, and more DNA extractions (as you sometimes end up extracting DNA more than once). About 20 years ago I created the first data base for this (and all the lab work, we record every PCR etc.) in a proprietary relational database (e.g., like FileMaker, ACCES etc.). We are now (well for a few years) hitting the limitations of "proprietary" (simply too many records and restrictions in terms of software, plugins, operating systems etc.). This have led me to the open source SQL databases, in our case mySQL/MariaDB.

Incredibly simple and capable. Works on any operating system and remote access is dead easy to set up in a secure manner (e.g., using SSH tunnels and key-based log in). You can make entry forms, etc. in HTML using PHP so users can access from anywhere. The degree of control, e.g., who has access to what database/tables/fields is truly staggering.

These databases (postgresql is another well-known) have been around for eons, most serves and web sites runs on mysql/portgresql and mariadb, which means that your database software will NOT become obsolete and the number of scripts and code and plugins to all kinds of programming languages etc. is equally extensive. It is also the choice databases for much of the genomic bioinformatics (e.g., STACKS for RAD sequencing) for all the above reasons. Records are saved in plain text, making it easy to recover in case of database corruption (not so for many proprietary database softwares).

Depending on your experience the learning curve may be a bit steep, but in these cases you know it will be worthwhile the investment for many years to come. As it is a generic system that implies you can configure any way you want and not have to rely upon some schema devised for somebody else's needs and purposes.

14. We are currently also looking into options to organize our databases better - one thing I came across is WILDBOOK:

http://www.wildme.org/wildbook/doku.php 15: I was forwarded your message by XXX at XXX, who thought our company's data management technology might be of interest to you. It is called Ref It Technology, which you can read about in some detail on our website: www.refittech.com . This technology uses Excel as an interface for Microsoft SQL Server databases. It is a different way to use the SQL software package, so that a single table-type can be used to store data for any type and number of variables and formats. Therefore, teams of people, who each might have some different and some identical variables, can store and share their data in a single SQL table-type. Also, because a single table-type is used for all types of data, it makes meta-studies, consolidation of databases, and divisions of databases by topic for various special purposes simple.

There is no database programming required. You simply need to own a copy of Microsoft SQL (the free 'Express' version works fine). The Ref It software configures the SQL database for you. And once the software is installed, a new ribbon shows up in your Microsoft Excel program, which allows you to interact with the uniquely configured SQL database, for sending, browsing, and retrieving data by search criteria, all the new ribbon in Excel.

Please let me know if you'd be interested in discussing this further. I could meet with you to show you a demonstration, even using examples of the types of data you will be storing.

AND HERE MY PREVIOUS POST WITH ANSWERS 1-11:

On 07.02.2015 09:46, evoldir@evol.biology.mcmaster.ca wrote: Dear EvolDir community!

I asked for sample management software a few days ago. Here is the original post:

—

we are searching a way to get rid of Excel tables of our samples in Dropbox or network drives. Would you be so kind and suggest solutions regarding the management of samples? Our samples are regular molecular ecology stuff. Sometimes we have multiple samples from the same individuum, and also multiple samples types. Otherwise we do not need anything special. It would be nice if the sample management could be

— / —

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

Sample management software answers

Dear EvolDir community!

I asked for sample management software a few days ago. Here is the original post:

—

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—

And these are the answers that reached me. I will return all answers to you without actually sorting out the ones that I think would not work so well. That is because your idea of such a software may be different from mine. Hope this is useful!

Cheers, Robert (robert.kraus@uni-konstanz.de)

1. We increasingly rely upon Google Spreadsheets. It's all saved in the cloud as part of Google Drive, is free, and it is of course very easy to share with multiple people such that certain lists of people can view the data and others can edit it. I suggest backing up regularly to a private spreadsheet, though, because if someone with edit access erases it, it's gone (same as for documents shared on networks.)

2. we purchased a FileMaker server license and five

client licenses installed on lab computers. We then created our own Filemaker database. It works great. The server software takes care of the backups and allows multiple users to modify the database while enforcing integrity of the data. You can publish the database on the web and restrict access. There is a bit of a learning curve though.

3. we have been looking into options to use a MySQL database for sample management. It has the flexibility that you can add any type of metadata you want provided you organise the database carefully from the begin on. However, I'm interested in any feedback you get from your query and would appreciate it if you could forward it to me.

4. we have established in our molecular lab a SQL database managed by the system OpenBIS from the ETH (http://www.cisd.ethz.ch/software/openBIS). Possibly it is a very big hammer on your data but it is very flexible and extensible over time. The simplest setting would be: Store your samples in the database and add observations as attachments (excel tables, etc.) to it. The next step would be to create database entries for the different experiments and you could link the samples to this (and could also backtrack from experiments to the samples afterwards, which is quite nice for supervisors or if you try to remember what you have done month ago).

The management/installation is not very easy but with a little knowledge about databases, SQL and linux doable in at least 2 weeks. A complete and sophisticated setup might need 4 weeks or even some month while learning the system better and better to get the whole workflow optimized.

5. Perhaps our VoSeq database would be of use to you? https://github.com/carlosp420/VoSeq and http://nymphalidae.utu.fi/cpena/VoSeq_docu.html 6. I would very much recommend JMP (www.jmp.com) as the data management and analysis platform. It's a popular statistical package and it's great as such (not cheap, though), but it is particularly good at data management. It allows to easily summarize data by any combination of columns, merge files by matching values two or more columns (with or without retaining non-matches or dropping multiples in either table), split and stack columns by specified values, etc. More expensive ProJMP version includes the same functions in the form of database management tool. Even more expensive JMP Genomics version includes all kinds of sequence, genotype an expression data analysis tools, but this maybe more than what you are looking for and it is expensive.

7. We do the things you mention with our software www.earthcape.com Please let me know if you want to have more details about it. Perhaps a skype call. It would be interesting to learn details of your needs and tell you about what we can offer.

8. We use Lab Collector, it has all the capabilities that you probably need and is user friendly and web based. Can be a little clunky for entering large quantities of data, but it is great when you have a whole team needing access to shared information.

— / —

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

Software HybridAllopolyploid GeneExpression

Hi everyone,

This is a quick announcement of HyLiTE, a new software package to study gene expression in hybrid and allopolyploid species.

Hybrids and allopolyploids are often an evolutionary short-cut to speciation. Although well studied in plants, they are also surprisingly common in animals and fungi.

Hybrids and allopolyploids carry at least two nearly-identical copies of each gene, which makes it challenging to determine the expression level of each gene copy ("homeolog"). Gene expression (either for individual genes or genome-wide) is usually measured by stringent read mapping, but this method has a very high error rate.

We have just released HyLiTE, a flexible, easy-to-use program with high read assignment accuracy that was specifically designed for bench biologists to explore patterns of gene expression following genome merger:

http://hylite.sourceforge.net The accompanying paper is available here:

Duchemin, W., P.-Y. Dupont, M.A. Campbell, A.R.D. Ganley and M.P. Cox. 2015. HyLiTE: Accurate and flexible analysis of gene expression in hybrid and allopolyploid species. BMC Bioinformatics 16:8.

http://www.biomedcentral.com/1471-2105/16/8
HyLiTE can be used on hybrids or allopolyploids with any number of parent species, particularly non-model organisms. Given the prevalence of hybrids and

allopolyploids in evolutionary studies (and limited genome resources for these mostly non-model species), we think that the HyLiTE software may be of interest to some in this community.

-Murray Cox

Murray Cox, Ph.D. | Associate Professor | Rutherford Fellow Institute of Fundamental Sciences | Massey University | New Zealand

+64-6-356 9099 x84747 | m.p.cox@massey.ac.nz | http://massey.genomicus.com murray.p.cox@gmail.com

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Software Microsatellite simulation inR

Hello all.

I just posted on GitHub a new R package (microsimr version 0.0.1) that simulates microsatellite data under the coalescent. At the moment, the package allows one to simulate microsat data under a diverse range of demographic scenarios, taking advantage of Hudson's ms coalescent simulator. There is a function that will save your simulated data as an input file for Migrate-N, so you can study the power of Migrate-N to estimate parameters of interest under the constraints of your study. Also, I take a slightly different approach to simulating the alleles from that of Murray Cox's microsat (details in the vignette), so it is possible to study rates of homoplasy in microsatellite data too, and how they might affect your downstream parameter estimates.

Current limitations:

1. Only outputs to Migrate-N, if there is interest in other programs I can certainly find the time to add output for additional formats.

2. Only simulates microsats using a symmetrical strict stepwise mutation model. This can easily be added to if there is interest.

3. I need to add an example to demonstrate how the data can be transformed to a GENIND object and thus be used with the adegenet package, and other R pop gen packages.

4. ms options must be entered manually, but could potentially be made easier.

5. No function to output degree of homoplasy.

If you have interest in the package, and would like to see any of these issues dealt with, or you have additional suggestions, please contact me directly or post a request in the Issues section of the GitHub page.

To get the package go to:

https://github.com/andersgs/microsimr And, follow the instructions.

The package is not yet available on CRAN.

Best.

Anders.

andersgs@gmail.com

Software TREEFINDER license change

Dear All!

Please note that I have changed the license agreement of my TREEFINDER software (www.treefinder.de):

Starting from 1st February 2015, I do no longer permit the usage of my TREEFINDER software in the USA. For all other countries, the old license agreement remains valid.

This is in accordance with the license agreement stated in the TREEFINDER manual since the earliest versions, which reserves me the right to change the license agreement at any time.

My reasons:

(1) I want to protest against American imperialism, which I regard as the cause of most of all evil in the world: wars, tyranny, poverty, migration.

(2) I want to protest against EU tyranny, which is mostly the result of US imperialism.

(3) I want to demonstrate my sovereignty, something I would welcome to see much more often in science and politics.

In particular, I dislike that the USA and the EU aggressively promote a way of life that conflicts with my own way of life.

After so many years of hard work on TREEFINDER, I have still not been paid any reward.

I want to stress that this license change is not against my colleagues in the USA, but against a small rich elite there that misuses the country's power to rule the world.

On the TREEFINDER download website I have collected many links to background information, including some in English language.

Regards,

Gangolf Jobb

Gangolf Jobb <gangolf@treefinder.de>

SouthAfrica VolResAssist SocialMolerats

SouthAfrica.ResearchAssistant.SocialMolerats

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

2 Positions:

15th of March 2015 to 14th of June 2015.

Mid-June 2015 to mid-September 2015.

We are looking for two voluntary field research assistants to conduct field research on the completely subterranean, highly social Damaraland mole-rat (Fukomys damarensis). Specifically, this project investigates the group augmentation hypothesis and how benefits of living large groups can generate selection for altruism in animals. We plan a large scale capture-mark and recapture experiment running over one year in which the voluntary research assistant would play an important role. Field work takes place in the southern Kalahari, Northern Cape province of South Africa. Entire groups of mole-rats will be captured and individually marked. Morphological measurements and tissue samples will be obtained before the release of the animals. The work is physically extremely demanding (long hours, heavy digging to capture mole-rats) and weather conditions are very challenging (heat during the day, very cold during the night). Field work will make trapping during the night necessary. The assistant will mostly be working along one more experienced scientist but will need to work independently at times.

Applicants should be enthusiastic, willing to work hard and keen to get involved in an ecological research project in the African bush. Research assistants are expected to be willing to work at night when trapping schedules require it and need to be fit as capturing mole-rats requires the capacity to do hard physical work (digging) in a challenging environment. Applicants must be holders of a driving license. A zoology related degree and/or previous field experience will be considered an asset. The successful applicants will work in a small team of 2 persons and hence need to be a team player and generally a person that enjoys collaboration under sometimes challenging and isolated circumstances.

Accommodation is provided, and research assistants are paid a monthly allowance to cover their food.

Applications received until the 12th of February 2015 are ensured full consideration. Later applications can be considered (particularly for the second time period). Dates for the second period are more flexible and applicants can indicate if they wish to commit for a longer period.

Further Information:

http://bit.ly/1zG67hJ To apply (CV + cover letter) or enquire further information contact:

Dr Markus Zöttl

Research associate

University of Cambridge

+441223336673

Mz338@cam.ac.uk

http://www2.zoo.cam.ac.uk/larg/MARKUSZOETTL.html Markus Zoettl <mz338@cam.ac.uk>

SSE HamiltonAward DeadlineFeb20

www.evolutionsociety.org SOCIETY FOR THE STUDY OF EVOLUTION

Dear SSE Colleagues:

Just a reminder that applications for the Hamilton Award are due Friday, February 20. The W.D. Hamilton Award (http://www.evolutionsociety.org/index.php?module=content&type=user&func=view&pid=15) for Outstanding Student Presentation will be given to a student who has presented an outstanding talk at the annual meeting. You must submit a 400-word abstract and talk title. Finalists will be notified by March 13. Finalists will present their papers during a day-long symposium of Hamilton award candidate talks. This year, finalists will receive a registration waiver and a $500 travel stipend from the SSE. Learn more and find the link to apply HERE (http://www.evolutionsociety.org/index.php?module=content&type=user&func=view&pid=15)

Please make note of another award deadline that is upcoming. Rosemary Grant Research Award (http://cms.gogrid.evolutionsociety.org/index.php?module=content&type=user&func=view&pid=16) - April 1

SSE Business Office PO Box 299 | St. Louis Missouri, 63166 314-577-9566 www.evolutionsociety.org Society for the Study of Evolution <hcacanindin@evolutionsociety.org>

SystematicBiology SpecialIssue

Special Issue of Systematic Biology, after MCEB2013 http://sysbio.oxfordjournals.org/content/current This issue, after the "Mathematical and Computational Evolutionary Biology" conference (MCEB), held at Montpellier in June 2013, contains three review papers that are freely available:

Cancer Evolution: Mathematical Models and Computational Inference Syst Biol (2015) 64 (1): e1-e25 doi:10.1093/sysbio/syu081 Niko Beerenwinkel, Roland F. Schwarz, Moritz Gerstung, and Florian Markowetz

Phylogenetics and the Human Microbiome Syst Biol (2015) 64 (1): e26-e41 doi:10.1093/sysbio/syu053 Frederick A. Matsen IV

The Inference of Gene Trees with Species Trees Syst Biol (2015) 64 (1): e42-e62 doi:10.1093/sysbio/syu048 Gergely J. SzöllÅsi, Eric Tannier, Vincent Daubin, and Bastien Boussau

Olivier Gascuel <gascuel@lirmm.fr> Olivier Gascuel <gascuel@lirmm.fr>

T H Huxley Award

The SSE Education Committee is pleased to announce the T. H. Huxley award, named in honor of Darwin's very public supporter, which provides funding for an SSE member to present at the National Association of Biology Teachers (http://www.nabt.org/ < http://www.nabt.org/websites/institution/index.php?p=10 >) annual conference. If you have an interesting project or educational activity to share with high school, community college or undergraduate faculty, consider applying for this award. Graduate students and postdoctoral fellows are encouraged to apply.

This years conference will be held Nov 11-14, in Providence, Rhode Island. The deadline for applying for the Huxley award is March 4. Apply here:

http://tinyurl.com/php87w4 Questions? Contact Louise Mead (lsmead@msu.edu) or Kristin Jenkins (kristin.jenkins@bioquest.org)

– Kristin P. Jenkins, PhD Director BioQUEST Curriculum Consortium bioquest.org

Kristin Jenkins <kristin.jenkins@bioquest.org>

UMaryland VolFieldAssist PlantInsectInteraction

Other: volunteer field assistance on plant insect interactions in eastern USA, summer 2015

Volunteer field assistance needed for research in eastern USA from June 15 V September 15, 2015, potential bachelor/master thesis.

Within my PhD project I am quantifying the interaction between the native plant species Silene stellata (Caryophyllaceae) and its specialized pollinating seed predator Hadena ectypa (Noctuidae) along a north-south gradient of their range and the implications of climate change on this interaction. I am offering a bachelor or master student to accompany my field work in summer 2015 with the potential to conduct his/her bachelor or master thesis within the project.

Details can be found under the following link: https://drive.google.com/file/d/0BzsO6ofdzOXZajc5cHljamhyM0E/view?usp=sharing For further information or any questions please contact: Nicola Seitz, seitz@umd.edu, phone: +49-157-52114695 <tel:%2B49-157-52114695>

Nicola Seitz <seitz@umd.edu>

UMBS UMichigan funding

The University of Michigan Biological Station (UMBS) has funding opportunities for graduate students who conduct research at the Station. Our fellowships page (http://www.lsa.umich.edu/umbs/students/studentresearchopportunities/studentresearchfellowships) has all of our fellowship information, including eligibility requirements, the application process and deadline (February 13, 2015), and contact information.

Prospective applicants should browse our Research Gateway (http://umbs.lsa.umich.edu/research/) to learn about the breadth of research that takes place at the Biological Station, the variety of habitats and research sites we have access to, and our specialized facilities. The Station has over a century of data in many fields and an equally long history of supporting regionally and nationally important field work. A nice visual overview of the Station is available here.

Interested students should direct questions to UMBS Associate Director Karie Slavik, (slavik@umich.edu).

– Alicia Farmer, Communications Coordinator University of Michigan Biological Station 734-764-5212

www.lsa.umich.edu/umbs/ < https://www.facebook.com/umichBIOSTATION > < https://twitter.com/UMBS > < https://www.youtube.com/channel/UC978qYs4y5YCLSmt1QZkbig >

farmeral@umich.edu

UTexas Austin UndergradSummerReserach

Dr. Tom Juenger's research group is currently seeking undergraduates interested in conducting research in Switchgrass biology. We are seeking undergraduate applicants for the The University of Texas at Austin Switchgrass Summer Research Program. This program is an opportunity for undergraduate students to participate in mentored independent research on the biology of Switchgrass. The program is funded through the NSF Research Experience for Undergraduates (REU) program and is associated with our ongoing interdisciplinary work on the ecology, physiology, and genomic responses of switchgrass to future climate change.

Summer students will be immersed in research and learn basic and applied biology through active participation. Working as part of our research team, they will contribute to group research projects, design short research projects, and present their work in an end-of-summer student symposium.

Who Should Apply? Undergraduates in the second or third year. Each REU position is supported for ten weeks, with a stipend of $4,500. The program runs from the first week in June until the first week of August 2013. Students will be housed in a UT dormitory, and the costs of the dormitory and meal plan are included in the program. Some funds will be available to help defray the cost of traveling to Austin.

Applications The application deadline is February 15, 2015. Applicants should submit a cover letter describing experience, interests and future career plans, along with a copy of their transcripts. Applicants should also ensure that two letters of recommendation are submitted on their behalf. Only applications that are complete will be considered. If acknowledgement of receipt is required, please request this in the application. Applications and requests for further information should be directed to:

Dr. Brandon Campitelli e-mail: brandon.campitelli@utexas.edu Subject: Switchgrass REU 2015 Mail: 1 University Station CO930, Austin 78712

For current information regarding ongoing research in the Juenger lab, please visit https://w3.biosci.utexas.edu/juenger_lab/ – Brandon E Campitelli, PhD Postdoctoral Fellow, Dept. of Integrative Biology College of Natural Sciences Research Educator, Biology of Biofuels Freshmen Research Initiative University of Texas at Austin

brandon.campitelli@utexas.edu

UToledo UndergradResearch PaidInternship Summer

Join our Land-Lake Ecology Team This Summer! Paid NSF Summer Research Experience for Undergraduates at the Lake Erie Center, The University of Toledo, OH

$5000 Stipend, 9 weeks, June 1 - July 31 plus paid dorm, roundtrip transportation & research expenses

- Fun, Exciting, Meaningful Field & Lab Research - Build the skills for your dream career - Fields: Environmental Sciences, Biology, Engineering, Chemistry, Geography, GIS - Develop life-long connections with top scientists, faculty, engineers, grad students & agencies - Study and help combat environmental problems: - Harmful Algal Blooms - Water Quality - Use & Apply Top Technology: Sensor networks, water quality, environmental DNA, next-gen sequencing, Geographic

Information Systems, ROVs, drones, etc. - Field trips: canoeing, lake sampling, wetlands - Social: Cedar Point, Mudhens baseball, concerts, kayaking - Rising college Juniors & Seniors preferred (rising Sophomores ok) - Must be U.S. citizen or permanent legal resident

Apply by Friday, March 27: http://www.utoledo.edu/nsm/lec/reu.html "Klymus, Katy Elizabeth" <Katy.Klymus@UToledo.Edu>

PostDocs

AustralianNationalU SpatialPhylogeneticBiodiversity

Postdoctoral Fellow in Biodiversity (one year)

Location: Australian National University, Canberra, Australia *Classification: *Academic Level A *Salary package: *$64,386 - $81,672 *Fixed Term: *12 Months

The Research School of Biology (RSB) of the Australian National University are seeking a Postdoctoral Fellow to work on an Australian Research Council funded project combining phylogenetic and spatial biodiversity data to investigate the evolution and diversification of the plant family Proteaceae. The Postdoctoral Fellow will carry out research towards the goals of this project, based in the Macroevolution & Macroecology Group (www.macroevoeco.com). The Postdoctoral Fellow will take a lead role in species distribution modelling, spatial and phylogenetic analyses, and the design and implementation of analyses to test aspects of biogeographic, ecological and evolutionary theory. The research will be entirely computer-based.

Applicants should have a PhD in evolution, ecology, biogeography, or a related field. Applicants should have demonstrated expertise in the analysis of phylogenetic and spatial biodiversity data. Applicants should be proficient in the use of a computer platform (preferably R) to handle data and perform high-level statistical analyses. Demonstrated ability to write scientific papers is essential.

For more information about the project, please contact marcel.cardillo@anu.edu.au or lindell.bromham@anu.edu.au

To apply, and to see the Position Description and Selection Criteria, go to the ANU Jobs page (http://jobs.anu.edu.au/cw/en/job/492878/postdoctoral-fellow).

Applications close March 11, 2015

marcel.cardillo@anu.edu.au

Brest France RayPopulationGenomics

A 18 months Post-Doc is proposed within the frame of the GenoPopTaille ANR project, to perform a population genomics study of the thornback ray, Raja clavata. The GenoPopTaille consortium consists in the collaboration of the EMH, HGS and LGPMM Ifremer laboratories (Nantes, La Tremblade), the LEMAR (UMR 6439, University of Western Brittany) and the APECS (Association pour l'Etude et la Conservation des Sélaciens).

Background and scientific context: A number of ray and shark species have severely declined since the the 20th century. The biology of these species is still poorly known and traditional fisheries stock assessment methods using fisheries catches and scientific survey data are often expensive and inapplicable for estimating their abundance due to the small numbers of observed individuals. Recently, a new method based on the genetic identification of parent-offspring pairs has been developed to estimate the absolute size of small populations. This method relies on the principle of capture-mark-recapture using genetic marking of parents and recapture via their offspring. The rapid progress of genomic methods during the last decade now allows for high-throughput sequencing and genotyping of large samples for several hundreds or thousands of genetic tags. The GenoPopTaille project will first use the RAD sequencing approach to evaluate the genetic structure and gene flow in thornback ray populations from the northeast Atlantic based upon several thousand of SNP (Single Nucleotide Polymorphism) tags. The most informative SNPs for the Bay of Biscay population will then be chosen to be genotyped for a large sample (~7000) of adults and juveniles for a large number (~200) of SNPs. These genetic data will be used to identify parent-offspring pairs. The number of parent-offspring pairs will be used in a population dynamics model for estimating the abundance of spawners in the Bay of Biscay.

Detailed Post-Doc project: The Post-Doc will be in charge of the RAD sequencing task. About 500 individuals, stemming from two-three sampling sites in the

Bay of Biscay and from 10-11 regions covering the entire geographic distribution range of the thornback ray, will be sequenced on thousands of SNPs. This genomic study will aim at addressing two issues: 1. Firstly, the population genetic structure of thornback ray will be investigaed over the whole distribution range of the species, from Iceland to the Mediterranean Sea. The goal of this first task will be to assess the level of genetic divergence and connectivity among the R. clavata populations. 2. Secondly, the most informative SNPs will be selected for conducting parentage analysis in the Bay of Biscay population. The best suited set of 192 SNPs will be defined, consisting in the loci with the highest statistical power to accurately identify the parent-offspring pairs. RAD libraries and sequencing will be performed at LGPMM (Ifremer La Tremblade), and bioinformatics will be conducted at LEMAR.

Profile of the candidate: The candidate must have a strong background in RAD sequencing and bioinformatics.

Expected starting date: as early as possible during the Spring 2015

Contacts: Sylvie Lapègue (sylvie.lapegue@ifremer.fr; LGPMM, Ifremer La Tremblade), Grégory Charrier (gregory.charrier@univ-brest.fr; LEMAR, University of Western Brittany, Brest)

gregory.charrier@univ-brest.fr

BrownU EvolutionaryMorphology

POSTDOCTORAL RESEARCH AND TEACHING ASSOCIATE IN VERTEBRATE MORPHOLOGY

The Department of Ecology and Evolutionary Biology at Brown University is seeking a Postdoctoral Associate to join the teaching staff of a highly collaborative, team-taught medical school human anatomy course, and to conduct research in vertebrate morphology. The primary teaching responsibility is in the Human Anatomy course for first-year medical students, with additional duties teaching advanced medical students and preparing anatomical teaching materials. Brown offers many opportunities for research collaborations with faculty in evolutionary morphology and excellent facilities for research. Applicants should contact a morphology faculty member to discuss potential research collaborations (Professors Elizabeth Brainerd, Stephen Gatesy, Thomas Roberts, and Sharon Swartz).

This position is available for the 2015-2016 academic year (anticipated start date is July 1, 2015) with a possibility for annual renewal for a maximum of three years total. Applicants must have potential for excellence in teaching and research, and all requirements for a doctoral degree completed before start of the position. Prior experience in a cadaver-based gross anatomy course preferred, but not required. Salary is NIH scale.

Applicants should submit a CV, statements of teaching philosophy and research interests, up to three representative publications, and names of three references. Application materials should be sent by e-mail to Ms. Kimberly Abbott (Kimberly_Abbott@Brown.edu). General questions about the position may be addressed to the course director, Dr. Dale Ritter (Dale_Ritter@Brown.edu). Application review will begin March 16, 2015.

Brown University is an Equal Opportunity Employer

Elizabeth Brainerd Professor, Department of Ecology & Evolutionary Biology Brown University, Box G-B210 Providence RI 02912 o: 401-863-9261

Beth Brainerd <elizabeth_brainerd@brown.edu>

CambridgeU EvolutionaryEcology

POST-DOCTORAL RESEARCH ASSOCIATE IN EVOLUTIONARY ECOLOGY

A post-doctoral research associate position, funded by the ERC, is available to work with Prof Rebecca Kilner in the Department of Zoology at the University of Cambridge, UK.

The post-doc will work on a project investigating whether parental care can drive evolutionary change, using burying beetles Nicrophorus spp as our model experimental organisms.

For further information about our research visit our website at nicrophorus.zoo.cam.ac.uk.

Duties will include:

Running a large-scale selection experiment; running or supervising complementary experiments in the lab or field; assisting in monitoring of beetle numbers at local field sites; collection and analysis of microsatellite data (or similar); data collection, analysis and interpretation; preparation of manuscripts for publication.

Essential knowledge, skills and experience for the role:

A PhD in evolutionary ecology or behavioral ecology or closely related subjects;

Ability to organise time, plan ahead and to work effectively independently;

Excellent data handling and data analysis skills;

Excellent communications skills (written and oral);

Ability to work in a team and strong interpersonal skills.

Desirable knowledge, skills and experience for the role:

Some post-doctoral experience;

Any relevant laboratory experience, particularly in carrying out selection experiments or experimental evolution;

Experience in collecting and analysing microsatellite data;

Experience of fieldwork with insects;

Background knowledge (e.g. from your undergraduate training) in entomology and microbiology;

Interest in natural history;

Some experience of managing others.

The post is available for up to 28 months, with a start date of 1 July 2015. The starting salary is £28,695 - £37,394 per annum.

Further information about the position, along with details about how to apply can be found here:

http://www.jobs.cam.ac.uk/job/6065/ The deadline for applications is 5pm GMT Thursday 5 March 2015. Interviews will be held during week beginning 23 March 2015.

Informal enquiries are welcomed and should be sent to Rebecca Kilner at

rmk1002@cam.ac.uk

Rebecca Kilner <rmk1002@cam.ac.uk>

DFO Halifax 2 SalmonPopulationGenomics

Population genomics of Atlantic salmon and the impact of escape of farmed salmon

We are currently recruiting two postdoctoral fellows to start early spring or fall 2015 working on population genomics of Atlantic salmon in eastern Canada. The positions will be associated with Dr. Ian Bradbury, Department of Fisheries and Oceans Canada and based out of Halifax, NS.

PDF #1. Escapes of farm salmon are both an economic loss and an environmental concern. Their effects on wild salmon populations will be a function of: (1) the presence of escapes and subsequent interbreeding (frequency and magnitude); (2) differences in traits that affect survival, competition and reproduction; (3) ability of natural systems to buffer against escapes through natural selection; and (4) our ability to mitigate impacts. The PDF will work collaboratively with other researchers (e.g., Dr. Ian Fleming, MUN) and students using population genomics, experimental crosses, and transplants to quantify the ecological and evolutionary impacts of escaped salmon and design mitigation measures.

PDF #2. SNP based identification of Atlantic salmon in North America. Atlantic salmon migrate from local rivers to northern feeding areas off West Greenland or the Labrador Sea. Genetic assignment of salmon caught at sea using the current microsatellite baseline allows only regional assignment and is insufficient for many management and conservation questions. This PDF will work collaboratively other researchers (e.g., MUN, Laval University) and use genome scans based on large SNP arrays and RAD sequencing to explore the genomic basis of fine scale adaptive variation and quantify homing / straying rates in this species. This information will ultimately be used to build a SNP panel for fine scale North American assignment and fisheries management.

There is flexibility and scope within both projects for the successful candidates to develop and address additional questions. PDFs should be prepared to share their enthusiasm for research and associated skills openly within and among the research groups, and by doing so, contribute to a dynamic research environment. While they will be based at DFO Halifax, candidates should be prepared to travel temporarily to Newfoundland for research.The ideal start date would be either May or August 2015.

Qualifications: The ideal candidates will possess a PhD; have research interests and training in the areas of population genomics, fish ecology and behaviour, and fish rearing; be capable of designing and undertaking both field and laboratory research; and have reasonable facility with the analysis of large data sets. Prospective candidates should email a cover letter, and CV to ian.bradbury@dfo-mpo.gc.ca. Review of applicants will begin March 1 2015 and continue until the positions are filled.

Ian Bradbury <ibradbur@me.com>

EBD Sevilla 5 EvolutionaryBiology

POLL FOR POSTDOCTORAL POSITIONS AT DOÑANA BIOLOGICAL STATION (EBD-CSIC), SPAIN Funded by the “Severo Ochoa” Excellence Program awarded by the Spanish Ministry of Economy and Competitiveness

The Doñana Biological Station (< http://www.ebd.csic.es/ >) seeks 5 Postdoctoral fellows for a one year contract with possibilities to be extended to the end of the project (June 30th, 2017) with the aim to conduct research in one of the following research lines:

Conservation biology Biological invasions Ecological synthesis Molecular ecology Evolutionary ecology Plant-animal interactions Wetland ecology

Applicants should have a Ph.D., a high publication record, and excellent writing and oral communication skills. Starting date: Summer 2015 Salary: 39,000 EUR approx. per yr. before taxes

Interested candidates should send the following documents: 1) Curriculum vitae, 2) cover letter with a description of research accomplishments and statement of overall scientific goals and interests (approximately 1000 words), 3) indication of the researchers at EBD with whom you have professional affinities, and 4) contact information for three references. All documentation in one pdf should be sent to rosa@ebd.csic.es or Fax: 34 954621125

The specific job positions will be announced in due course at http://www.ebd.csic.es Deadline for interested applicants: March 6th, 2015

If interested in Plant-Animal Interactions with an epigenetic component please contact Conchita Alonso <conalo@ebd.csic.es>

Dr. Conchita Alonso Phone: +34 954466700 Estación Biológica de Doñana, CSIC Fax: +34 954621125 Avda Américo Vespucio s/n e-mail: conalo@ebd.csic.es E-41092 Sevilla http://www.plant-animal.es SPAIN

Conchita Alonso <conalo@ebd.csic.es>

ECWP Morocco PostCopulatorySexualSelection

Postdoctoral Position: post-copulatory sexual selection

04/02/2015

We are seeking applicants for a two-year postdoctoral position to work on a project dealing with post-copulatory sexual selection in the houbara bustard. The houbara bustard is an endangered bird species living in semi-desert areas in North Africa and central Asia. The Emirates Center for Wildlife Propagation (ECWP) has promoted a captive breeding program in Morocco aiming at producing houbara bustards to reinforce natural populations in North Africa. The captive breeding involves a large number of adult birds of known age and pedigree. Reproduction is based on the collection of sperm and the artificial insemination of females. This offers a unique opportunity to address experimentally a number of issues related to post-copulatory sexual selection (sperm competition and cryptic female choice) in a non-domesticated species. The houbara bustard is an excellent model species to study sexual selection for several reasons. The houbara bustard has a lek-based mating system and females have been shown to copulate with different males in nature as witnessed by the high frequency of multiple paternity. Males have elaborate secondary sexual traits that are supposed to be used by females during mate choice. Traits describing sperm quality (number of sperm per ejaculate) have been shown to be heritable and can therefore respond to selection. Finally, sperm traits (but to a lesser extent secondary sexual traits) decline with male age.

The postdoc will run and supervise experiments aiming at testing the potential effect of sperm competition and cryptic female choice when females mate promiscuously with mates that vary in their levels of relatedness and in their age. In addition to the fundamental interest of investigating post-copulatory sexual selection in relation to kinship and aging, the results gathered will prove beneficial to optimize the management of the large number of birds involved in the captive breeding.

All the experiments are run at the ECWP in Missour (Morocco) where the post-doc will be based most of the time (the breeding season lasts from February to June). To ensure the necessary communication with the local staff in Morocco, the applicant must be able to communicate in French. Regular meetings will be organized with the project supervisors in Abu Dhabi, U.A.E (Yves Hingrat and Loïc Lesobre) and France (Michel Saint Jalme and Gabriele Sorci).

Applicants should have a PhD in evolutionary biology and a strong background in sexual selection. Applicants who are already familiar with the techniques of quantification of sperm quality will be given the priority.

The position will start in March 2015. Applicants are requested to send as soon as they wish a CV (with list of publications) and an application letter including the name of three referees to Yves Hingrat (yhingrat@reneco-hq.org) and Gabriele Sorci (Gabriele.sorci@u-bourgogne.fr). Review of applications will be conducted as soon as we receive them and will stop when we find a suitable candidate. The postdoc will be based in Morocco, at ECWP (at least during the breeding season and experiments). The breeding season of Houbara in the captive breeding in Morocco extends from January to June. During the first year (2015) the successful applicant will mainly learn ECWP breeding management and analyze the existing database which will allow her/him to design proper experiments for the 2016 season. The two year period is extendable with regards to preliminary results and the need for complementary experiments.

The successful applicant will be under contract with Reneco Wildlife Preservation (PoBox 61741, Abu Dhabi, UAE), the consulting company managing ECWP. Food and accommodation are provided when on the project ECWP. Salary: commensurate with experience and qualifications.

Some recent literature that has been produced on this system

Preston, B.T., Saint Jalme, M., Hingrat, Y., Lacroix, F., Sorci, G. 2015. The sperm of aging male bustards retards their offspring's development. Nature Communications 6: 6146.

Chargé, R., Sorci, G., Saint Jalme, M., Lesobre, L., Hingrat, Y., Lacroix, F., Teplitsky, C. 2014. Does recognized genetic management in supportive breeding prevent genetic changes in life-history traits? Evolutionary Applications 7: 521-532.

Chargé, R., Teplitsky, C., Hingrat, Y., Saint Jalme, M., Lacroix, F., Sorci, G. 2013. Quantitative genetics of sexual display, ejaculate quality and size in a lekking species. Journal of Animal Ecology 82: 399-407.

Chargé, R., Sorci, G., Hingrat, Y., Lacroix, F., Saint Jalme, M. 2011. Immune-mediated change in the expression of a sexual trait predicts offspring survival in the wild. PLoS ONE 6: e25305.

Preston, B., Saint Jalme, M., Hingrat, Y., Lacroix, F., Sorci G. 2011. Sexually extravagant males age more rapidly. Ecology Letters 14: 1017-1024.

Chargé, R., Saint Jalme, M., Lacroix, F., Cadet, A., Sorci, G. 2010. Male

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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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EMBL Barcelona ComputationalBiol

Postdoctoral Position for a Computational Biologist at the EMBL/CRG Systems Biology Unit

Our laboratory, at the EMBL/CRG Systems Biology Unit in Barcelona, is looking for an excellent and highly motivated computational postdoc to investigate the functional and evolutionary impact of transcriptomic diversification in vertebrates. The major goal of the project - funded by the European Research Council (ERC) - is to identify and characterize the transcriptomic novelties associated with the origin and evolution of the vertebrate brain.

The research will involve comparative genomic and transcriptomic analysis of the different processes involved in transcriptomic diversification (alternative splicing, alternative polyadenylation, alternative promoters and RNA editing), using RNA-seq from multiple vertebrate and invertebrate species. The study of neuronal-specific microexons (see Cell 2014, 159:1511-23 for details), expected to be crucial for terminal neurogenesis and synaptic function, will be particularly relevant. In addition to these questions, the candidate will be encouraged to develop his/her own scientific ideas and participate in multiple intra- and inter-group collaborations.

The applicant is expected to be passionate about evolution and transcriptomics. Extensive experience in RNA-seq analyses and good programming skills (preferably in perl or python, and R) are required. Previous experience in alternative splicing analysis and a strong background in statistics would be an advantage. The applicant should be able to work rigorously, independently and flexibly. The candidate will be responsible for his/her own project within the research group, including carrying out experiments, data analysis and interpretation. Fluency in English (spoken and written) is expected. The position has a fully covered, competitive salary for up to five years, but the applicant will also be encouraged to apply for independent funding.

The Institute The Centre for Genomic Regulation (CRG) is an international biomedical research institute of excellence, based in Barcelona, Spain, whose mission is to discover and advance knowledge for the benefit of society, public health and economic prosperity.

The breadth of topics, approaches and technologies at the CRG permits a broad range of fundamental issues in life sciences and biomedicine to be addressed. Research at the CRG falls into four main areas: gene regulation, stem cells and cancer; cell and developmental biology; bioinformatics and genomics; and systems biology.

With more than 350 scientists from 41 countries, the CRG's excellence is based on an interdisciplinary, motivated and creative scientific team that is supported by high-end and innovative technologies.

The centre's other main strategic goals are: to translate basic scientific findings into benefits for health and economic value for society; to provide advanced and high quality training to our scientists; and to communicate and establish a bilateral dialogue with society.

For further information: www.crg.eu *Requirements*

Studies:

- PhD in Biology-related areas

Technical skills required:

- Experience in RNA-seq analyses. - Programming proficiency (ideally in perl or python, and R).

Additional beneficial skills:

- Good background in statistical analyses. - Experience in research on alternative splicing.

Languages:

- Fluent level of English

Soft skills:

- Passion for evolutionary molecular biology. - A highly motivated and organized candidate, capable of dealing with multiple ongoing projects. - Capable of working in a group, and with a high degree of work autonomy.

The Offer

- Duration: 1 year renewable contract up to 5 years. - Estimated annual gross salary: A competitive salary will be provided, which will be well matched relative to the cost of living in Barcelona, and adjusted according to experience. - Starting date: as soon as possible from April 2015.

We offer work in a highly stimulating environment with state-of-the-art infrastructure, providing the successful applicant with unique opportunities to develop a strong technical portfolio.

Application Procedure All applications must include:

1. A cover letter.
2. A full CV including contact details.
3. Two contacts for further references.

All applications must be addressed to Dr. Irimia and be submitted to the following email address: mirimia@gmail.com. Please include as email subject the reference "Postdoc-Bioinfo1".

Deadline: Please submit your application by *28th February 2015*

Centre de Regulació GenÃ²mica (CRG) Doctor Aiguader 88, 08003 Barcelona (Spain)

Manuel Irimia <mirimia@gmail.com>

GoetheU Frankfurt FungalEvolutionaryGenomics

Postdoc Fungal Evolutionary Genomics

A postdoctoral research position in fungal evolutionary genomics is available in the lab of Prof. Imke Schmitt at the Senckenberg Biodiversity and Climate Research Centre and Goethe University Frankfurt. The successful candidate will investigate genomic evolutionary processes in fungal communities, species or populations as a response to environmental factors. He or she will be involved in projects related to the study of environmental adaptation in fungal communities and/or lichen-symbiotic fungi.

The applicant should hold a Ph.D. in evolutionary or computational biology, genetics, mycology, ecology or a related field. The ideal candidate has a biological training, background in bioinformatics with skills in programming (scripts and analysis pipelines), next generation sequence analysis, genome assembly and annotation. Competitive candidates will have a strong record of prior publication, preferably in genome scale data analysis (including comparative genomics, population genomics, metagenomics/metabarcoding or molecular evolution), and speak fluent English.

My lab and the entire institute provide a very supportive atmosphere. The broader research environment at Senckenberg and Goethe University offers postdoctoral fellows chances for collaboration with experts in fields ranging from molecular ecology and evolution, phylogenetics, to macroecology and climate change biology (modeling and statistics). Attractive computing infrastructure is available (high-RAM computers, clouds, and clusters). Frankfurt, a vibrant city in the center of Germany, provides ample cultural and recreational opportunities and excellent infrastructure for travel. We offer a competitive salary (TV-H E 13 according to the German public service pay scale), full benefits, and training opportunities. The position is available for three years starting May 1^st 2015.

Please send your application before March, 15th 2015 preferably by e-mail (attachment in a single pdf document), mentioning the reference of this position (Ref. #8.3) and including a cover letter detailing research interests and experience, a C.V., a copy of your PhD certificate, and a list of three professional references. Please be sure to highlight skills and experience related to genome assembly, statistics, bioinformatics, or programming and send your application to the address below

Prof. Dr. Katrin Böhning-Gaese

c/o Senckenberg Gesellschaft für Naturforschung

Senckenberganlage 25

60325 Frankfurt

E-Mail:recruiting@senckenberg.de

Informal enquiries to Imke Schmitt (imke.schmitt@senckenberg.de) before the application are welcome.

Prof. Dr. Imke Schmitt Goethe Universität Frankfurt and Senckenberg Gesellschaft für Naturforschung Biodiversity and Climate Research Centre Senckenberganlage 25 60325 Frankfurt Germany

Tel. 0049 (0)6975421855 email: imke.schmitt@senckenberg.de website: http://www.bik-f.de/root/index.php?page_id=434 Imke Schmitt <imke.schmitt@senckenberg.de>

HarvardU BacterialVariation

POSTDOCTORAL RESEARCH FELLOW

STREPTOCOCCUS PNEUMONIAE ANTIGENIC VARIATION

LIPSITCH LABORATORY

DEPARTMENTS OF EPIDEMIOLOGY AND IMMUNOLOGY & INFECTIOUS DISEASES

HARVARD T.H. CHAN SCHOOL OF PUBLIC HEALTH

POSTED 22 FEBRUARY 2015

A postdoctoral research fellowship is available for work in the Lipsitch Laboratory at Harvard T.H. Chan School of Public Health to study phenotypic and antigenic effects of sequence variation in surface proteins of Streptococcus pneumoniae.

Genomic analysis has indicated extensive sequence variation and hotspots of recombination in surface proteins of S. pneumoniae (1, 2). Two lines of evidence suggest that these phenomena result from selection for escape from host immune responses: concentration of nonsynonymous changes within identified antibody targets and, among these, within epitope regions (3); age-specific variation in gene content, such that nonessential surface proteins (or common alleles of conserved surface proteins) are more common among isolages from younger (presumably immunologically naïve) carriers of S. pneumoniae (2, 4). Such results would be expected if these genes or their common alleles are net-beneficial in younger/more naïve hosts but are subject to immune responses that select against their presence in more immunologically experienced persons. However, there is little direct, mechanistic evidence for hypothesis that losing or diversifying these antigens produces an immune escape benefit for the bacteria.

As part of an interdisciplinary R01-funded project involving (a) mathematical transmission modeling, (b) population genomics, (c) analysis of human sera from a pneumococcal carriage study for comparison with the sequences of subsequently carried pneumococci, and (d) mechanistic studies in the laboratory of the specificity of anti-protein immunity in pneumococci, we are seeking a postdoctoral fellow to design and carry out assays to measure the impact of allele-specific immunity against particular surface proteins on bacterial fitness, as well as assays of allele-specific variation in the function of these proteins. The aim is to test the hypothesis that varying or losing these proteins is beneficial in the presence of specific antibodies. Studies will include characterization of allele-specific antibody binding specificity and function (eg opsonization, adhesion-blocking). They will also include functional assays of the allelic variants of the surface proteins in the presence and absence of antibody.

The postdoctoral fellow will be part of a larger multidisciplinary research team within the Center for Communicable Disease Dynamics (which Dr. Lipsitch directs), including researchers in population genomics and transmission dynamics of multiple infectious diseases. For more information about the group see http://www.hsph.harvard.edu/marc-lipsitch/ . Opportunities for projects in some of these areas may be available depending on interests.

Applicants should have a doctorate and publication record in experimental microbiology, immunology, molecular biology and/or biochemistry and an interest in evolutionary problems. Interested candidates should send a letter of inquiry and CV with 2+ references to Marc Lipsitch, mlipsitc@hsph.harvard.edu.

REFERENCES

1. Croucher NJ, Harris SR, Fraser C, Quail MA, Burton J, van der Linden M, McGee L, von Gottberg A, Song JH, Ko KS, Pichon B, Baker S, Parry CM, Lambertsen LM, Shahinas D, Pillai DR, Mitchell TJ, Dougan G, Tomasz A, Klugman KP, Parkhill J, Hanage WP, Bentley SD. 2011. Rapid pneumococcal evolution in response to clinical interventions. Science 331:430-434. http://www.ncbi.nlm.nih.gov/pmc/articles/PMC3648787/ 2. Croucher NJ, Finkelstein JA, Pelton SI, Mitchell PK, Lee GM, Parkhill J, Bentley SD, Hanage WP, Lipsitch M. 2013. Population genomics of post-vaccine changes in pneumococcal epidemiology. Nat Genet 45:656-663. http://www.ncbi.nlm.nih.gov/pmc/articles/PMC3725542/ 3. Li Y, Gierahn T, Thompson CM, Trzcinski K, Ford CB, Croucher N, Gouveia P, Flechtner JB, Malley R, Lipsitch M. 2012. Distinct effects on diversifying selection by two mechanisms of immunity against Streptococcus pneumoniae. PLoS Pathog 8:e1002989. http://journals.plos.org/plospathogens/article?id=10.1371/journal.ppat.1002989 4. Regev-Yochay G, Hanage WP, Trzcinski K, Rifas-Shiman SL, Lee G, Bessolo A, Huang SS, Pelton SI, McAdam AJ, Finkelstein JA, Lipsitch M, Malley R. 2010. Reemergence of the type 1 pilus among Streptococcus pneumoniae isolates in Massachusetts, USA. Vaccine 28:4842-4846.

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ImperialCollege London 2 SpeciationGenomics

2 postdocs in Speciation Genomics on Lord Howe Island's Palms in Savolainen Lab, Imperial College London

http://www.imperial.ac.uk/people/v.savolainen The main research objective is to analyse genetic data and infer:

postdoc 1:

To identify candidate loci for speciation

To validating candidate loci from above by rescuing wild-type phenotypes in Arabidopsis mutants by introducing orthologous palm genes

To evaluate the strength of post-zygotic isolation

postdoc 2:

To disentangle the underlying genetics controlling the mutant red- stemmed phenotype

FOR MORE DETAILS AND TO APPLY, FOLLOW THESE LINKS:

https://www4.ad.ic.ac.uk/OA_HTML/OA.jsp?page=/oracle/apps/irc/candidateSelfService/webui/VisVacDispPG&OAHP=IRC_EXT_SITE_VISITOR_APPL&OASF=IRC_VIS_VAC_DISPLAY&akRegionApplicationId=821&transactionid=1856497030&retainAM=Y&addBreadCrumb=RP&p_svid=45647&p_spid=1713236&oapc=15&oas=9Er_CvHXgG4kBYRochRxnQ. . https://www4.ad.ic.ac.uk/OA_HTML/OA.jsp?page=/oracle/apps/irc/candidateSelfService/webui/VisVacDispPG&akRegionApplicationId=821&transactionid=1957440653&retainAM=Y&addBreadCrumb=S&p_svid=45668&p_spid=1714184&oapc=7&oas=4LVYRH-iBmziPuWw7ZHQBg. . Prof. Vincent Savolainen Deputy Head, Department of Life Sciences Imperial College London, Silwood Park Campus Buckhurst Road, SL5 7PY Ascot, Berks, UK Tel: +44 (0)20 7594 2374 Fax: +44 (0)20 7594 2339 v.savolainen@imperial.ac.uk skype vincent.savolainen1 www3.imperial.ac.uk/people/v.savolainen

"Savolainen, Vincent" <v.savolainen@imperial.ac.uk>

KielU EvolutionaryEcol

Although it is mainly a Postdoc position in Ecology, applicants with an evolutionary background are particularly welcome!

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Postdoc in Vegetation Ecology

The Institute for Ecosystem Research of Kiel University, Germany, announces a vacancy for a Postdoc position in the field of vegetation ecology starting on April 1st. The position will run for 3 years with the possibility of prolongation for another 3 years (TVL E 14, 100%)

We are looking for a highly qualified and motivated postdoctoral fellow with a keen interest in research in vegetation ecology and with ambition to stay in academia. The ideal candidates profile should imply a focus on community ecology or evolutionary ecology that fits into the scope of the newly established Geobotany group (including research in biodiversity ecosystem function, global environmental change and plant invasion ecology). Eligible candidates must hold an outstanding university degree (MSc) and PhD in ecology/botany, environmental sciences or related disciplines. Previous postdoctoral research would be advantageous.

We expect knowledge in ecological statistics with strong analytical and data handling skills and profound experience in the R environment. Knowledge of Central European vegetation and flora and previous experience of field or experimental work is advantageous. Excellent writing skills in English, good work ethic, and creative thinking are desired.

Candidates are supposed to teach in German in courses on plant identification, excursions and lab courses in vegetation ecology in the programs of BSc and MSc of Biology (4 contact hours). The successful candidate is encouraged to initiate new research projects and to supervise bachelor, master and doctoral students. This position permits and supports the development of independent research ideas and further qualifications (habilitation). We offer a stimulating working environment at the interface between Biology and Geography with plenty of possibilities for collaborations within Kiel University. The group is involved in the international research platform BEF-China (DFG Research Unit 891) and has established active international collaborations that can be integrated into new research.

Kiel University is an equal opportunity employer and aims to increase the number of women in research and teaching. Applications by females are most welcome. Kiel University has been certified by the Hertie Foundation as a family-friendly institution and is committed to further the compatibility of work and family life. The university supports the employment of disabled persons. Persons with disabilities will, with appropriate qualifications and aptitudes, be employed preferentially. Applications by people with a migration background are particularly welcome.

Applications in English should include a letter of interest with a description of relevant experience, CV, a list of publications, a short description of the proposed research (max. 2 pages), authenticated documents and the names and email addresses of two references. Applications should be sent as one pdf file to aerfmeier@ecology.uni-kiel.de by February 28, 2015. The selection of the postdoctoral candidate will be based on his or her academic record and proposed research project.

For more information please contact Prof. Dr. Alexandra Erfmeier, Institute for Ecosystem Research, Geobotany, Kiel University, Olshausenstr. 75, 24118 Kiel, Germany, Tel +49-431-880-1010; aerfmeier@ecology.uni-kiel.de, http://www.ecosystems.uni-kiel.de . Alexandra Erfmeier <aerfmeier@ecology.uni-kiel.de>

LouisianaStateU 2 Phylogenetics

Two postdoctoral researcher positions are available in the computational evolutionary biology lab of Jeremy M. Brown at Louisiana State University. Research in the Brown lab is broadly centered on the use of phylogenetic approaches to understand organismal history and molecular evolution.

Position 1 is part of a project funded by the National Science Foundation to develop and apply a suite of related statistical approaches for assessing the fit of stochastic models to sequence and trait data. The Brown lab is collaborating extensively on this project with the lab of Bob Thomson at the University of Hawaii V Manoa, as well as the developers of RevBayes and the authors of various R packages.

Position 2 is not tied to a specific project, but research connected to other areas of active inquiry in the Brown lab will be strongly preferred. These areas include the development of new techniques for extracting information from large collections of phylogenetic trees, the exploration of new models and priors for Bayesian phylogenetics, and the investigation of genome-wide phylogenetic and evolutionary patterns.

Review of applications for both positions will begin on Feb. 16th. Applicants are asked to submit a cover letter describing their research interests and background, a CV, and the names of three references.

Informal inquiries are strongly encouraged and can be directed to jembrown@lsu.edu. More information on the Brown lab is available at http://www.phyleauxgenetics.org/ . LSUs Dept. of Biological Sciences has a particular strength in computational evolutionary genetics. LSU continues to invest heavily in the computational sciences, with a recent focus on computational biology. Outstanding resources are available through the Center for Computation and Technology (http://www.cct.lsu.edu/home) and the Louisiana Optical Network Initiative (http://www.loni.org/).

Baton Rouge is located in South Louisiana, one of the most culturally unique locations in the United States (http://louisianatravel.com/). The surrounding area has excellent food, music, festivals, and outdoor recreation. LSUs campus is just over an hours drive from New Orleans and allows easy access to much of the Gulf Coast.

Details for Position 1:

Responsibilities: Work with a computational biologists to write software, in collaboration with developers of RevBayes and various R comparative methods packages. Also responsible for testing new methods by analyzing exemplar data sets. Required Qualifications: Ph.D. or equivalent degree in Evolutionary Biology, Computer Science, Statistics, Applied Mathematics or a related discipline; A.B.D. candidates will be considered, but must have Ph.D. by May 31, 2015; previous experience with programming and phylogenetic analyses. Additional Qualifications: Previous software development experience as part of a team; programming experience using C++ and R; previous experience writing and publishing scientific manuscripts in peer reviewed journals. An offer of employment is contingent on a satisfactory pre-employment background check. Application deadline is February 16, 2015, or until a candidate is selected. Apply online and view a more detailed ad at: https://lsusystemcareers.lsu.edu Position #032424 Quicklink: https://lsusystemcareers.lsu.edu/applicants/Central?quickFind=58866 Details for Position 2:

Responsibilities: Conduct novel, cutting-edge research in phylogenetics and/or molecular evolution. Required Qualifications: Ph.D. or equivalent degree in Evolutionary Biology, Computer Science, Statistics, Applied Mathematics or a related discipline; A.B.D. candidates will be considered, but must have Ph.D. by May 31, 2015; previous experience with programming and phylogenetic analyses. Additional Qualifications: Previous software development experience; programming experience using C++, Java, Python, and/or R; previous experience mentoring younger researchers; previous experience writing and publishing scientific manuscripts in peer reviewed journals. An offer of employment is contingent on a satisfactory pre-employment background check. Application deadline is February 16, 2015, or until a candidate is selected. Apply online and view a more detailed ad at: https://lsusystemcareers.lsu.edu Position #032333 Quicklink: https://lsusystemcareers.lsu.edu/applicants/Central?quickFind=58879 Jeremy M. Brown Assistant Professor Louisiana State University Dept. of Biological Sciences 202 Life Sciences Building Baton Rouge, LA 70803

(225) 578-1745

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LSUMuseum CollectionsVertEvolBiol

Postdoctoral Position in Collections-based Vertebrate Evolutionary Biology

The Museum of Natural Science at Louisiana State University is seeking an enthusiastic and highly motivated Postdoctoral Researcher/Lab Manager to join our multidisciplinary research team working on various aspects of collections-based vertebrate systematics, phylogeography, and population genetics using massively parallel sequencing.

Candidate will conduct collections-based research in coordination with one or more of the Curators. The candidate will also be responsible for managing the Museum's shared molecular genetics laboratory and helping with the laboratory supervision of graduate, undergraduate, and high school research assistants. Ongoing projects in the lab include systematics, phylogeography, and population genetics studies of birds, fish, mammals, reptiles and amphibians. The person in this position will be part of the Museum's vibrant academic community, attending seminars, participating in journal clubs, etc.

More information about the position and instructions for applying can be found at this web site: https://lsusystemcareers.lsu.edu/applicants/-Central?quickFind=58972 Required qualifications: Ph.D. in Biology or related discipline; A.B.D. candidates will be considered as long as the degree is conferred by the effective date of the appointment; experience in molecular methods, evolutionary biology, GIS, and computational biology; strong publication record; strong interpersonal skills; ability to manage an active laboratory.

Review of applications will begin 3 March 2015. LSU is an Equal Opportunity-Affirmative Action employer.

Questions about the position can be emailed to Robb Brumfield (robb at lsu.edu)

Robb Brumfield <robb@lsu.edu>

McMasterU IntegratingGenomicsCognition

We are looking for a prospective postdoc who is interested in applying genetic and genomic approaches for research on the evolution of animal cognition and behaviour.

We are part of a large and highly interactive group working at the interface of genetic, genomics, cognition and behaviour. We consist of about a dozen faculty, several postdocs and three dozen graduate students.

Prospective candidates are invited to read relevant material on our web sites (https://www.msu.edu/~idworkin/ and http://psych.mcmaster.ca/dukas/) and then contact either of us via email (dworkin@mcmaster.ca or dukas@mcmaster.ca) by February 15, 2015. Please include a CV and eprints in pdf format.

The position is open to Canadian citizens and permanent residents within five years of completing their PhD who have a strong publication record.

McMaster University is located in Hamilton, Ontario, a culturally diverse city of 500,000 people, located less than an hour from Toronto. Hamilton offers a great quality of life and is experiencing a post-industrial revival. Resources include easy access to natural wonders such as Niagara Falls and the Niagara Escarpment, an expanding network of bike paths, seasonal climate, and a burgeoning food and nightlife scene.

Ian Dworkin Department of Biology McMaster University dworkin@mcmaster.ca

Ian Dworkin <dworkin@mcmaster.ca>

Milan Bioinformatics

Post V Doctoral Position in Bioinformatics (Centro Mafalda Luce V Milan V Italy)

Description A post-doctoral position for a biologist with a strong background in bioinformatics is available in the Laboratory of Molecular Psychiatry and Neurogenetics at the Mafalda Luce Center for Pervasive Developmental Disorders (Milan). In tight conjunction with its homologous laboratory at University Campus Bio-Medico in Rome, this team investigates the genomic, transcriptomic and functional bases of autistic disorder and of other neuropsychiatric disorders of childhood. Biomaterials are obtained primarily from patients diagnosed, clinically characterized and treated at the same Center or at the Child and Adolescent Neuropsychiatry Unit at University Campus Bio-Medico, which encompasses both laboratories. In reference to clinical neurogenetic testing, after a training period the Candidate will be responsible for the bioinformatic analysis of clinical array-CGH data performed using the Agilent platform (180K) and genome-wide transcriptomics, while second generation sequencing and RNA-seq will also soon be implemented.

Qualifications Candidates must possess a PhD in biology with a strong background in bioinformatics applied to molecular biology and to large microarray-based data sets (mandatory: array-CGH and genome-wide transcriptomics; very useful: second generation sequencing and RNA-seq). Some seniority and a demonstrated capacity to work independently are a clear advantage. Fluency in spoken and written English is mandatory. Salary will be based on age and prior experience.

Estimated starting date: May 1, 2015

Location: Milan (Italy)

Address inquiries with a complete CV by email to Prof. Antonio Persico at a.persico@unicampus.it:

Antonio M. Persico, M.D. Assoc. Prof. in Child & Adolescent NeuroPsychiatry Lab. of Molecular Psychiatry & Neurogenetics Univ. Campus Bio-Medico Via Alvaro del Portillo 21 I-00128 Rome Italy

Ignazio Stefano Piras <I.Piras@unicampus.it>

MNHN Paris EcolFuncMorphPaleobiology

Postdoctoral researcher in functional morphology and paleobiology

Project title: Morphological convergence and functional inferences: an integrative study of the masticatory apparatus in rodents and extinct notoungulates.

Supervisors: Guillaume Billet (UMR7207; billet@mnhn.fr), Anthony Herrel (UMR7179; anthony.herrel@mnhn.fr) and Raphäel Cornette (UMR7205; cornette@mnhn.fr).

Location: Muséum National d'Histoire Naturelle, Paris, France

Salary: 2500Euro/month (± 2000 Euro net) depending on experience.

We are looking for a postdoctoral researcher in functional morphology and paleontology to work on a project investigating a typical case-study of repeated morphological convergence in the masticatory apparatus of mammals. The project focuses on the rich mosaic of resemblances found in several groups of extant rodents and extinct notoungulates. The postdoctoral researcher will quantify the shape of the masticatory apparatus and identify areas of mechanical constraints based on 3D models and using geometric morphometric and finite element approaches. Moreover, the postdoctoral researcher will evaluate the main chewing directions by examining dental microwear patterns and will use invivo cineradiographic studies in order to characterize the kinematics associated with variation in muzzle shape in selected extant rodents. The goal of this project is to integrate these results within a comprehensive framework in order to characterize the convergence observed in the masticatory apparatus of rodents and notoungulates, and to provide more robust functional inferences for the latter.

Expertise in the anatomy and functional analysis of the masticatory apparatus and solid knowledge of its evolution within mammals are requirements for the position. Experience with geometric morphometric methods and the interpretation of fossil material is considered as an additional plus for the project.

Candidates should send (1) a letter of motivation, (2) a full CV, and (3) two letters of recommendation to the following e-mail address: billet@mnhn.fr DEADLINE to send your application: March 16, 2015.

Please contact Guillaume BILLET, or any of the other supervisors for additional information.

– Anthony Herrel Associate Editor Herpetological Journal, The European Journal of Anatomy & Functional Ecology Branch Editor Functional anatomy of amphibians and reptiles Zookeys Editorial board member J. Zoology & Zoology

UMR 7179 C.N.R.S/M.N.H.N. Département d'Ecologie et de Gestion de la Biodiversité, 55 rue Buffon, Bat Anatomie Comparee, CP 55, 75005, Paris Cedex 5, France e-mail: anthony.herrel@mnhn.fr - phone: ++33-140798120 - fax: ++33-140793773 URL: www.anthonyherrel.fr anthony.herrel@mnhn.fr

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MNHN Paris EvolFuncMorphology

Postdoctoral researcher in evolutionary functional morphology

Project title: Form-function relationships and the evolution of arboreal locomotion in mammals

Supervisors: Anthony Herrel (UMR7179; anthony.herrel@mnhn.fr), Marc Herbin (UMR7179; herbin@mnhn.fr), Raphäel Cornette (UMR7205; cornette@mnhn.fr) and Stéphane Peigné (UMR7207; peigne@mnhn.fr).

Location: Muséum National d'Histoire Naturelle, Paris, France

Salary: ±2500Euro/month (± 2000 Euro net) funded by the LabEx BCDiv. Salary

will vary with experience based on national salary scales defined by the CNRS. We are looking for a postdoctoral researcher in functional morphology to work on a project investigating the evolution of arboreal locomotion in mammals. The postdoctoral researcher will quantify the functionally relevant properties of the musculature of the limbs (muscle mass, physiological cross sectional area) using specimens from the comparative anatomy collections at the MNHN. Moreover, the postdoctoral researcher will quantify the shape of limb bones in arboreal mammals based on 3D surface scans and using geometric morphometric approaches. One of the goals of this study will be to make better inferences on the locomotor ecology and life-style in extinct animals. As such the project will focus more specifically on carnivorans and primates given the presence of well preserved fossil material.

Expertise in geometric morphometrics and experience with dissection are requirements for the position. Experience with comparative methods and the interpretation of fossil material is considered as an additional plus for the project.

Candidates should send (1) a letter of motivation, (2) a full CV, and (3) two letters of recommendation to the following e-mail address: anthony.herrel@mnhn.fr

The deadline for submission of applications is May 1st, 2015.

Please contact Anthony Herrel, or any of the other supervisors for additional information.

– Anthony Herrel Associate Editor Herpetological Journal, The European Journal of Anatomy & Functional Ecology Branch Editor Functional anatomy of amphibians and reptiles Zookeys Editorial board member J. Zoology & Zoology

UMR 7179 C.N.R.S/M.N.H.N. Département d'Ecologie et de Gestion de la Biodiversité, 55 rue Buffon, Bat Anatomie Comparee, CP 55, 75005, Paris Cedex 5, France e-mail: anthony.herrel@mnhn.fr - phone: ++33-140798120 - fax: ++33-140793773 URL: www.anthonyherrel.fr anthony.herrel@mnhn.fr

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MNHN Paris EvolutionFunctionalMorph

Postdoctoral researcher in evolutionary functional morphology

Project title: Form-function relationships and the evolution of arboreal locomotion in mammals

Supervisors: Anthony Herrel (UMR7179; anthony.herrel@mnhn.fr), Marc Herbin (UMR7179; herbin@mnhn.fr), Raphäel Cornette (UMR7205; cornette@mnhn.fr) and Stéphane Peigné (UMR7207; peigne@mnhn.fr).

Location: Muséum National d'Histoire Naturelle, Paris, France

Salary: ±2500Euro/month (± 2000 Euro net) funded by the LabEx BCDiv. Salary will vary with experience based on national salary scales defined by the CNRS.

We are looking for a postdoctoral researcher in functional morphology to work on a project investigating the evolution of arboreal locomotion in mammals. The postdoctoral researcher will quantify the functionally relevant properties of the musculature of the limbs (muscle mass, physiological cross sectional area) using specimens from the comparative anatomy collections at the MNHN. Moreover, the postdoctoral researcher will quantify the shape of limb bones in arboreal mammals based on 3D surface scans and using geometric morphometric approaches. One of the goals of this study will be to make better inferences on the locomotor ecology and life-style in extinct animals. As such the project will focus more specifically on carnivorans and primates given the presence of well preserved fossil material.

Expertise in geometric morphometrics and experience with dissection are requirements for the position. Experience with comparative methods and the interpretation of fossil material is considered as an additional plus for the project.

Candidates should send (1) a letter of motivation, (2) a full CV, and (3) two letters of recommendation to the following e-mail address: anthony.herrel@mnhn.fr

The deadline for submission of applications is May 1st, 2015. Please contact Anthony Herrel, or any of the other supervisors for additional information.

– Anthony Herrel Associate Editor Herpetological Journal, The European Journal of Anatomy & Functional Ecology Branch Editor Functional anatomy of amphibians and reptiles Zookeys Editorial board member J. Zoology & Zoology

UMR 7179 C.N.R.S/M.N.H.N. Département d'Ecologie et de Gestion de la Biodiversité, 55 rue Buffon, Bat Anatomie Comparee, CP 55, 75005, Paris Cedex 5, France e-mail: anthony.herrel@mnhn.fr - phone: ++33-140798120 - fax: ++33-140793773 URL: www.anthonyherrel.fr Anthony Herrel <anthony.herrel@mnhn.fr>

MonashU EvolutionaryEcol FairyWrens

POSTDOCTORAL RESEARCH FELLOW: Quantitative molecular ecologist to study telomere dynamics in fairy-wrens

ORGANISATION: Monash University

LOCATION: Melbourne, Australia

Start date: between April and Sep 2015

Prof Anne Peters at Monash University, Melbourne, Australia, in collaboration with Prof Simon Verhulst, Groningen University, The Netherlands, is seeking an experienced Quantitative Molecular Ecologist to explore the ecology of molecular senescence (telomere attrition). Telomeres shorten as organisms age and short telomeres are associated with greater predisposition to diseases, accelerated organismal senescence and shorter lifespan. Telomere shortening rate is known to vary with external influences and individual quality. This project will use longitudinal sampling of telomere length in individual fairy-wrens, of known age and pedigree. The telomere information will be combined with state of the art statistical methods to study telomere dynamics in relation to life-history and ecology, to disentangle effects of senescence and selective disappearance, and to assess environmental and genetic effects on telomere attrition rate.

As the successful candidate, you will join Anne Peters group studying behavioural and evolutionary ecology of fairy-wrens, based at Monash University (Melbourne, Australia). You will be expected to optimise and implement existing qPCR protocols for use in fairy- wrens and apply these to blood/DNA samples (2000 longitudinal samples). You will further be expected to maintain consistently high research output in the form of quality publications, supervise and train students, develop and submit grant proposals to external funding agencies, contribute more generally to research activities of the group, and participate in appropriate career development activities. The position (Level A, starting salary ~$75 p.a. with annual increments) is for three years subject to satisfactory annual progress.

Requirements: - A PhD in molecular ecology, with extensive experience in qPCR, preferably of telomeres - A publication track record in high-quality journals that clearly reflects the ability to conduct and publish research in the field of molecular ecology - Demonstrated evidence of a strong interest in applying state-of-the-art molecular methods to current evolutionary and ecological questions with meticulous attention to detail and high quality lab work. - Strong quantitative skills in the R-environment are highly advantageous, especially animal modelling framework - Ability to work independently - Enthusiastic about collaborative research - Have the ability to communicate effectively with other scientists at the interface of lab and field ecology - Have a strong command of English

For further details about the host and institution see: https://sites.google.com/site/petersresearchgroup/ http://monash.edu/science/about/schools/biological-sciences/ and http://www.rug.nl/staff/s.verhulst/

Send a letter of interest about your research achievements and interests to Anne Peters (anne.peters@monash.edu). This call for expressions of interest will shortly be followed by a call for application through an online application system with a short deadline (t.b.a.). Interested suitable candidates are strongly encouraged to contact Anne for further information.

Anne Peters <anne.peters@monash.edu>

Montpellier DomesticationGenomics

Postdoctoral position in plant domestication, 2 years.

RESEARCH TOPICS:

The post-doctoral will investigate plant domestication in the African continent. Original genomic datasets of 4 different species with wild and cultivated forms will be available to address their evolutionary history, place of origin and identifying genes associated with crop adaptation to different environments. The postdosctorate will analyze and modelize domestication processess, with the aim to develop geographical modelisation. Different social science datasets will be also available and we will use them to also test specific hypotheses associated with domestication history. The position will be jointly supervised by Prof. O François from TIMC-IMAG < http://www.google.fr/url?sa=t&rct=j&q=&esrc=s&source=web&cd=2&ved=0CCsQFjAB&url=http%3A%2F%2Fwww-timc.imag.fr%2FOlivier.Francois%2Fteaching.html&ei=YbbMVOLHOMLqUqOshIgF&usg=AFQjCNEnbWrLpvvM7hrG2Agzp7pEEF97Hw&sig2=-

eB7GBQx4wqsWMug-Fsw9wQ&bvm=-bv.85076809,d.d24 > in Grenoble and Dr Yves Vigouroux, IRD, Montpellier. The post-doctoral will be located in Montpellier, France

Start of the postdoctoral position: September, 2015. Earlier or later starting dates are possible.

REQUIRED OF CANDIDATES:

PhD degree obtained in population genetics or evolutionary biology. Experience or desire to develop expertise in population genetic modeling. Experience with NGS data is expected, but not require.

APPLICATION MATERIALS:

CV; statement of academic interests and goals (1 page max.); two academic references.

FUNDING:

The initial position is available for one year, with extension already funded up to two years. The project is funded by the Agence Nationale de la Recherche, France.

– Yves Vigouroux Responsable de l'Equipe Anthropisation et Dynamique de la Diversité Génétique -DYNADIV IRD - Institut de Recherche pour le Développement 911 avenue AGROPOLIS BP 64501, 34394 Montpellier cedex 5 France Tel : 33 (0)4 67 41 62 45 ; Fax : 33 (0)4 67 41 62 22 Email : yves.vigouroux@ird.fr

Web : https://sites.google.com/site/-plantbiodiversityadaptation/ yves.vigouroux@ird.fr

Munich EvolutionaryNeuronalBiol

The Parmenides Center for the Conceptual Foundations of Science is offering a research stipend for a candidate with a Ph.D (preferably with successful postdoc experience) to investigate the possible links among evolutionary biology, neuronal dynamics and insight psychology.

Within the advertised topic the successful candidate is free to pursue an individual, high-quality research programme, also possibly including concepts and methods of statistical physics. Writing and communication skills in English are mandatory and some command of German is welcome.

The stipend is up to 2.500 EUR per month for a maximum of one year.

Applicants should send their CV, a motivation letter and a research plan of up to 3 pages to Prof. Eors Szathmary (szathmary.eors@gmail.com), the Director of the Center by the 15th of February. The fellowship begins on the 1st March the earliest.

Thank you in advance!

Best regards,

Carsten

Carsten Freitaeger Parmenides Foundation Kirchplatz 1 82049 Pullach Tel +49.89.4520935.0 Fax +49.89.4520935.31 Skype: Parmenides.Foundation carsten.freitaeger@parmenides-foundation.org

Carsten Freitäger <carsten.freitaeger@parmenides-foundation.org>

NorthCarolinaStateU Biocomplexity

NC State University Distinguished Postdoctoral Fellow in Biological Complexity

North Carolina State University is embarking on a new university-wide interdisciplinary initiative in biological complexity encompassing systems genetics, behavioral neurogenetics and neurogenomics, genome-environment interactions, ecological genetics, systems ecology, climate change, and computational biology and bioinformatics.

Associated with the new initiative in biological complexity is a distinguished postdoctoral fellowship program. Applicants are expected to be near completion of a terminal doctorate degree, have a strong research record with evidence of exceptional scholarship, and embrace interdisciplinary research. Fellows will receive competitive stipends and independent research funds to initiate an innovative research program with guidance from a multidisciplinary mentoring committee in areas covered by the initiative in biological complexity.

To apply for a fellowship, go to https://jobs.ncsu.edu/-postings/48719. Provide a cover letter, curriculum vitae, a three-sentence statement of the most significant scientific problem(s) to be addressed in the near future, and statements of research interests. Three letters of recommendation should be sent to trudy_mackay@ncsu.edu. Review of applications will begin immediately, and continue until the position is filled. The start date can be as soon as June 1, 2015.

NCSU is an AA/EO employer. All qualified applicants will receive consideration for employment without regard to race, color, national origin, religion, sex, age, veteran status or disability. In its commitment to diversity and equity, NC State University seeks applications from women, minorities, and persons with disabilities. NC State welcomes all persons without regard to sexual orientation. ADA Accommodations: please call 919-515-3148.

Melissa Robbins <merobbi3@ncsu.edu>

Otago EvolutionaryGenomics

Postdoctoral Fellow Department of Zoology Division of Sciences UNIVERSITY OF OTAGO

Applications are invited for the 3-year, fixed-term position of Postdoctoral Fellow at the Univeirsity of Otago. We seek an energetic and dedicated scientist to carry out evolutionary and developmental genomic research on alpine insects. The successful candidate will be working on a Marsden-funded research project titled 'Use it or lose it: unravelling the genetic basis of flight-loss in New Zealand's alpine insects'. The project is led by Professor Jon Waters and Associate Professor Peter Dearden.

The research will combine evolutionary and developmental genomic approaches. A PhD and research experience in evolutionary or developmental genetics is essential. Experience in bioinformatics would be an advantage.

The appointment is expected to start within the period July-October 2015.

https://otago.taleo.net/careersection/2/jobdetail.ftl?lang=en&job=1500256 Specific enquiries may be directed to Professor Jon Waters, Principal Investigator of the Mardsen funded project, Department of Zoology, Tel 03 479 5847 email jon.waters@otago.ac.nz. http://www.otago.ac.nz/Zoology/staff/otago008938.html Applications close 23 February 2015.

Professor Jon Waters Associate Dean of Research, Sciences Department of Zoology University of Otago Dunedin, New Zealand Ph NZ-3-4795847 http://www.otago.ac.nz/Zoology/staff/otago008938.html jon.waters@otago.ac.nz

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Otago EvolutionaryGenomics updatedURL

Postdoctoral Fellow - Evolutionary Genomics Department of Zoology Division of Sciences UNIVERSITY OF OTAGO

Applications are invited for the 3-year, fixed-term position of Postdoctoral Fellow at the University of Otago. We seek an energetic and dedicated scientist to carry out evolutionary and developmental genomic research on alpine insects. The successful candidate will be working on a Marsden-funded research project titled 'Use it or lose it: unravelling the genetic basis of flight-loss in New Zealand's alpine insects'. The project is led by Professor Jon Waters and Associate Professor Peter Dearden.

The research will combine evolutionary and developmental genomic approaches. A PhD and research experience in evolutionary or developmental genetics is essential. Experience in bioinformatics would be an advantage.

The appointment is expected to start within the period July-October 2015.

Postdoctoral Fellow - Zoology < https://otago.taleo.net/careersection/2/jobdetail.ftl?lang=en&job=1500256 >

Specific enquiries may be directed to Professor Jon Waters, Principal Investigator of the Marsden-funded project, Department of Zoology, Tel 03 479 5847 email jon.waters@otago.ac.nz.

Applications close 23 February 2015.

Professor Jon Waters Associate Dean of Research, Sciences Department of Zoology University of Otago Dunedin, New Zealand Ph NZ-3-4795847 http://www.otago.ac.nz/Zoology/staff/otago008938.html jon.waters@otago.ac.nz

Jonathan Waters <jon.waters@otago.ac.nz>

PennStateU PopulationGenetics

The DeGiorgio lab (http://www.personal.psu.edu/-mxd60/) at The Pennsylvania State University is recruiting a highly motivated postdoctoral scholar. The position requires a PhD degree in biology, genetics, bioinformatics, statistics, computer science, or a related field. Our lab uses mathematical and computational approaches to study evolutionary relationships within and among species. We work on both theoretical and applied problems in statistical population genetics, human evolutionary genomics, and phylogenetics. Candidates interested in research projects within these three broad research categories are encouraged to apply. Our lab is solely computational, and so candidates should have knowledge of at least one programming language (C, C++, Java, Perl, Python, etc), familiarity with either R or Matlab, and experience using a Unix or Linux environment. A complete application must be submitted electronically at https://app2.ohr.psu.edu/Jobs/-External/EVMS2_External/currentap1.cfm#55772 and will include a current CV, a cover letter describing your research interests, copies of copies of three representative publications, and contact information for three references. Review of applications will begin immediately and continue until position is filled. This is a fixed-term appointment funded for one year from date of hire with possibility of re-funding.

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 minorities, women, veterans, disabled individuals, and other protected groups.

mikedegiorgio@gmail.com

QueensU PhD PDF SeabirdAdaptation

I am looking for one or two PhD or MSc students or a post-doctoral fellow to join my research team studying adaptation in seabirds. We have two main study systems:

1) Band-rumped storm-petrels represent an exciting case of repeated parallel evolution of sympatric allochronic races (populations separated by breeding time - basically, feathered sticklebacks). Initial studies in my lab documented the pattern of divergence. We are now investigating the mechanisms of parallel adaptation and speciation using genomic methods. The new project will entail combination of molecular data with an existing large data set to estimate heritability of various morphological and life history traits. Other projects within this study system are possible. Field work on barren tropical islands will be required.

2) Thick-billed Murres breed throughout the north Atlantic, Pacific and Arctic Oceans, and are increasingly challenged by climate change. The need, and the potential, for a species to adapt to anthropogenic change depends on the plasticity of key traits such as breeding time and heat tolerance. I am looking for a new student to combine genetic data with an existing large dataset to study the fitness effects and heritabilities of several physiological and life history traits. Field work on a remote arctic island will be required. This student will be co- supervised by Dr. Kyle Elliott (McGill University).

Applicants must have some background in evolutionary genetics. Practical experience with genomics and bioinformatics is an asset. The successful applicant(s) will join a dynamic group of faculty and students studying ecology and evolution at Queen's University. Please send a resume or curriculum vitae, informal transcript, and contact information for two academic references to Dr. Vicki Friesen (address below). Acceptance is conditional on scholarship funding through either Queen's University or an external agency. Positions are not restricted to Canadians. Please contact vlf@queensu.ca for further information.

Dr. Vicki Friesen, Professor Department of Biology, 4443 Biosciences, 116 Barrie Street, Queen's University, Kingston, ON K7L 3N6, Canada Tel: 613-533-6156 Fax: 613-533-6617

Haida Saying: Treat the Earth well: it is not given to us by our parents, it is loaned to us by our children.

Vicki Friesen <vlf@queensu.ca>

RJB Madrid PlantEvolution

A postdoctoral research fellowship is available in the lab of Dr. Pablo Vargas (RJB, Royal Botanical Garden of Madrid, Spain) to participate in a variety of highly collaborative projects related to the phylogeny and evolution of plant genomes. They are collaborative projects with the lab of Dr. Toni Gabaldón (CRG, Centre for Genomic Regulation, Barcelona, Spain).

The successful candidate will work with collaborators to analyse comparative genomics and phylogenomics of seven genomes using a reference genome or reference assembly. The projects primarily include analyses of bioinformatics, phylogenomics, and comparative genomics involving extensive data at a genome-scale. Transcriptomes will serve for comparative genomics. The position is based at the Royal Botanic Garden of Madrid and includes opportunities for travel to Barcelona to work with the CRG team. The initial appointment is for one year.

The position offers a salary subject to experience. Start date as soon as possible. Review of applications will begin on March 15, 2015; however applicants will be considered until the position is filled.

Required Qualifications:

- A Ph.D. in computational biology, evolutionary genetics/genomics, phylogenomics, bioinformatics and related fields. - Experience with manipulating and analyzing genomic, transcriptomic and NGS sequence data. - Some record of prior publication in genome-scale data analysis, including bioinformatics pipeline construction, phylogenomics, and/or genome structure and evolution - Strong communication and interpersonal skills, including a proven ability to work both independently and as part of a team

Desired Qualifications: (ideal applicant; applicants without these skills will be also considered)

- Proficiency in computer programming - Experience with standard molecular laboratory techniques - Experience with the analysis of traditional molecular phylogenetic data sets

The successful applicant will be expected to work/collaborate with another postdocs and graduate students in Madrid and Barcelona.

To apply, submit a cover letter stating your research accomplishments and interests, qualifications relevant to the position (especially in reference to the required and desired qualifications listed above), a curriculum vitae, and the names and contact information for three references.

Inquiries about the position may be directed to Pablo Vargas (vargas@rjb.csic.es).

Pablo Vargas Ph.D. Senior Scientist Royal Botanical Garden of Madrid (CSIC) Plaza de Murillo 2, 28014 Madrid http://www.rjb.csic.es/jardinbotanico/-jardin/contenido.php?Pag=413&tipo=cientifico&cod=-96&len=es Toni Gabaldón Ph. D. Senior Scientist Centre for Genomic Regulation Calle C/ Dr. Aiguader, 88 (PRBB Building) 08003 Barcelona, Spain http://-big.crg.cat/comparative_genomics Pablo Vargas Gómez <vargas@rjb.csic.es>

Singapore ViralGenomics

Postdoctoral Opportunity at Duke-NUS Graduate Medical School, Singapore

We are currently recruiting a post-doc to work with Prof. Mariano Garcia-Blanco in the Emerging Infectious Disease program (https://www.duke-nus.edu.sg/content/-garcia-blanco-mariano). The group studies host factors of /flavivirus/ infection (primarily dengue and yellow fever viruses) in human tissue culture and mosquitoes. The group is located in a dynamic, well-funded and well-equipped environment (https://www.duke-nus.edu.sg/), with access to cutting-edge genomic and proteomic facilities.

The project is to study the interaction of non-coding /flaviviral/ RNA and the host innate immune response. Using proteomics, cell culture and molecular biology techniques, the researcher will characterize the interaction between viral non-coding RNA and proteins, determine the role of the interaction in infection, identify interacting immune factors, and search for drugs disrupting those interactions. The project should provide a basic understanding of how viral non-coding RNA alters the host immune response during infection and result in identification of drugs targeting these interactions.

The ideal candidate will have experience with cell and molecular biology techniques, virology and protein biochemistry. The candidate will also have a track record of publications, a high level of intellectual engagement and excellent problem-solving skills. The ability to work independently without supervision is essential.

Singapore is a safe, lively and stimulating country with a profound commitment to supporting cutting edge scientific research. Salary is attractive and will depend upon experience. The position is a one-year contract renewable for up to 3 years. Only selected candidates will be invited for interview.

Please send a CV and cover letter to:

Julien.pompon@duke-nus.edu.sg

alex.ward@duke-nus.edu.sg

– Julien Pompon, PhD | Senior Research Fellow Emerging Infectious Diseases | Duke-NUS Graduate Medical School 8 College Road, Singapore 169857 | www.duke-nus.edu.sg Julien Pompon <julien.pompon@duke-nus.edu.sg>

SLU Alnarp PlantHerbivore PollinatorInteractions

A 2-year postdoc position is available at SLU, Alnarp:

In strawberries herbivore-damaged plants deter pollinators, leading to reduced pollination success. However, wild plant genotypes, as well as domesticated varieties, differ in their resistance against herbivores.

The aim of this postdoc project is to investigate whether pollination success is improved when wild strawberries evolve stronger resistance, and during plant breeding for improved resistance in domesticated varieties. The postdoc will have access to a large common garden with 100 wild plant genotypes (Fragaria vesca) that differ in several plant traits , including their resistance against herbivores.

The full ad can be downloaded here: http://www.slu.se/sv/om-slu/fristaende-sidor/aktuellt/lediga-tjanster/lasmer/?eng=1&Pid=1700 Johan

Johan A. Stenberg Associate Professor

Sveriges lantbruksuniversitet Swedish University of Agricultural Sciences

Department of Plant Protection Biology PO Box 102, SE-230 53 ALNARP Visiting address: Sundsvägen 14 Mobile: +46 70 622 00 42 johan.stenberg@slu.se, www.slu.se/stenberg Johan A Stenberg <Johan.Stenberg@slu.se>

SpelmanCollege Georgia 3 EvolBiology TeachingEmphasis

I would like to share these three postdoctoral positions with the evodir community. The positions are broadly defined but we are looking people with evolutionary/bioinformatics training that are interested to integrate research and teaching in an undergrad liberal art college environment.

Thanks,

Yonas

CURE Postdoctoral Fellowships

(Three Positions)

Spelman College is piloting a postdoctoral fellowship program that combines a traditional principal-investigator directed postdoctoral research experiences with mentored teaching experiences. Founded in 1881, Spelman College is a private four-year liberal arts college located in Atlanta, GA. The oldest historically Black college for women in the United States, Spelman is a member of the Atlanta University Center Consortium and Atlanta Regional Consortium for Higher Education.

Eligibility:

(1) Graduate students that will complete their requirements for the Ph.D. prior to the Fellowship start date of June 1, 2015, or Ph.D. scholars who have completed their dissertation within the last three years (on or after August 1, 2012);

(2) Ph.D. must be in an eligible research-based field in STEM to include: Biology, Biochemistry, Chemistry, Computer Science, Mathematics, Physics, or a related science discipline. Preference will be given to candidates with interdisciplinary training.

Qualifications: Commitment to a career in teaching and research, experience working with underrepresented groups and interest in the scholarship of undergraduate teaching and learning are highly valued.

Responsibilities: Conduct research within a specific field guided by a designated PI; publish scientific manuscripts under the direction of the PI; help develop investigative-based modules for existing undergraduate science courses; and contribute to the training and mentoring undergraduate research students.

Term: Postdoctoral awards may be up to three years (36 consecutive months), given continued successful progress.

Review of applications will begin immediately with a materials received and closing deadline of March 13, 2015.

Competitive salary and an excellent benefits program are available. To apply for the position, please upload: a letter of interest, including job code, which identifies the position sought; curriculum vitae (with contact information); a one-page statement of teaching philosophy; statement of scholarly, creative or research interests.

Applicants selected for further review will be required to provide official undergraduate and graduate school transcripts, as well as three letters of recommendation sent directly from the referee or dossier. Address all referee or dossier letters to: Spelman College, Provost Faculty Human Resources Office, Attn: Ms. Karla H. Williams, Manager of Faculty Human Resources, 350 Spelman Lane, SW, Box 1209, Atlanta, GA 30314.

PLEASE APPLY BELOW

Spelman College is an EOE/Minority/Female/Disabled/Veteran/Title IX Employer and participates in E-Verify

Yonas Tekle <yonastekle@gmail.com>

Stockholm MeiofaunaTaxonomy

Post-doctoral researcher

A postdoc position is available in the research group of Ulf Jondelius at the Swedish Museum of Natural History, Stockholm.

We are looking for a highly motivated postdoc with interest in animal diversity and taxonomy for a project aiming to survey the diversity of the flatworm group Macrostomorpha with emphasis on the Swedish fauna. Macrostomorphs are free-living microscopic worms that live predominantly in the marine environment, but also in fresh water. They are an abundant component of the littoral meiofauna.

Live specimens will be collected, documented and preserved for histology and DNA-sequencing. Sequence data will be used to delimit named and newly discovered species, which will be taxonomically described. The phylogeny of various groups within Macrostomorpha will be reconstructed. Sediment samples for a metagenetic study of several meiofauna groups will be collected and analyzed within the project aiming to provide new insights into meiofauna distribution and abundance patterns.

Qualifications The ideal candidate has a recent PhD in zoology or marine biology, an interest in marine and limnic fieldwork, experience in taxonomy of microscopic animals, proficiency in analysis of DNA sequence data and a record of publishing in scientific journals.

Criteria for selection Selection will be based on scientific merits including the quality of the PhD thesis and published scientific work, the applicants documented competence in subjects of relevance for the research field, proficiency in English and teamwork skills. The PhD degree should have been received no more than three years before the deadline for applications.

Starting date is May 1, 2015, although this is negotiable. Initial appointment is for one year with the possibility of extension for a further two years. The project will be carried out in cooperation with colleagues at the University of Basel.

For more information, please contact professor Ulf Jondelius (ulf.jondelius@nrm.se). Union representative is Bodil Kajrup, SACO-S. Both can be reached at telephone number + 46 8 519 540 00.

How to apply Applicants should submit (1) a cover letter describing your research interests and background, (2) a detailed CV (including publications), and (3) the contact details of three references as a single pdf document to rekrytering@nrm.se or to Swedish Museum of Natural History, P.O. Box 50007, SE-104 05 Stockholm, Sweden, no later than February 27, 2015. Mark your application with dnr 2.3.1-49-2015

Ulf.Jondelius@nrm.se

TorontoScarborough FishPopulationGenomics

Postdoctoral position in population genetics at University of Toronto Scarborough

A one year postdoctoral position is available to carry out a next generation sequencing study on the role of waterfalls as geographic barriers for Great Lakes fishes. The project has important conservation implications, particularly with respect to the ability of invasive species to cross physical barriers.

Applicants are expected to have some background in genomic approaches to population studies.

A complete application package includes a CV, a short description of past research accomplishments and future goals, and the names and e-mail addresses of at least 2 references. Evaluation of applications starts immediately and will continue until a suitable candidate is found. Application materials should be sent via email to Nathan Lovejoy at lovejoy@utsc.utoronto.ca

This fellowship is a joint project sponsored by the University of Toronto and Fisheries and Oceans Canada.

lovejoy@utsc.utoronto.ca

UAgder Norway EvolutionaryMarineGenomics

Post-doctoral Research Fellow in Evolutionary Marine Genomics at the Faculty of Engineering and Science. Ref 5/15

The University of Agder (UiA) invites applications for a full-time, fixed-term appointment as Post-doctoral Research Fellow in Evolutionary Marine Genomics at the Faculty of Engineering and Science, Department of Natural Sciences for a period of two years. The position will mainly be located in Kristiansand, Norway. However, the appointee may be required to stay for a period at the Institute of Marine Research, Fl©devigen (IMR). The preferred start date is 1 May 2015 (negotiable with the Department).

The marine group at the Department of Natural Sciences comprises around 20 people including Professors, Professors II, Researchers II, Post-doc and PhD fellows. The Post-doctoral Fellow will also benefit from the recently established Center for Coastal Research < https://www.facebook.com/-marinecenternorway?ref=hl > (CCR) in cooperation with University of Oslo, Institute of Marine Research, GRID-Arendal, NIVA and Telemark University College.

The postdoctoral-fellow will primarily work in an ongoing international project entitled Adaptation or plasticity as response to large scale translocations and harvesting over a climatic gradient in the marine ecosystem?± funded by the Research Council of Norway (RCN) under the Havkyst programme. This project aims at improving our understanding of adaptive processes in marine fish in response to human and climatic stressors. During its development, large datasets will be generated by means of Next-Generation Sequencing (NGS) approaches, focusing the analysis on Rads and transcriptomics data. The candidate will also have the opportunity to get involved in other ongoing projects at CCR as well as to develop own initiatives.

The Post-doctoral Fellow will be expected to take part in a binding cooperation with the research group and contribute to an active research environment that will give opportunities for personal and professional development. The appointee must have the ability to work in a goal-oriented, organised, focused, and independent manner. During the assessment process emphasis will be placed on the applicants PhD work, examination results as well as any other previous research and development work. Relevant practical experience, personal suitability and good teamwork skills will also be emphasised.

The successful candidate should hold a PhD in a relevant field such as ecology, evolution, genetics/genomics, aquaculture or bioinformatics. Applicants with a PhD in medical science and experience in NGS data analysis are also welcome. The qualified candidate should have strong computational skills and/or experience with the major techniques in Bioinformatics. In addition, he/she will be familiar with Linux/Unix systems as well as programming in script-based language, e.g. Phython and/or Perl. Experience with laboratory protocols in molecular biology and rearing fish in tanks is an advantage, but not required.

Information about the appointment criteria for a Post-doctoral Research Fellow can be found in the Regulations Concerning Terms and Conditions of Employment for the Post of Post-doctoral Research Fellow, Research Fellow, Research Assistant and Resident, available for download here < http://www.uia.no/en/vacancies2 >.

The Norwegian public service is committed to reflect the diversity of society and the personnel policy of the University of Agder aims to achieve a balanced workforce. All qualified persons are therefore encouraged to apply for the position irrespective of cultural background, gender, age or disability.

Short-listed applicants will be invited for interviews and with permission from the applicant the University will also conduct a reference check before appointment.

Appointment is made by the University of Agders Appointments Committee for Teaching and Research Positions. The successful applicant will have rights and obligations in accordance with the current regulations for the public service.

The position is remunerated according to the State salary scale, salary plan 17.510, code 1352 Post-doctoral Research Fellow, salary grade 60 -72 (NOK 509.100-639.500). A 2 % compulsory pension contribution to the Norwegian Public Service Pension Fund is deducted from the pay according to current statutory provisions.

Applicants are asked to submit their application and CV online. Please use the link Send application±.

The following documentation should be submitted online:

* Copies of diplomas, transcripts and letters of reference * Complete list of scientific publications * A description of research interests, background for the problem that the applicant wishes to study and its relevance for the above mentioned project * Summary

— / —

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

UAlabama Bee PopulationGenomics

A NSF-funded postdoctoral research position in the field of landscape genomics is available in Jeff Lozier's lab in the Department of Biological Sciences at the University of Alabama (http://bama.ua.edu/~jlozier).

The available position will involve the study of evolutionary and functional genetics of local adaptation in North American bumble bees. In addition to interacting with the Lozier lab, the selected applicant will work closely with Michael Dillon (University of Wyoming; http://www.uwyo.edu/mdillon/) and James Strange (USDA-ARS Pollinating Insect Research Unit and Utah State, Logan, UT; http://goo.gl/uJFqxS) on an interdisciplinary effort to understand the consequences of abiotic heterogeneity on morphological, physiological, and genomic variation across complex mountain landscapes of CA, OR, and WA.

The open position is for a highly motivated postdoctoral research associate whose primary objective will be to oversee next generation population genomic and transcriptomic analyses of field-collected and experimental samples.

Responsibilities will include participating in fieldwork, laboratory work, and will be especially focused on computational and statistical analysis of genomic and RNAseq data. The ideal candidate should have experience with next generation sequencing, ideally with emerging methods for population-level genomic (e..g, RADseq, Pool-seq) or RNAseq analysis, and possess laboratory genetics skills, excellent computational skills (e.g., familiarity with GIS, UNIX, R, or other programming languages, as well as open-source genetics software), and the ability to effectively manage large data sets. The applicant should be creative and independent, have excellent organizational, communication, and writing skills, and a publication record in evolutionary biology, population genetics, molecular ecology or other related fields. A general interest in pollinator biology and related field experience would be advantageous, but applicants with diverse research backgrounds are encouraged to apply

. Candidates must have received a Ph.D. in a relevant field by the start date.

Funding is available for at least two years, potentially longer, with annual renewal dependent on performance evaluation, and will include a competitive salary and full benefits. The University of Alabama offers a range of professional development opportunities. Application review will begin in late February, 2015 and will continue until the position is filled. Start date is negotiable, but the successful applicant should ideally be able to begin working in the position by summer (May 1-Sept 1) 2015.

Applicants interested in the position are encouraged to contact Jeff Lozier (jlozier@ua.edu) when applying. Applicants must officially apply by submitting an application to the Spring 2015 Biological Sciences Departmental postdoctoral pool at facultyjobs.ua.edu (requisition number 0809316): https://facultyjobs.ua.edu/postings/36373 . Materials should include: 1. Cover letter mentioning the “Pollinator Landscape Genomics” position, a description of past research accomplishments and future research goals, and the names and contact information for 3 references (maximum of two pages). 2. Curriculum vitae

About the University of Alabama: The University of Alabama is the flagship campus of the University System of Alabama, with an enrollment of over 35,000 students. The University is committed to achieving excellence as one of the country’s primary centers of research and education. It is located in the vibrant college town of Tuscaloosa, AL, which boasts many cultural and athletic activities. The campus also benefits from the close proximity to the Birmingham metropolitan community.

The University of Alabama is an Affirmative Action/Equal Opportunity Employer. Women and minorities are encouraged to apply.

jlozier@ua.edu

UAlabama PopulationGenomics

A NSF-funded postdoctoral research position in the field of population genomics is available in Jeff Lozier$B!G(Bs lab in the Department of Biological Sciences at the University of Alabama (http://bama.ua.edu/~jlozier). Note that this is a repost of an earlier ad for this open position, containing just a few clarification on dates below.

The available position will involve the study of evolutionary and functional genetics of local adaptation in North American bumble bees. In addition to interacting with the Lozier lab, the selected applicant will work closely with Michael Dillon (University of Wyoming; http://www.uwyo.edu/mdillon/) and James Strange (USDA-ARS Pollinating Insect Research Unit and Utah State, Logan, UT; http://goo.gl/uJFqxS) on an interdisciplinary effort to understand the consequences of abiotic heterogeneity on morphological, physiological, and genomic variation across complex mountain landscapes of CA, OR, and WA.

The open position is for a highly motivated postdoctoral research associate whose primary objective will be to oversee next generation population genomic and transcriptomic analyses of field-collected and experimental samples.

Responsibilities will include participating in fieldwork, laboratory work, and will be especially focused on computational and statistical analysis of genomic and RNAseq data. The ideal candidate should have experience with next generation sequencing, ideally with emerging methods for population-level genomic (e..g, RADseq, Pool-seq) or RNAseq analysis, and possess laboratory genetics skills, excellent computational skills (e.g., familiarity with GIS, UNIX, R, or other programming languages, as well as open-source genetics software), and the ability to effectively manage large data sets. The applicant should be creative and independent, have excellent organizational, communication, and writing skills, and a publication record in evolutionary biology, population genetics, molecular ecology or other related fields. A general interest in pollinator biology and related field experience would be advantageous, but applicants with diverse research backgrounds are encouraged to apply. Candidates must have received a Ph.D. in a relevant field by the start date.

Funding is available for at least two years, potentially longer, with annual renewal dependent on performance evaluation, and will include a competitive salary and full benefits. The University of Alabama offers a range of professional development opportunities. Applications received will be reviewed by the end of next week (March 6) and applicants will be contacted by the second week of March, however review of applications will continue until the position is filled. Start date is negotiable, but the successful applicant should ideally be able to begin working in the position by summer/fall 2015.

Applicants interested in the position are encouraged to contact Jeff Lozier (jlozier@ua.edu) when applying. Applicants must officially apply by submitting an application to the Spring 2015 Biological Sciences Departmental postdoctoral pool at facultyjobs.ua.edu (requisition number 0809316): https://facultyjobs.ua.edu/-postings/36373 . Materials should include: 1. Cover letter mentioning the $B!H(BPollinator Landscape Genomics$B!I(B position, a description of past research accomplishments and future research goals, and the names and contact information for 3 references (maximum of two pages). 2. Curriculum vitae

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The University of Alabama is an Affirmative Action/Equal Opportunity Employer. Women and minorities are encouraged to apply.

Jeffrey D. Lozier Assistant Professor Department of Biological Sciences Box 870344 University of Alabama, Tuscaloosa AL 35487 jlozier@as.ua.edu

jlozier@ua.edu

UArizona 2 GenomicsInvasiveSpecies

Two postdoctoral research positions funded by the United States Department of Agriculture are available to work with Dr. Katrina Dlugosch (http://dlugoschlab.arizona.edu/) and Dr. David Baltrus (http://cals.arizona.edu/research/baltruslab) at the

University of Arizona on the ecological genomics of microbial interactions with the invasive plant yellow starthistle (Centaurea solstitialis). We are investigating the evolution of species interactions during range expansion and their impact on the spread of invading populations, and we are seeking postdoctoral researchers with interests and experience in these areas.

One successful candidate will be responsible for next-generation genomic sequence generation and bioinformatic analyses, particularly by 1) surveying plant-associated microbial communities in the native (European) and invaded (North American) ranges of yellow starthistle, using 16S metagenomics and culture-based sequencing of field-collected specimens, and 2) quantifying rates of gene flow across the genome in invading plant populations using a high-throughput RADseq next-generation approach. Preferred start date in May 2015. To apply, submit a statement of interest and curriculum vitae to job #57623 at https://www.uacareertrack.com A second successful candidate will be responsible for 1) mapping QTL associated with the genetic basis of variation in resistance to bacterial pathogens using large-scale greenhouse experiments and genome-wide RADseq markers, and 2) quantifying population-level impacts of infection using phenotypic data collection in combination with existing demographic models in collaboration with Dr. Sarah Swope (Mills College). Preferred start date in late 2015 or early 2016. To apply, submit a statement of interest and curriculum vitae to job #57624 at https://www.uacareertrack.com Positions are for one year, with reappointment for up to two additional years subject to satisfactory performance. Review of applications will begin March 2, 2015 and continue until filled.

Minimum qualifications *PhD in Biology or a related field *Authorship of peer-reviewed publications of research in a field related to the position *Strong communication skills *Ability to work independently and in a team

Preferred Qualifications (Applicants without these skills will be considered): *Experience producing and analyzing molecular genetic data, particularly next-generation genomic data *Experience culturing bacterial colonies *Experience rearing plants under standard greenhouse conditions *Experience collecting and documenting field specimens

Inquiries about the positions may be directed to Dr. Katrina Dlugosch (kdlugosch@email.arizona.edu).

Katrina M. Dlugosch, Assistant Professor Ecology & Evolutionary Biology, University of Arizona kdlugosch@email.arizona.edu | http://dlugoschlab.arizona.edu katrina.dlugosch@gmail.com

katrina.dlugosch@gmail.com

UBern 2 Biodiversity

Two Postdoctoral Researchers, Biodiversity Synthesis, University of Bern

Applications are invited for two, 3-year, postdoc positions conducting ecological synthesis in the Biodiversity Exploratories (_http://www.biodiversity-exploratories.de_). One postdoc will be supervised by Prof. Markus Fischer and the other by Prof. Eric Allan, both at the University of Bern in Switzerland.

The Biodiversity Exploratories project involves collaboration between over 50 research groups and examines relationships between environmental change (land-use intensification), biodiversity and ecosystem functioning in forests and grasslands. It has generated uniquely comprehensive biodiversity and ecosystem function datasets, including detailed land-use data, diversity data from a wide range of groups such as bacteria, fungi, arthropods, plants and vertebrates and data on many different ecosystem services. The synthesis project aims to utilise these data for combined analyses and therefore to create synergies between the different research groups, thus providing added value for the whole project.

We are seeking highly motivated applicants interested in the causes and consequences of biodiversity change, community ecology and/or ecosystem service research. As well as conducting synthesis analyses, applicants are expected to interact frequently with members of the Biodiversity Exploratories community and to organise workshops.

Applicants should have a PhD in ecology, or related discipline, and strong analytical skills, including familiarity with advanced statistical techniques and manipulation of large datasets (preferably using R). The positions will be based at the Institute of Plant Sciences in Bern, which offers a stimulating, international research environment and excellent facilities (_www.botany.unibe.ch/planteco_). Bern is also a beautiful city with a high quality of life.

Please send your application by email (as a single PDF by email) to _eric.allan@ips.unibe.ch_. Applications should include a CV, names and addresses of two references, a one page description of your research interests and a list of publications. Applications will be reviewed from 5^th March 2015 until the position is filled.

For queries on the application process or more information on these positions, please contact Prof. Eric Allan _eric.allan@ips.unibe.ch_

– Dr. Eric Allan, Institute of Plant Sciences University of Bern Altenbergrain 21 CH-3013 Bern email: eric.allan@ips.unibe.ch phone: +41 31 631 4992 http://www.ips.unibe.ch/content/biodiversity/-index_eng.html http://www.researchgate.net/profile/-Eric_Allan Eric Allan <eric.allan@ips.unibe.ch>

UCalifornia Berkeley 2 Drosophila

UC Berkeley, Two Postdoctoral Positions in Evolutionary and Functional Genomics

Two postdoctoral positions are available in the group of Doris Bachtrog at the University of California, Berkeley.

One project focuses on the formation of heterochromatin on evolving Y chromosomes in Drosophila, using functional genomics and computational analysis, combined with developmental biology approaches. The second project focuses on the evolution of reproductive barriers in incipient Drosophila species, using both experimental evolution and population genomics approaches. Our group shares space and weekly lab meetings with other members of the Center for Theoretical Evolutionary Genomics at UC Berkeley (http://cteg.berkeley.edu/).

Applicants for the position must have either a background in high-throughput genomics techniques, Drosophila genetics and husbandry, and/or computational population and evolutionary genomics analysis. Programming and bioinformatics skills are required.

Funds are available to support these positions for up to three years. The positions are immediately available and the search continues until the positions are filled.

To apply, please submit (by email) a CV, a brief description of research interests (no more than one page), and the names and contact information for three references to Doris Bachtrog (dbachtrog@berkeley.edu).

For further information about our research program, please visit our website (http://ib.berkeley.edu/labs/-bachtrog/).

Doris Bachtrog University of California, Berkeley Department of Integrative Biology Center for Theoretical Evolutionary Genomics Berkeley, CA 94720-3140 phone: (510)-325-9547

Doris Bachtrog <dbachtrog@berkeley.edu>

UCambridge Phylogenetics

*** Postdoc in Phylogenetics & Biodiversity, Cambridge ***

The Ecosystems and Global Change Group in the Department of Plant Sciences at the University of Cambridge (http://www.plantsci.cam.ac.uk/research/-andrewtanentzap) is seeking a full-time Research Associate with interests in plant and animal diversification, biogeography, and computational phylogenetics. Based in central Cambridge, the postholder will join an existing project focused on mapping the evolutionary potential of the world's biodiversity. They will be responsible for generating time-calibrated phylogenetic trees and using them to estimate evolutionary rates.

Applicants should have a PhD in evolutionary biology, ecology, or a closely related field, and strong skills in phylogenetic and macro-evolutionary modelling. A track record of publication in leading peer-reviewed journals is essential. Laboratory experience with DNA sequencing is desirable, as is experience with tools such as DPPDiv, BEAST, and MrBayes. Interest in conservation science is helpful.

Fixed-term: The funds for this post are available for 22 months in the first instance.

To apply online for this vacancy, please click on the 'Apply' button at http://www.jobs.cam.ac.uk/job/6094/. This will route you to the University's Web Recruitment System, where you will need to register an account (if you have not already) and log in before completing the online application form.

Applicants should provide a CV, the filename of which should be "CV-followed by your name", including contact details of two academic referees, and a covering letter addressing the selection criteria.

For further information see http://-www.jobs.cam.ac.uk/job/6094/ Please quote reference PD05272 on your application and in any correspondence about this vacancy.

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

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

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

UCanterbury EvolutionNetworks

Postdoctoral research fellowship Stouffer Lab, School of Biological Sciences, University of Canterbury, Christchurch, New Zealand

We invite applications for a postdoctoral research fellowship to study the structure, dynamics, and evolution of ecological networks in the Stouffer Lab < http://stoufferlab.org/ > (School of Biological Sciences, University of Canterbury, New Zealand).

Requirements: The ideal candidate has a strong quantitative background, demonstrated research excellence, and a PhD in ecology, engineering, applied mathematics, physics, computer science, or related fields. Programming experience in both a compiled language (C or C++ preferred) and one or more scripting languages (such as Python or R) is highly desirable.

Position details: The position is part of a Fast-Start grant from the Marsden Fund Council, administered by the Royal Society of New Zealand. The salary will be in the range of NZ$55,000-65,000 per year (depending on experience), and the starting date is negotiable. The initial appointment will be made for 1.5 years, with renewal dependent on progress, mutual agreement, and funding availability.

How to apply: Applicants should submit (1) a cover letter describing their research interests and background, (2) a detailed CV (including publications), and (3) the contact details of three references to daniel.stouffer@canterbury.ac.nz. The cover letter should also include possible starting dates.

Review of applications will start immediately and will continue until the position has been filled.

Dr. Daniel B. Stouffer Senior Lecturer School of Biological Sciences University of Canterbury Christchurch, New Zealand

http://stoufferlab.org @StoufferLab

daniel.stouffer@canterbury.ac.nz

UConnecticut PlantComparativeGenomics

The Wegrzyn lab invites applications for a post-doc position in the Department of Ecology and Evolutionary Biology at the University of Connecticut. We focus on developing computational approaches that integrate next generation sequence data to address questions in comparative genomics in non-model plants, particularly forest trees. The lab has the following ongoing projects: 1) Understanding the evolution of alternative translation initiation using RNA-seq data 2) Developing new approaches to gene prediction to improve annotation of complex genomes 3) Comparative analysis of conifer specific gene families

REQUIREMENTS:

Ph.D in Genetics, Evolutionary Biology, Bioinformatics, Computational Biology, or other related field.

Track record of publications in comparative genomics.

Programming skills in Python, Perl, Java, C++, R or other language.

Experience with Linux and high performance computing environments.

Demonstrated ability in developing/applying statistical or machine learning methods in computational biology.

Experience in genome scale data analysis including RNA-Seq data, network analysis, biological sequence analysis or other relevant computational genomics experience.

Highly motivated for interdisciplinary research, excellent communication skills, and the ability to work independently as well as within a research group.

HOW TO APPLY:

Initial appointment is one year, with possible extension. Interested applicants should send their C.V., research statement, available start date, and contact information for three references to jill.wegrzyn@uconn.edu.

jillylee@gmail.com

UFlorida AppliedEvolutionaryPhysiology

A postdoctoral position in applied ecological and evolutionary stress physiology is available in Dan Hahn's lab at the University of Florida.

Our work takes a vertically integrated approach to understanding both the plastic mechanisms that organisms use to rapidly respond to environmental perturbation, and the consequences of this rapid physiological plasticity for organismal performance from evolutionary and applied perspectives.

The initial appointment will be for 2 years starting as early as summer 2015, with extension for additional years based on performance. The postdoctoral associate is expected to spend 2/3-3/4 of their time on a project centered around understanding how exposure to hypoxic and/or hypercapnic atmospheres can alter the physiology of insects to promote cross-resistance to other stressors (i.e., hormesis). The remaining 1/3-1/4 of time will be available for other creative activities related to the postdoctoral associates interests, particularly if they pertain to other projects in our lab group (see Additional Projects Section below).

The Main Project: Exposure to low-oxygen environments can be damaging in the long term, but many insects are highly resistant to short-term exposures to hypoxia and hypercapnia. In fact, short term exposures to modified atmospheres can promote cross-tolerance to other stressors, including oxidative stressors. Here we will investigate how exposure to modified atmospheres can affect insect physiology to impart resistance to irradiation stress (from gamma sources or x-rays). Specifically, the postdoc will: 1) study the effects of modified atmospheres on irradiation tolerance on several insect pests, 2) investigate the fundamental physiological mechanisms that are associated with enhanced resistance to irradiation stress, and 3) use this knowledge in a physiologically guided approach to developing biomarkers for irradiation stress and resistance. Applications for this work include expanding the use of low-dose irradiation as an alternative to chemical pesticides to prevent the movement of insect pests in fresh fruits and vegetables. This work is a recent area of inquiry in our lab that has implications for both our basic understanding of ecological and evolutionary physiology and applications to agriculture and international trade. Although we have not published much in this area yet, two related papers from our lab on irradiation biology in the context of sexual selection and biological control by the sterile insect technique and one general review of irradiation as a phytosanitary treatment are listed below.

Lopez-Martinez, G., and D.A. Hahn. 2012 Short-term anoxic conditioning hormesis boosts antioxidant defenses, lowers oxidative damage following irradiation, and enhances male sexual performance in the Caribbean fruit fly, Anastrepha suspensa. Journal of Experimental Biology, 215:2150-2161.

Lopez-Martinez, G. and D.A. Hahn. 2014. Early-life hormetic treatments decrease irradiation-induced oxidative damage, increase longevity, and enhance sexual performance during old age in the Caribbean fruit fly. PLoS One 9(1): e88128. doi:10.1371/journal.pone.0088128

Hallman, G.J., N.M. Brilz, L.J. Zettler, and I.C Winborne. 2010. Factors affecting ionizing radiation phytosanitary treatments, and implications for research and generic treatments. Journal of Economic Entomology. 103:1950-1963.

The postdoctoral fellow must be interested in working at the boundary between basic and applied sciences and must be interested in working in a multidisciplinary and collaborative atmosphere. Knowledge of physiology, respirometry, biochemistry, multivariate data analysis, and high-throughput screening, or strong interest in learning these techniques is needed. International applicants are encouraged to apply, but a strong command of spoken English is a must for this position in addition to demonstrating the ability to effectively write peer-reviewed manuscripts in English.

The Setting: The University of Florida is located in Gainesville and offers a rich scientific community for evolution, ecology, physiology/cell biology, and genomics that spans many departments including Entomology and Nematology (the academic home for this appointment), Biology, Wildlife, Forestry, the Genomics Institute, the US Department of Agriculture, and the College of Medicine. Our lab currently includes 3 postdoctoral associates, 3 PhD students, and 9 undergraduates with which you would interact daily. There will be substantial opportunities for interdisciplinary training across units at our institution and within our network of collaborators, as well as additional training opportunities in teaching/instruction and scientific outreach to the public. Our group has an excellent record of career development with former postdocs and students placed in tenure-track academic positions, biotech industry positions, and government science. We strongly recognize the value

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UHeidelberg BioinformaticsGenomics

BIOINFORMATICS POSTDOC IN FUNCTIONAL 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, preferably also with experience in data mining and comparative or evolutionary genome analyses.

We have been interested in a range of topics related to the functional evolution of genomes across mammals. In the framework of our research, we are generating comprehensive sets of RNA-seq data for a large collection of germline and somatic tissues from representatives of all major mammalian lineages (placental mammals, marsupials, and the egg-laying monotremes) and evolutionary outgroups (e.g., birds). In conjunction with various high-throughput genomic and epigenomic datasets, we are using these transcriptome data to study the functional (expression) evolution of mammalian genomes across gene types, lineages, tissues, developmental stages, chromosomes and sexes.

The postdoctoral fellow will perform integrated evolutionary/bioinformatics analyses based on data produced in our lab and available genomic data. The specific project will be developed together with the candidate.

The language of the institute is English, and its members form a highly international group. The ZMBH is located in Heidelberg, a beautiful international city next to the Odenwald forest and Neckar river.

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/) and also our website at the University of Lausanne (Switzerland, http://www.unil.ch/cig/kaessmann), where our lab is currently located (before moving to Heidelberg October 1, 2015).

Please submit a CV, statement of research interest, and names of three references to: Henrik Kaessmann (h.kaessmann@zmbh.uni-heidelberg.de or Henrik.Kaessmann@unil.ch).

– Henrik Kaessmann, Ph.D. Full Professor ZMBH Im Neuenheimer Feld 282 69120 Heidelberg, Germany

Selected recent publications:

Cortez, D., Marin, R., Toledo-Flores, D., Froidevaux, L., Liechti, A., Waters, P.D., Grützner, F., and Kaessmann, H. (2014) Origins and functional evolution of Y chromosomes across mammals. Nature 508: 488-493.

Necsulea, A., Soumillon, M., Warnefors, M., Liechti, A., Daish, T., Zeller, U., Baker, J.C., Grützner, F., and Kaessmann, H. (2014) The evolution of lncRNA repertoires and expression patterns in tetrapods. Nature 505: 635-640.

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., Schütz, F., Daish, T., Grützner, F., and Kaessmann, H. (2012) Mechanisms and evolutionary patterns of mammalian and avian dosage compensation PLoS Biol. 5:e1001328.

Brawand, D., Soumillon, M., Necsulea, A., Julien, P., Csárdi, G., Harrigan, P., Weier, M., Liechti, A., Aximu-Petri, A., Kircher, M., Albert, F.W., Zeller, U., Khaitovich, P., Grützner, F., Bergmann, S., Nielsen, R., Pääbo, S., and Kaessmann, H. (2011) The evolution of gene expression levels in mammalian organs. Nature 478: 343-348.

Henrik.Kaessmann@unil.ch

UMemphis BeetlePhylogenomics

A 2-year postdoctoral research fellowship is available in the lab of Dr. Duane McKenna (University of Memphis) to participate in a variety of highly collaborative projects related to the phylogeny and evolution of beetles and beetle genomes.

The successful candidate will work with collaborators to establish a bioinformatic pipeline for the NSF-funded 1K Weevils Project (anchored phylogenomics, comparative genomics), analyze beetle data in association with the 1KITE Beetle Subproject (phylogenomics, transcriptomes), and contribute to beetle genome and comparative genomics projects in the McKenna Lab, e.g., in collaboration with the Insect 5000 Genomes Project. These are primarily bioinformatics, phylogenomics, and comparative genomics projects involving extensive analysis of genome- and transcriptome-scale data sets. The position is based at the University of Memphis, but includes opportunities for travel to work with collaborators. The initial appointment is for one year, renewable for one additional year provided the first year review shows satisfactory progress. The position offers a competitive salary plus benefits. Start date is flexible, though interested individuals are encouraged to apply immediately. Review of applications will begin on February 9, 2015; however applicants will be considered until the position is filled.

Required Qualifications:

- A Ph.D. in computational biology, evolutionary genetics/genomics, phylogenomics, bioinformatics, or a related field. Advanced ABDs may be considered if degree completion is imminent - Experience with manipulating and analyzing genomic and transcriptomic NGS sequence data - A strong record of prior publication in genome-scale data analysis, including bioinformatics pipeline construction, phylogenomics, and/or genome structure and evolution - Strong communication and interpersonal skills, including a proven ability to work both independently and as part of a team

Desired Qualifications: (Ideal applicant; applicants without these skills will be considered)

- Proficiency in computer programming - Experience working with arthropods (especially insects) - Experience with standard molecular laboratory techniques - Experience with the analysis of traditional molecular phylogenetic data sets

The successful applicant will be expected to work/collaborate with another postdoc and with graduate students in the McKenna Lab.

To apply, submit a cover letter stating your research accomplishments and interests, qualifications relevant to the position (especially in reference to the required and desired qualifications listed above), a curriculum vitae, two representative publications, and the names and contact information for three references (submit at: http://workforum.memphis.edu/postings/8680). Inquiries about the position may be directed to Duane McKenna (dmckenna@memphis.edu).

Duane D. McKenna Ph.D. Assistant Professor Department of Biological Sciences Associate, Program in Bioinformatics Associate, W. Harry Feinstone Center for Genomic Research University of Memphis 3774 Walker Avenue Memphis, TN 38152

phone: (901) 678-1386 email: dmckenna@memphis.edu website: https://umdrive.memphis.edu/dmckenna/-public/index.html "Duane McKenna (dmckenna)" <dmckenna@memphis.edu>

UMichigan Herpetology

Postdoctoral position in the ecology, evolution, and systematics of squamate reptiles

A two year postdoctoral research position is available in the Rabosky Lab at the University of Michigan. Multiple projects are available, including:

(1) Comparative evolutionary ecology of squamate reptile communities, particularly Australia, the southwestern United States, and the Neotropics. This project will potentially involve field studies of squamates and the collection of ecological and phenotypic data from a broad range of species in some of the world's most species-rich squamate communities. We are particularly interested in novel and innovative approaches to acquiring ecological data about a broad range of difficult-to-observe and/or rare species (e.g., many snakes). Such approaches potentially include stable isotope ecology, remote sensing, radio/satellite telemetry, and population genomics.

(2) Systematics of Australian skinks: phylogenetics, species delimitation/discovery, and taxonomy.

(3) Comparative analyses of macroevolutionary dynam-

ics (speciation, extinction, and phenotypic evolution) across evolutionary radiations of squamate reptiles, to understand how and why major squamate lineages vary in species richness and morphological / ecological diversity. Expertise in computational biology and/or assembly of large ecological, morphometric, or phylogenetic datasets is desirable.

(4) Speciation and biogeography in Australian squamates, particularly from arid and semi-arid regions of the continent. This project requires experience with the generation and analysis of high- throughput DNA sequence data (e.g., RADseq).

The ideal candidate will have a keen interest in the ecology and evolution of squamate reptiles and skills compatible with one or more of the projects outlined above. A strong publication record relevant to one of the areas listed above is essential. The position offers exceptional opportunities for independent research, career development, and quantitative skills training.

Applications should be sent to drabosky at umich.edu. Please include a detailed cover letter describing your research interests and background, a C.V., and contact information for three references. Review of applications will begin on March 9, 2015 and will continue until the position is filled. Any questions about the position can be directed to Dan Rabosky (http://www.lsa.umich.edu/eeb/people/faculty/-ci.raboskydaniel_ci.detail).

Dan Rabosky Assistant Professor & Curator of Herpetology Museum of Zoology & Department of Ecology and Evolutionary Biology University of Michigan Ann Arbor, MI 48109-1079 USA

drabosky@umich.edu http://www-personal.umich.edu/-˜ drabosky http://www.lsa.umich.edu/ummz/ drabosky@umich.edu

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UMinnesota ComputationalMicrobialEvolution

Postdoctoral Position Metabolic modeling of microbial species interactions

BioTechnology Institute/Department of Ecology, Evolution and Behavior

University of Minnesota

The Harcombe lab invites applicants for a postdoctoral position to develop computational approaches to quantitatively predict the dynamics of microbial communities. We use genome-scale metabolic models to investigate the mechanistic basis of social interactions and Eco-Evolutionary processes (see PMID 24794435). We strive to connect intracellular metabolism to emergent community behavior in systems ranging from simple communities that have been engineered in the lab, to complex communities associated with pathogen suppression in agricultural soils. We are particularly interested in improving ability to simulate the evolutionary dynamics that arise from antibiotic production in spatially structured environments.

We are seeking motivated candidates that are interested in connecting microbial physiology to evolutionary ecology. Candidates should have experience with Matlab, Python, and Java. Previous work with constraint-based modeling of metabolic networks, microbiology, and evolutionary ecology are beneficial. Candidates should be comfortable interacting with computational biologists, microbiologists and evolutionary ecologists.

Please submit a CV and cover letter with references by March 1. The initial appointment will be for one year, with the option for extension. Candidates should have a PhD (or be close to completion) in a relevant field, and have a demonstrated record of productivity. The University of Minnesota is an equal opportunity employer.

For further details please contact William Harcombe (harcombe at umn dot edu).

harcombe@umn.edu

UNebraska Lincoln POEFellowPopulationBiology

POPULATION BIOLOGY POSTDOCTORAL RESEARCH FELLOWSHIP

THE UNIVERSITY OF NEBRASKA-LINCOLN is seeking applications for a 2-year postdoctoral position in the Population Biology Program of Excellence.

The goal of the Population Biology-POE Postdoctoral Fellowship is to stimulate synergistic interactions between faculty and postdoctoral scholars interested in the broad area of Population Biology. Qualified candidates are required to develop a single, coherent 2-year research project under the guidance of two or more faculty advisors, one of whom must be in the Ecology, Evolution & Behavior (EEB) section in the School of Biological

Sciences (http://biosci.unl.edu/research-specializations). The second advisor may be in the School of Biological Sciences (including EEB), the Institute of Agriculture and Natural Resources (ianrhome.unl.edu/colleges), Mathematics (http://www.math.unl.edu) or in another UNL department. While in residence, the postdoctoral fellow will be expected to teach a graduate seminar on a topic of his/her choice (Year 1), and to help organize a local symposium (Year 2). Applications must include a CV, a 1-page description of previous or current research and a 2- 3 page description of proposed research as well as a brief description of possible seminar and symposium topics. In addition, the applicant must arrange for two recommendation letters from non-UNL faculty, and one from each of the proposed UNL faculty sponsors (a total of 4 letters) to be emailed to the address below. The expected salary will be $45,000. The position does not include research funds so it is anticipated that these needs, if modest, can be met through contributions from the faculty sponsors and should be addressed in the proposal.

Application materials should be emailed to: Dr. Gwen Bachman at: gbachman1@unl.edu. The subject line should read 'Population Biology Post-doc application'. Applications should be received by 15 April 2015 in order to ensure full consideration. We strongly encourage applications from women and members of minority groups. The University of Nebraska is committed to a pluralistic campus community through affirmative action, equal opportunity, work-life balance, and dual careers. We assure responsible accommodation under the Americans with Disabilities Act.

Kristi Montooth Associate Professor of Biology University of Nebraska kmontooth2@unl.edu

Kristi Montooth <kmontooth2@unl.edu>

UNewEngland Australia PlantSpeciationGenomics

Postdoctoral Research Fellow (Plant Speciation Genomics)

We are seeking a highly motivated postdoctoral researcher to fill an ARC Discovery-funded postdoctoral position. The project will involve whole-genome shotgun sequencing of many individuals across 10 woodland Eucalyptus species. This widespread genus of Australian trees includes several hybridising species that co-occur in woodlands across large portions of Eastern Australia, offering an unusual degree of replication for studying comparative landscape genomics and the role of interspecific gene flow in local adaptation. A second aim of the project is landscape genomic association studies on thousands of trees to identify environmentally adaptive loci. A third aim will be to validate adaptive loci segregating in hybrid progeny by growing seedlings in climate chambers phenotyping stress response with plant phenomics.

To be considered for this position applicants must have a PhD in Evolutionary Genetics, Genomics or a related area, with an excellent research record relative to opportunity, including articles in high quality, peer-reviewed journals. In addition the successful applicant will have research experience in population genomics, admixture analysis and/or landscape genomics.

This is a full-time fixed-term position available for 2 years, with the possibility of further appointment, subject to the availability of funding. The successful candidate will be expected to participate actively in the School and to interact with undergraduate and postgraduate students in the research group. The research fellow will join Dr Rose Andrew's research group at UNE, which conducts genome-enabled research on adaptation and speciation in a range of organisms (e.g. orchids, sunflowers, feral cats). This project is a collaboration with Professor Justin Borevitz at the Australian National University, who specialises in plant genomics for climate adaptation and high-throughput phenotyping.

Informal enquiries may be directed to Dr Rose Andrew, phone: +61 2 6773 3160 or email rose.andrew@une.edu.au. To find out more about the school visit: https://www.une.edu.au/about-une/-academic-schools/school-of-environmental-and-rural-science About UNE and Armidale: The University of New England, as Australia's oldest regional university, has a long history of excellence in research across many major fields of study, including Ecology and Botany. The School of Environmental and Rural Science is home to the N.C.W. Beadle Herbarium and has strengths in animal and plant genetics, and evolutionary biology. Armidale a vibrant university city recognized as a centre fo culture, is well served with art, music, theatre, sport and public and private education. To explore our region visit: www.armidaleregion.com.au/ and/or www.experiencethehighs.com.au/ * 2 years fixed-term, full-time * $75,717 Salary to $81,196 Salary per annum (Level A) * Plus up to 17% employer superannuation contribution. Optional salary packaging is available.

Closing Date: 15 March 2015 Reference No: 215020 Applicants must provide a response to each of the selection criteria contained in the position statement at www.un.edu.au/jobs-at-une, where applications are also to be lodged. Equity principles underpin all UNE policies and procedures.

Dr Rose Andrew Lecturer in Molecular Ecology School of Environmental and Rural Science University of New England Armidale, NSW, 2351 AUSTRALIA Ph: +61 2 6773 3160 rose.andrew@une.edu.au http://www.une.edu.au/staff-profiles/randre20 https://sites.google.com/site/roseandrewresearch/

randre20@une.edu.au

UOregon MicrobialEcologyEvolution

Postdoctoral Research Scholar Institute of Ecology and Evolution Posting: 14431 Location: Eugene Closes: Open Until Filled

Revised Posting

Postdoctoral Position in Microbial Ecology and Evolution

Jessica Green at the University of Oregon (http://pages.uoregon.edu/green/) is currently seeking a postdoctoral researcher to collaborate on the Seagrass Microbiome Project (http://seagrassmicrobiome.org). Applicants should have a Ph.D. in a biological, computational, mathematical, or statistical field and strong writing skills. The ideal candidate will have experience developing and applying models to understand the ecology, evolution, and/or function of complex systems. Experience in the analysis of environmental sequence data is highly desirable, but not required.

The successful candidate will have the opportunity to creatively and independently tackle one or more of the science questions outlined in the Seagrass Microbiome Project grant proposal (http://seagrassmicrobiome.org/2014-grant-proposal/), funded by the Gordon and Betty Moore Foundation. The successful candidate will interact regularly with team members Jonathan Eisen (http://phylogenomics.wordpress.com), Jay Stachowicz http://www-eve.ucdavis.edu/stachowicz/stachowicz.shtml, and Jenna Lang (http://jennomics.com/) at the University of California, Davis through weekly tele-conferencing and also through regular visits to the UC Davis campus. At the University of Oregon, the candidate will benefit from ongoing microbiome research programs including the Microbial Ecology and Theory of Animals Center for Systems Biology (http://meta.uoregon.edu/) and the Biology and Built Environment Center (http://biobe.uoregon.edu/).

The position is available for 1 year with the possibility for renewal depending on performance. The start date is flexible. Please email questions regarding the position to Jessica Green (jlgreen@uoregon.edu).

To apply

A complete application will consist of the following materials:

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

(2) CV (including publications)

(3) names and contact information for three references

Submit materials to ie2jobs@uoregon.edu. Subject: Posting 14431

To ensure consideration, please submit applications by March 10, 2015, but the position will remain open until filled.

Women and minorities encouraged to apply. We invite applications from qualified candidates who share our commitment to diversity.

The University of Oregon is an equal opportunity, affirmative action institution committed to cultural diversity and compliance with the ADA. The University encourages all qualified individuals to apply, and does not discriminate on the basis of any protected status, including veteran and disability status.

– 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

UOulu Bioarcheologal

The Faculty of Humanities of the University of Oulu, Finland, announces a three-year Postdoctoral Researcher Position in bioarcheological research community to start at the beginning of May, 2015.

Description

Bioarchaeological research community (BARC) at University of Oulu, Finland, is looking for a talented and research-oriented postdoctoral researcher. This position is for three years. The postdoctoral researcher is expected to make a contribution to multidisciplinary research of this research community by bringing in expertise in at least one of its areas of research.

This research community was rated as outstanding (6/6) in the most recent research assessment exercise at the University of Oulu in the category on the threshold of international breakthrough in 2013. It examines the effects of environmental and cultural changes on both humans and animals in northern Europe focusing on Finland and neighboring regions. The effects of neolithization, modernization and urbanization are under particularly close scrutiny. The main study materials include archaeological materials (biological and non-biological materials), museum collections and clinical samples. A broad range of methods and techniques are thus utilized from those used in archaeological and historical research to those used in bone imaging and biomolecular research. Due to this multidisciplinary research, this research community includes four research teams divided between three faculties. The four research teams are as follows:

The Post-Pleistocene Evolution of Human Skeleton (Docent Markku Niskanen, Archaeology, Faculty of Humanities) utilizes osteometric and bone imaging techniques to examine temporal and geographic variation in human body size, body shape and skeletal robusticity and how these are related to environmental and cultural changes. Bioarchaeology of human-animal interactions: biomolecular and osteoarchaeological analyses of human and animal bones (Prof. Jouni Aspi, Biology, Faculty of Science) explores human-animal relationships (e.g. domestication) through ancient DNA (aDNA), stable isotope and osteological analyses. Material culture and the modernization of the north (Dr. Timo Ylimaunu, Archaeology, Faculty of Humanities) examines the development of society from the medieval period to the present. The focus is on examining the dynamics of modernization, globalization and consumption processes and human-environmental relationship in Northern Fennoscandia as a part of the globalizing world. Human Biology and Comparative Anatomy (Prof. Juha Tuukkanen, Anatomy and Cell Biology, Faculty of Medicine) concentrates on functional relationship in morphology between temporally distinct populations. The main research focus is temporal trends in overall skeletal morphology, bone microstructure and biomechanical properties.

The postdoctoral researcher is expected to carry out research and participate in publishing research results in peer-reviewed journals. Some teaching and/or administrative duties may be included, but would take 10% of the working hours at the maximum. It is our hope that this position would help the postdoctoral researcher to develop his/her own scientific networks through research collaboration, and that this position would be a step towards a position as a more senior and independent researcher able to develop his/her own projects.

This position is officially based at the Faculty of Humanities, University of Oulu, Finland. In practice, the postdoctoral researcher will work in facilities, which best suit his/her actual work for this research community.

Qualifications

The candidates research should interface with research conducted in one or more of the four research teams. He/she must have earned his/her doctorate no more than seven years before the application deadline. This doctoral degree should be in archaeology (including historical archaeology, osteoarchaeology, biomolecular archaeology), biological anthropology, biology, biomedicine or a related field. In addition, he/she should have a record of scientific achievements (e.g. peer-review publications). International mobility and experience of teaching and/or academic supervision are advantages. In addition, we appreciate ability for independent research, high motivation and efficiency, as well as ability to co-operate and work as a research team member.

We are primarily (but not exclusively) searching for a researcher, who is familiar with bioinformatics and computational genomics. Previous experience in handling NGS data using scripts and analysis pipelines is desirable. Other highly useful skills and/or experiences include computer programming, population genetics, wet lab analysis, genome assembly and annotation, and/or paleodietary studies (e.g. stable isotope analyses).

Representatives of other fields of research (general archaeology, historical archaeology, osteoarchaeology, etc.) are, however, strongly

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UOulu PopulationStatisticalGenomics

Post doc in population and statistical genomics at the University of Oulu

Post doctoral position for two years available in the Population and statistical genomics (PSG) research team http://www.oulu.fi/popstatgen at the University of Oulu, in the Genetics and Physiology unit.

The team consists of five different research groups, dealing with genomics of adaptation of plant populations (Outi.Savolainen at oulu.fi), with conservation genetics of especially large carnivores (Jouni.Aspi at oulu.fi), of statistical genomics, especially variable selection methods (Mikko.Sillanpaa at oulu.fi), systematics and evolutionary genetics of Lepidoptera and of social insects (Marko.Mutanen at oulu.fi) and human cancer functional genomics (Gonghong.Wei at oulu.fi).

The post doc will be associated with one of these groups to conduct research on topics studied in the group. Some 10-20 % of the time will be allocated to shared interests of the whole team. We seek a highly motivated Ph.D. with interest in the topics represented by the groups, expertise in population genomics and bioinformatics and international experience. The position will be based on the Linnanmaa campus, where all groups except for the cancer biology group are based. Applications should include a letter describing your interest, your CV and list of publications, and names of three possible persons to ask for letters of reference. All the materials should be submitted as one single pdf to kirjaamo@oulu.fi, by March 23rd, 2015.

For the official announcement, please see https://www.saimanet.com/certiahome/open_job_view.html?did=5600&jc=1&id=0000863&lang=en . For information, please be in touch with Outi.Savolainen@oulu.fi and/or the other PIs.

Outi Savolainen <Outi.Savolainen@oulu.fi>

UPM Spain PlantVirusCoevolution

*_POSTDOCTORAL POSITION AVAILABLE_*

In *Plant-Virus Interaction and Co-Evolution*

*_Research topics_*: The long-term goal of the group is to understand*the evolution of plant-virus interactions*. Within this broad field of research the post-doctoral scientist to be recruited will participate in defining a specific programme of research on the*Evolutionary Ecology of Virus Emergence, specifically on how ecosystem simplification affects infection patterns, host range evolution and virulence of multihost plant viruses.*

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*_Period_*: Two years starting any time from now.

*_Conditions_*: Contract conditions will be equivalent to those of the Spanish “Juan de la Cierva” Postdoctoral Programme.

(http://www.idi.mineco.gob.es/portal/site/MICINN/menuitem.dbc68b34d11ccbd5d52ffeb801432ea0/?vgnextoid=bf96e5b0a21f9410VgnVCM1000001d04140aRCRD&vgnext
67a04939e6b42410VgnVCM1000001d04140aRCRD)

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*_Requisites_*: Experience in evolutionary biology of host-parasite interactions or/and virus evolution or/and plant evolutionary ecology or/and population genetics of plants.

INTERESTED CANDIDATES PLEASE CONTACT

Prof. *FERNANDO GARCÍA-ARENAL *fernando.garciaarenal@upm.es

BEFORE *FEBRUARY 28^th * 2015

For further information about the group: http://www.cbgp.upm.es/plant_virus.php *__*

*_Recent publications of the group related to the above-specified topics:_***

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Fraile A. /et al/. (2011). Rapid genetic diversification and high fitness penalties associated with pathogenicity evolution in a plant virus*. /Molecular Biology and Evolution/*/./ 28: 1425-1437.

Pagán I. /et al./ (2012). Effect of biodiversity changes on disease risk: Exploring disease emergence in a plant-virus system. */PLoS Pathogens/ *8:e1002796.

Rodelo-Urrego M. /et al. /(2013). Landscape heterogeneity shapes host-parasite interactions and results in apparent plant-virus co-divergence. */Molecular Ecolog/**/y/*22: 2325 -2340.

García-Arenal F. & Fraile A. (2013). Trade-offs in host range evolution of plant viruses. */Plant Pathology/*62 - S1: 2 - 9.

Betancourt M. /et al./ (2013). Virulence evolution of a generalist plant virus in a heterogeneous host system*/. /**/Evolutionary Applications/*6: 875 - 890

Elena S.F. /et al./ (2014). Evolution and emergence of plant viruses. */Advances in Virus Research/*88: 162 - 191.

Fraile A. /et al/ (2014). Host resistance selects for traits unrelated to pathogenicity that affect fitness in a plant virus. */Molecular Biology and Evo/**/lution/*31: 928 - 939.

Pagán I. /et al/. (2014). Vertical transmission selects for reduced virulence in a plant virus and for increased resistance in the host. */PLoS Pathogens/* 10: e1004293.

Hily J. M. /et al/. (2014). The relationship between host lifespan and pathogen reservoir potential: An analysis in the system /Arabidopsis thaliana-Cucumber mosaic virus/. */PLoS Pathog/ens *10: e1004492.

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*For additional information on CBGP, please visit **http://www.cbgp.upm*** fernando garcia arenal <fernando.garciaarenal@upm.es>

Uppsala Sweden PlantGenetics

Dear colleagues,

We have a vacant Postdoc stipend in plant genetics and genomics with particular focus on sex chromosome turnover in willows

Where: Department of Plant Biology, Swedish University of Agricultural Sciences, Uppsala, Sweden

Project description: We are looking for a postdoc that will work with research on the genetics of sex determination and sex chromosome turnover in willows (Salix; Salicaceae). Species in this family can be dioecious with male and female flowers on different individuals and among these species different sex determination mechanisms have evolved. The main task for the postdoc is to study sex determination mechanisms in willows to learn about the rate of sex chromosome turnover in the Salix genus. We are mainly working with the basket willow Salix viminalis for which we have several mapping populations, an association mapping population, a draft genome sequence assembly, RNA-seq data from several individuals and tissues and genotyping-by-sequence data both from one mapping population and the association mapping population. The postdoc will have access to all these resources. Duties include genome wide association mapping, RNA-seq analyses, work with whole genome sequence data, PCR amplification of sex linked markers and RNA and DNA-extractions. However, as there are different ways to study these issues and we would be happy to design the specific subprojects to match the skills and interests of the successful candidate.

Qualifications: We are looking for a highly motivated candidate with a PhD degree in evolutionary genetics, population genetics, genomics, bioinformatics or in similar subjects. Documented scientific qualifications within the research field are required. Good collaborative skills are necessary. The applicant should have the ability to work independently, to take own initiatives and to have a strong interest in producing high quality research and writing scientific publications. The ranking of the candidates will be based on the proven scientific competence within the research area of the position.

Type of employment: Postdoc stipend, one year with (excellent) possibility to extend up to two years.

Employment: Full time (100 %)

How to apply: The application should include: 1) description of previous and current research interests especially in evolutionary genetics, genomics and bioinformatics (1-2 pages) 2) CV including list of publications 3) a copy of your PhD-degree diploma 4) names and contact details (address, email address and phone number) to at least two reference persons. The application should be written in English.

Starting date as soon as possible or as agreed upon.

For further information contact: Sofia Berlin Kolm sofia.berlin@slu.se +4618673375.

We welcome your application marked with Ref no. SLU ua SLU ua 319/2015. Please submit your application to the Registrar of SLU, P.O. Box 7070, SE-750 07 Uppsala, Sweden or registrator@slu.se no later than March 2, 2015.

The ad can also be found at: http://www.slu.se/sv/om-slu/fristaende-sidor/aktuellt/lediga-tjanster/las-mer/-?eng=1&Pid=1757 Kind regards, Sofia

Sofia Berlin Kolm, Associate Professor Department of Plant Biology Uppsala BioCenter, SLU, Box 7080, S-750

07 UPPSALA, SWEDEN

Phone: +46-18 67 33 75 E-mail: sofia.berlin@slu.se

Sofia Berlin Kolm <Sofia.Berlin@slu.se>

UppsalaU ComputationalMolecularEvolution

Investigating insertion and deletion in genomic inference — A post-doctoral fellowship in molecular evolution is available working with Simon Whelan at Uppsala University, Sweden. The postdoc will join a project working on the development and application of phylogenetic methods for studying insertion and deletion both within protein families and on the genome scale.

The project has two broad aims. The first is to apply probabilistic methods weve been developing for studying insertion and deletion rates from aligned or unaligned sets of sequences. We will use these estimated rates to study how patterns of insertion and deletion vary through the genome, both in genes and intergenic DNA, and how evolutionary forces affect these fundamental processes. The second aim of the project is to use this acquired knowledge of insertion and deletion to filter or rearrange multiple sequence alignments to better reflect the true homologous relationships between bases or residues. These approaches will be assessed through their ability to correctly estimate sequence divergence, natural selection and phylogeny using both empirical and simulation data sets. There is also the possibility for the fellow to develop their own research interests, providing they fit within the broad scope of the project outlined above.

The fellowship will be located at the Evolutionary Biology department at the Evolutionary Biology Centre (EBC), Uppsala, Sweden. Uppsala is a leading centre for evolution and ecology research, with a large number of research groups in the subject area. The Evolutionary Biology department (http://www.ebc.uu.se/Research/IEG/evbiol/?languageId=1) is a diverse and multicultural department, with interests both computational- and laboratory-based research groups working on evolutionary genomics, speciation, population genetics and phylogenetics. The fellowship will be supported by the Carl Tryggers Stiftelse (CTS) and will be initially for one year, with the possibility of extending for an additional year. Details of this fellowship are available (in Swedish; Google Translate works reasonable well) at http://www.carltryggersstiftelse.se/ and CTS make the final appointment of the fellow based on the conditions outlined there. The fellowship would be expected to start as soon as possible after the beginning of April'15. If you have any questions regarding the research project or anything else about the fellowship please contact me.

Please send your application to simon.whelan@ebc.uu.se in a single pdf file containing the following information:

* Cover letter; * CV, including publication record; * A brief statement (max. 2 page) outlining your research interests, experience, and ambitions; and * Contact information (name/address/phone/e-mail) for 2-3 referees.

The recruitment will be ongoing until a suitable candidate is found, with the first round of decisions being made around March 1st.

Regards,

Simon Whelan

Simon Whelan | Evolutionary Biology Centre, Uppsala University T: +46-(0)18-4716483

simon.whelan@ebc.uu.se

UPretoria LifeHistoryEvolution

POST-DOCTORAL PROJECT AVAILABLE: TELOMERE SHORTENING IN RELATION TO LIFE HISTORY CHANGES

Funding is available to test the prediction that longevity in flies is associated with patterns of reproductive effort, and that these patterns are linked to evolutionary history and the cellular processes that may underpin ageing.

Key to the project are selection lines that we have already established. We select for age of reproduction by permitting female marula flies, Ceratitis cosyra, to lay eggs into artificial oviposition substrates at different ages. Selection will continue for at least 20 generations before testing for differences in nutrient intake and ageing mechanisms, but longevity and reproductive effort is determined intermittently as the selection regime progresses.

We are seeking a Post-Doctoral Researcher to coordinate the maintenance of the selection lines central to this project, to test how accumulation of oxidative damage and telomere shortening affects ageing and reproduction in this species, and to assist with training postgraduate students.

We have secured funding for the Post-Doctoral Researcher to be trained to assay telomere length and oxidative damage by Dr Jon Blount at the University of Exeter in the UK, as well as attendance of local and international scientific meetings. However, the successful candidate will now need to apply for a UP Postdoctoral Fellowship to fund living expenses in South Africa (R150000/year for two years plus once-off relocation allowance). The successful candidate will be assisted to develop a strong application.

Minimum requirements - A PhD in Biochemistry, Biological Sciences, Entomology, Genetics, or Zoology - A record of publication in international, ISI-listed journals - Proven track record of collaborative research - Commitment to accuracy and ethical research behaviour - Experience in the use of appropriate statistical analyses - Excellent written and oral communication skills in academic English

A background in ageing research, biochemical analyses, molecular genetics, or working with insect models are all highly advantageous.

All interested persons that meet the minimum requirements are encouraged to apply. Applications must include an application letter that provides evidence for the minimum requirements for the position, a CV with the names and contact details of two academic referees including the PhD supervisor, and copies of academic transcripts that indicate eligibility for the award of a PhD degree.

The Post-Doctoral Researcher will be based in the Department of Zoology and Entomology on the Hatfield Campus of the University of Pretoria, and mentored by Dr. Chris Weldon, Dr Ruth Archer (Max Planck Institute for Demographic Research, Rostock, Germany), Dr. Jon Blount (University of Exeter), and Prof. Sue Nicolson.

Queries and written applications should be directed by email to Dr. Chris Weldon (cwweldon@zoology.up.ac.za).

Applications close: 30 March 2015

Dr. Chris Weldon Senior Lecturer - Entomology

FliES | Flies of Economic Significance Research Group Department of Zoology and Entomology University of Pretoria Private Bag X20 Hatfield 0083 South Africa

http://www.up.ac.za/zoology/?q=user/156/research http://sites.google.com/site/cwweldon/ Chris Weldon <cwweldon@zoology.up.ac.za>

UQueensland Australia AlgalGenomicsBioinformatics

** Research Officer / Senior Research Officer **

A postdoctoral research-focused position is available at the University of Queensland, Brisbane, Australia. The University of Queensland's Institute for Molecular Bioscience is a leading global research institute. IMB was established in 2000 as UQ's first research institute and is the cornerstone of one of the largest bioscience research precincts in Australia.

This position is created within a Discovery Projects grant funded by the Australian Research Council to understand the evolutionary transition of the dinoflagellate algae Symbiodinium to coral reef symbiont. Coral reefs are sustained by symbiosis between Symbiodinium and the coral host, and breakdown of this symbiosis under environmental stress results in coral bleaching and eventual death. Through genome sequencing of eight Symbiodinium isolates from reef corals plus two free-living relatives, the Project aims to identify genes that have been gained, lost or shared, or are under adaptive selection, along the trajectory from free-living forms to symbionts.

The person appointed to this position will be responsible for assembly, analysis and interpretation of genome-scale sequence data from Symbiodinium and related species within the Discovery Project. The successful applicant will collaborate as appropriate in the identification of potential genomic signatures of symbiosis and adaptive selection. There are opportunities to address individually-developed and collaboratively-generated research questions, and to supervise honours, masters and/or doctoral students.

This is a full-time, fixed term appointment for 2 years (with the possibility of renewal pending funding) at Academic Research Level A or B. The level of appointment will be commensurate with the successful applicant's qualifications and experience.

For Level A, the remuneration package will be in the range AUD 76864 - 82510 per annum, plus employer superannuation contributions of up to 17% (total package AUD 89930 - 96536 per annum).

For Level B, the remuneration package will be in the range AUD 86853 - 103138 per annum, plus employer superannuation contributions of up to 17% (total package

AUD 101618 - 120671 per annum).

Applicants should possess a PhD in molecular biology, microbiology, marine biology, genomics, bioinformatics or a related discipline, with significant data-management, computational and statistical components. He or she should have at least three years' full-time experience (during the PhD and/or otherwise), or its equivalent, in a relevant area of molecular biology, microbiology, genomics, bioinformatics or a related field. Experience in scientific programming and/or scripting and familiarity with working under UNIX environment are essential. Applicants should also have excellent knowledge of a modern scripting language and Bayesian and frequentist statistics, and of the R package or similar. A demonstrated high-level ability to write scientific papers in clear, grammatically correct English is also essential.

Contact Information Professor Mark Ragan (m.ragan@uq.edu.au) The University of Queensland Institute for Molecular Bioscience

More info: http://jobs.uq.edu.au/caw/en/job/-497083/research-officer-senior-research-officer
c.chan1@uq.edu.au

USDA ARS Gainesville PopulationGenomics

Two postdoctoral research positions in population genomics are available in the laboratory of DeWayne Shoemaker, Agricultural Research Service, Gainesville, Florida.

Our current research program largely focuses on functional, population and evolutionary genomics studies of fire ants (genus Solenopsis). Examples of current projects include the use of population genetic and genomic tools and approaches to understand the genetic underpinnings of fire ant social behavior, the patterns of genome-wide gene flow and introgression among fire ant species, the genetic architecture of species differences, the consequences of recent invasions of fire ants into new environments and reproductive biology and life history of fire ants and other ants.

We are looking for someone to join us on a project that uses NGS methods (particularly genotyping-by-sequencing) to investigate population structure, gene flow, introgression, and species delimitation in fire ants. Successful candidates will be encouraged to work on additional projects, depending on personal interests and demonstrated abilities. The lab is located within the Fire Ant Research Unit at the Center for Medical, Agricultural and Veterinary Entomology in Gainesville, Florida and maintains close interactions with labs that work on insect genetics at the University of Florida. Initial appointments are for one year with the possibility of extension based on performance and available funding. Desired qualifications: Ph.D. in genetics, evolutionary genomics or related field, interest and expertise in population and evolutionary genomics, bioinformatics experience of managing and analyzing large-scale genomic data sets, programming experience in any scripting language (e.g. PERL or Python), and evidence of excellence in research and high productivity.

To apply, please send a brief description of research interests (1-2 pages), a CV, and contact information for three references to dewayne.shoemaker@ars.usda.gov. Start date is flexible and can be immediate. Positions are open until filled.

"Shoemaker, Dewayne" <Dewayne.Shoemaker@ARS.USDA.GOV>

USheffield UK EcoEvoResistance

We have a 3-year post doc position available for an evolutionary ecologist with strengths in population modelling and evolutionary theory.

*** Deadline 4th March *** Application Portal: http://-bit.ly/1Kdbpkb *** Informal enquiries to Dylan Childs: d.childs@sheffield.ac.ukÂ

The position is part of a collaborative BBSRC LoLa funded project (http:// www.bgri.info) examining the evolution of multiple herbicide resistance (MHR) in Alopecurus myosuroides ("black-grass"). The LoLa comprises five interlinked work packages studying MHR at scales from molecular genetics through to farm-scale modelling of the environmental consequences of resistance evolution and management. The consortium is led by Prof. Rob Edwards (University of Newcastle), with Co-investigators Dr Dylan Childs (University of Sheffield), Prof Rob Freckleton (University of Sheffield), Dr Paul Neve (Rothamsed Research) and Prof Ken Norris (Zoological Society of London). We are an internationally leading team of researchers with complementary expertise in the biotransformation of synthetic compounds, weed ecology and evolution, quantitative population biology, and environmental risk assessment.

The role requires familiarity with eco-evolutionary theory and modelling, as well as working as part of a multi-disciplinary team. We are interested in developing both general and system-specific models for the evolution of resistance. Based at the University of Sheffield, the successful applicant will be responsible for modelling the eco-evolutionary dynamics of multiple resistance at the within- and among-field scales, both in our model black-grass system and more general contexts. The overarching question is, what are the genetic, life history and ecological factors that promote or constrain the evolution of MHR? This research will be used to: 1) determine the key drivers of MHR evolution across different agroecosystems; 2) generate predictions about local and regional patterns of resistance; and 3) act as a platform for other studies with the project collaborators.

The University of Sheffield has strong commitment to science underpinning sustainable food production. The Department of Animal and Plant Sciences (APS) is one of the largest departments in the UK devoted to the study of whole organism biology, with 45 permanent academic staff, over 50 research fellows/associates and approximately 50 research students from different nationalities. The department contains the largest concentration of organismal biologists in the UK, and is ranked 5th in the UK (2014 REF results) for biology research with 70% of its research activity judged as “world-leading” or “internationally excellent”. The project is allied to a new translational research centre at the University of Sheffield, entitled “Plant Production and Protection (P3). The main focus of this centre is to exploit knowledge from fundamental research in plant biology for development of innovative tools in sustainable crop production and protection.

d.childs@sheffield.ac.uk

UToledo FishGenomics eDNA

Postdoctoral Researcher: Fish environmental DNA and NGS

Great Lakes Genetics/Genomics Laboratory, University of Toledo Lake Erie Center, Toledo, OH Closing Date: February 28, 2015 http://www.utoledo.edu/nsm/lec/-research/glgl/index.html Description: The research project is to help develop, test, and publish a Next-generation sequence assay for detecting and identifying all Great Lakes native and invasive fish species, including those anticipated to invade, from environmental DNA and plankton samples. The postdoctoral research associate will organize large DNA sequence databases, train and co-supervise students and technicians, and be thoroughly competent and experienced in bioinformatics, DNA extraction, PCR, DNA sequencing, and population genetic and systematic evolutionary data analyses.

Qualifications: Ph.D. degree required in hand. Publication of Ph.D. results in peer-reviewed journals required. Excellent recommendation from former advisors required. Teaching and supervisory experience preferred. Grant funding record preferred. Data management experience, bioinformatics, and data analysis experience in molecular phylogenetics and population genetics required. DNA extraction, PCR, DNA Sequencing (both Sanger and Illumina MiSeq), sequence alignment and GenBank experience required. Familiarity with QIIME, Unix/Linux operating systems and writing script in Perl is a plus. Strong communication (written, oral) skills required. Experience in working with fishes strongly preferred. Strong personnel interaction skills and experience in training others required. Oral research presentation experience at national or international scientific conferences required. Fish specimen collection experience Vstrongly preferred.

How to Apply: Send (1) cover letter, (2) CV, (3) copies of graduate and undergraduate transcripts (unofficial are fine) and (4) 2 letters of reference. Please combine items (1), (2) and (3) together as a single PDF. Have letters of reference sent by writers, separately. Have all application materials sent to: Dr. Stepien at carol.stepien@utoledo.edu.

Competitive salary, full benefits. Beautiful well-funded lab (by NSF, USEPA, ARS, Sea Grant) on Lake Erie (with view) at Lake Erie Center field station 20-25 minutes from main University of Toledo campus. The Great Lakes Genetics Laboratory currently has another postdoc, 3 Ph.D. students, a full-time technician, and 2 undergraduate researchers.

The University of Toledo is an Equal Access, Equal Opportunity, Affirmative Action Employer and Educator and is committed to increasing the diversity of our campus.

For questions or inquiries contact Carol Stepien Distinguished University Professor and Director Lake Erie Center and Dept. Environmental Sciences 6200 Bayshore Rd. Toledo, OH 43615 Phone: 4195308362 Fax: 4195308399 carol.stepien@utoledo.edu

“Klymus, Katy Elizabeth” <Katy.Klymus@UToledo.Edu>

UUtah HerbivoreMicrobiomeBiodiversity

Biodiversity and Metagenomics of the Herbivore Microbiome

The Dearing lab at the University of Utah invites applications for a postdoctoral fellow to participate in a collaborative study to understand the gut microbiome of mammalian herbivores with respect to detoxification of plant defensive compounds. Our investigations suggest 1) the microbiome in the foregut of woodrats is critical for the ingestion of dietary toxins, 2) microbial biodiversity is important in this process and 3) previous exposure to toxins shapes the microbiome. For more information on previous research, see:

http://biologylabs.utah.edu/dearing/Lab/-publications.html This postdoctoral position will focus on the influences of host evolutionary history and diet in sculpting the diversity and function of the mammalian microbiome. One component of this will be a broad survey of microbiomes and phylogeny across the woodrat genus (*Neotoma). *The ideal candidate will have a strong interest and experience in microbial ecology and metagenomics, with experience in gut systems preferably of vertebrates. Basic bioinformatic and molecular skills are required. Fieldwork for small mammal collection will be necessary; prior experience preferred but not required. The candidate should have a demonstrated record of publication with at least one first authored publication in press, and will be expected to work well in a collaborative environment. The Dearing lab provides a strong training and career development environment for candidates interested in academic positions.

Applications will be reviewed as they are received until the position is filled. The preferred start date is June 15, 2015. Please send cover letter, C.V., statement of research experience and interests that includes career goals (1-2 pgs), pdfs of papers, and contact information (emails, phone numbers and professional relationship) for at least 3 professional references to Dr. Denise Dearing, denise.dearing@utah.edu; please put 'Microbiome Postdoctoral Applicant' in the Subject Line.

jaelmalenke@gmail.com

UUtah PlantAnimalMolEvol

*Postdoctoral Fellowship: **Molecular Evolution of Plant-Animal Interactions*

Plant-Animal Interactions: The Dearing lab at the University of Utah invites applications for a postdoctoral fellow to participate in a study to understand the coevolution of mammalian herbivores and plant defensive compounds. This collaborative project will investigate the role of a subfamily of detoxification enzymes with respect to dietary strategy. Few mammalian herbivores are capable of dietary specialization. Our preliminary data suggest the cytochrome P450 2B subfamily is critical in the biotransformation of plant secondary compounds, particularly terpenes. These enzymes may play a key role in dietary specialization since substrate specificity and catalytic efficiency of CYP2B enzymes can be greatly affected by small changes in amino acid sequence. The change of even a single amino acid, particularly in critical regions such as a substrate recognition site, can have notable effects on metabolism of substrates. Thus, the structure and copy number of CYP2B genes may be key in an herbivore's ability specialize on a terpene-rich diet. The future work consists of characterizing and comparing the amino acid sequences of CYP2B enzymes of specialist and generalist woodrats (*Neotoma spp.*) and possibly other terpene feeders. We are currently sequencing the genome of *Neotoma lepida* with assembly expected by April 1, 2015. The successful applicant will use this new genomic information to amplify and sequence CYP2B genes from a variety of wild mammalian species, compare predicted protein sequence with respect to degree of dietary specialization, and characterize the function of the proteins purified from heterologous expression systems to determine the structural basis of functional differences. The applicant may also conduct enzyme assays. This research is a collaborative project with Dr. James Halpert, UConn and provides possibilities for interactions with his research group.

For more information on previous research, see:

http://biologylabs.utah.edu/dearing/-Lab/pdf/2012_journal_pone.pdf http:/-/biologylabs.utah.edu/dearing/Lab/pdf/-2009_expression_biotrans_magnanou.pdf The ideal candidate will have experience accessing and evaluating genomic data, using molecular techniques, experience with biochemical analyses and have an interest in addressing questions of molecular evolution, molecular ecology or plant-animal interactions. Animal collection fieldwork is possible. The candidate should have at least one first authored publication in press. The Dearing lab provides a strong training and career development environment for candidates interested in academic positions.

Applications will be reviewed as they are received. The preferred start date is July 6, 2015, with an earlier start date possible. Please send a cover letter, C.V., statement of research interests that includes career goals (1-2 pgs), pdfs of papers, and contact information (emails and phone numbers) for at least 3 professional references to Dr. Denise Dearing, *denise.dearing@utah.edu *; please put '*Postdoctoral Applicant CYP2B*' in the Subject Line.

jaelmalenke@gmail.com

Vienna 2 ExpEvolutionDrosophila

Experimental Evolution in Drosophila

2 postdoctoral positions are available at the Institute of Population Genetics, Vetmeduni Vienna (Austria). The research focus of the Institute of Population Genetics is on understanding the genetics of adaptation. This central question in evolutionary biology is being tackled using up-to-date methods and a variety of approaches, including experimental evolution, quantitative genetics, functional genetics, empirical population genetics, bioinformatics and statistics.

The successful candidate will be part of a team of scientists studying adaptation of experimental Drosophila populations to temperature stress. Since our experimental evolution study is performed under controlled environmental conditions with a high level of replication we have a powerful system to successfully employ a combination of DNA sequencing, RNA-Seq and Chip-Seq to characterize the architecture of adaptation in an out-crossing species. With some of our populations having already evolved up to 100 generations, this project provides the opportunity to follow adaptive trajectories through time.

We are looking for a candidate with a good quantitative training and experience in handling large data sets. A background in population genetics and/or experience with the analysis of RNA-Seq and Pool-Seq data are a bonus.

The positions are available for at least two years starting April 2015 , but the exact starting date is negotiable. The application should be emailed to christian.schloetterer@vetmeduni.ac.at as a single pdf containing CV, list of publications, a statement of research interests, and the names of three references with contact details. While the search will continue until the position is filled, applications should be received by 5.3.2015 to ensure full consideration.

Background: 1: Franssen, S.U., et al. (2015) Patterns of linkage disequilibrium and long range hitchhiking in evolving experimental Drosophila melanogaster populations. Molecular Biology and Evolution 32, 495-509 2: Orozco-terWengel, P., et al. (2012) Adaptation of Drosophila to a novel laboratory environment reveals temporally heterogeneous trajectories of selected alleles. Molecular Ecology 21, 4931-4941 3: Schlötterer, C., et al. (2015) Combining experimental evolution with next-generation sequencing: a powerful tool to study adaptation from standing genetic variation. Heredity in press 4: Schlötterer, C., et al. (2014) Sequencing pools of individuals - mining genome-wide polymorphism data without big funding. Nature Reviews. Genetics 15, 749-763 5: Tobler, R., et al. (2013) Massive habitat-specific genomic response in D. melanogaster populations during experimental evolution in hot and cold environments. Molecular Biology and Evolution 31, 364-375

Julia Hosp <Julia.Hosp@vetmeduni.ac.at>

Vienna 3 Population Genetics

Dear all:

We would like to draw your attention to up to 3 postdoctoral positions available in the Institute of Population Genetics at the Vetmeduni in Vienna. The positions are for up to 4 years, and are awarded on a competitive basis by the university.

The groups at the Institute of Population Genetics comprise an international group of researchers applying cutting-edge statistical and molecular methods to evolutionary questions, including using experimental evolution to uncover the nature of genetic basis of adaptive phenotypic variation, population genetic inferences about the process of adaptation, and phylogenetic tree reconstruction. English is the common language spoken at the institute.

Potential supervisors are Christian Schlötterer, Carolin Kosiol, and Andrea Betancourt: See http://www.vetmeduni.ac.at/en/population-genetics/research/research-groups/ for additional information on their research interests, and http://www.vetmeduni.ac.at/en/research/young-scientists/postdoc-programme/ for proposed research topics and other details.

Informal inquires can be directed to the potential supervisor directly at (first name).(last name) at vetmeduni.ac.at (with Schlötterer spelled 'schloetterer' in this case).

Formal applications should be sent directly to the university, following the instructions here: http://www.vetmeduni.ac.at/en/research/young-scientists/postdoc-programme/ Vienna provides and excellent environment for young researchers. It is home to a number of research groups working in population genetics and related areas (see http://www.univie.ac.at/evolvienna/), many of whom participate in a training grant funding Ph.D. students working in population genetics http://www.popgen-vienna.at/ Vienna is particularly attractive to Drosophila researchers, as it is home to the VDRC Stock Center, and a high-profile Drosophila research community, most notably at the IMP (http://www.imp.ac.at/) and the IMBA (http://www.imba.oeaw.ac.at/).

In addition to a stimulating scientific environment, Vienna also offers an extraordinarily high quality of life. Affordable housing, excellent public transport, great restaurants, a range of international schools, two operas, two music centers, many theaters and museums in combination with a pleasant climate make Vienna one of the most attractive cities in Europe.

Cheers, Christian Schlötterer, Carolin Kosiol, and Andrea Betancourt

– Institute of Population Genetics Department of Biomedical Sciences Vetmeduni Vienna Veterinärplatz 1 A-1210 Wien Austria/Europe

Andrea Betancourt <andreajbetancourt@gmail.com>

WorkshopsCourses

Arizona Lepidoptera Aug16-25

Announcing the Sixth Annual Lepidoptera Course, 16 V 25 August, 2015.

Held at the Southwestern Research Station (SWRS) in the Chirichahua Mountains in SE Arizona (a 2 1/2 hour drive from Tucson), the focus of the Lep course is to train graduate students, post-docs, faculty, state and federal employees, and serious citizen-scientists in the classification and identification of adult Lepidoptera and their larvae. Topics to be covered include the biology and systematics of major families of Lepidoptera, an introduction to adult and larval morphology with a focus on taxonomically-important traits, extensive field work that concentrates on both collecting and photographing adults and larvae, collecting and curatorial techniques, genitalic dissection, larval classification, use (and abuse) of DNA barcoding, and general topics in Lepidoptera systematics, ecology, and evolution.

With its extensive series of Sky-Island mountain ranges, SE Arizona has the highest Lepidoptera diversity in the US. With low desert scrub, oak and mixed oak-pine woodland, lush riparian, juniper, Douglas fir, and mountain meadow habitats all within a 40 minute drive from the station, the SWRS is an ideal location from which to sample this diversity (of both habitats and species).

If you want to interact with other Lepidoptera enthusiasts, see a spectacular Dysschema, identify the Organ of vom Rath, sort through trap samples with hundreds of species, learn about diversity of Lepidoptera , and enjoy the vistas of the SE Arizona, then this course will provide a unique experience.

Partial list of Invited instructors (subject to change) Rich Brown (Mississippi Entomological Museum), Jennifer Bundy (RD4AG), Chris Grinter (Illinois Natural History Survey), Don Harvey (Smithsonian), Sangmi Lee (Arizona State University), Chris Schmidt (Canadian National Collection), Bruce Walsh (University of Arizona)

For more information, see http://research.amnh.org/-swrs/education/lepidoptera-course or www.lepcourse.org or contact Bruce Walsh at jbwalsh@u.arizona.edu You can also see photos and comments from students in the 2011 course at their facebook site, “2011 Lep Course, SWRS SEAZ”.

“Walsh, James Bruce - (jbwalsh)” <jbwalsh@email.arizona.edu>

AuburnU BioinformaticBootcamp May11-15

Second Annual Bioinformatics Bootcamp

High throughput sequencing technology has rapidly changed life sciences. As such the need for bioinformatics skills has become critical. From May 11th to 15th, a Bioinformatics Bootcamp will be held at Auburn University introducing researchers to basic bioinformatics skills related to high throughput sequencing data. Previous experience is not required and the course will cost $350.

The workshop will be run by Drs. Scott Santos, Les Goertzen, and Ken Halanych. Topics will include: 1) Working in the unix command-line environment 2) Sequence assessment and quality control 3) Genomic and transcriptomic assembly 4) Annotation methodologies 5) Differential expression among genes/transcriptomes/treatments 6) Identification of SNPs in genomic and transcriptomic assemblies 7) Phylogenomics

Additionally we will have a keynote lecture by Dr. Paul Stothard of the University of Alberta.

Information for applications can be found at www.auburn.edu/bioinformatics .Questions can be addressed to bioinformatics@auburn.edu.

ken@auburn.edu

Barcelona NetworkTools Apr20-24

Dear colleague,

This is the last call for the workshop “NETWORK TOOLS IN BIOSCIENCES”. Webpage:

http://www.transmittingscience.org/courses/syst-bio/-networks/ INSTRUCTORS: Dr. Diego Rasskin-Gutman (Institut Cavanilles de Biodiversitat i Biologia Evolutiva, Spain) and Dr. Borja Esteve-Altava (Institut Cavanilles de Biodiversitat i Biologia Evolutiva, Spain).

DATES: April, 20-24, 2015. 34 teaching hours.

PLACE: Facilities of the Centre de Restauració i Interpretació de Els Hostalets de Pierola, Els hostalets de Pierola, Barcelona (Spain).

Many features and processes of biological systems can be well represented by networks of interacting elements. In the last decades, network analysis has provided new insights into the organization and functioning of complex biological systems such as brain wiring, genetic regulation, or ecological dynamics. A basic knowledge on network modelling and network analysis will provide biologists a better understanding of cutting-edge research in their fields. This course will introduce participants into the analysis of complex biological systems using network models. Students will learn the basics of network analysis: gathering information, building network models, and interpret the outcomes of their analysis. This course combines theoretical introduction and computing practices using the free software environment R. Previous knowledge in R is not required. Participants are encouraged to bring their own data for practicing. Emphasis is placed on offering participants a wide overview of network modelling in biology and the many available software tools to do it.

Organized by: Transmitting Science, the Institut Catalá de Paleontologia Miquel Crusafont and the Council of Hostalets de Pierola.

Please feel free to distribute this information between your colleagues if you consider it appropriate.

With best regards

Soledad De Esteban Trivigno, PhD.

soledad.esteban@transmittingscience.org

Cairns Behaviour2015 Animations Aug9-14

Are you interested in the “Virtual Reality”-Symposium at Behaviour2015 in Cairns this summer?

Then also consider to participate in the following workshop about VR-systems and computer animations:

.....

Announcement for a workshop at Behaviour2015 in Cairns, Australia (9-14th August 2015)

“Virtual Reality systems and computer animations in animal behavior research”

Date: Friday 14th August 2015 Time: TBC Room: TBC

Virtual reality (VR) systems and computer animations are promising but yet possibly underestimated methods for the use in behavioral research. Sharing many advantages, both methods are ideal for standardized, repetitive testing of behavior. Computer animations allow replacing experimental animals by their virtual counterparts that can be manipulated in any way and who behave totally predictable. The same counts for virtual environments that are created according to specific and predefined landmarks for testing navigational skills or discrimination abilities in a certain animal. Both methods inevitably combine aspects of biology and computer science which leaves many scientists reluctant to use them. Fear of possibly high technical requirements and the lack of know-how are the main reasons.

This workshop will be discussion based, offering introductions to the different methods with two step-by-step tutorials and a more detailed look at DOs and DON'Ts:

- Introduction to VR systems for freely moving model organisms and discussion of possible ways of implementation in research and constraints to keep in mind depending on different experimental animals.

- Short overview of useful techniques and software to create and animate virtual animals.

- Step-by-step tutorial for creating a 2D computer animation of a spider with Adobe products. This method is not restricted to the use with spiders but might also be applied with other animals.

- Introduction to the novel and free software tool /anyFish/ with a tutorial describing its functions. /AnyFish/ was developed to create 3D animations of fish for the use in behavioral experiments.

Participation is recommended for early stage scientists (PhDs and early PostDocs). Participants can follow the step-by-step tutorials with their own laptops (software and additional files needed). Specifics are given after registration. By the end of this workshop, participants should have a better idea of existing programs and tools and how to implement them in their research. The workshop also serves to form a network of scientists using VR and computer animations to share future knowledge and advice.

To participate please contact Stefanie Gierszewski via email: gierszewski@chemie-bio.uni-siegen.de <mailto:gierszewski@chemie-bio.uni-siegen.de>

This workshop is a supplement to the “Virtual Reality”-Symposium held at Behaviour2015: http://iec2015-symposium.wix.com/virtual-reality Dipl.-Biol. Stefanie Gierszewski Department of Chemistry & Biology Institute of Biology Research Group Ecology & Behavioral Biology University of Siegen Adolf-Reichwein-Str. 2 D-57068 Siegen phone: +49(0)271-740-2093 Fax: +49(0)271-740-4182

JOIN our “Virtual Reality”-Symposium at Behaviour2015 in Australia!

gierszewski@chemie-bio.uni-siegen.de

Cameroon UndergraduateFieldResearch Jun21-Jul15

Drexel University and the Central African Biodiversity Alliance (www.CABAlliance.org) are offering an undergraduate field research course in Cameroon from June 21 - July 15, 2015.

This 3.5 week course will pair US students with African students in field-based research projects focused on a suite of diverse taxa to inform conservation practice under climate change in central Africa. The course will be team-taught, including lectures and field-instruction by professors from Drexel, UCLA, U. Hong Kong, U. Halle Wittenberg (Germany), U. Buea (Cameroon), The Higher Institute of Environmental Sciences (Cameroon) and the National University of Equatorial Guinea. Lectures will take place in Yaounde, the capitol of Cameroon. Students will carry out field research projects at Mbam & Djerem National Park and Ebo Forest, both with excellent opportunities for viewing some of Africas most iconic wildlife. Detailed information about the course is available at www.CABAlliance.org . The course is heavily subsidized by an NSF-PIRE award. Space is very limited, and spots are filling quickly. All US students should apply through Drexel Study Abroad (http://studyabroad.drexel.edu/index.cfm?FuseAction=3DPrograms.ViewProgram&Program_ID=47722). Applications from US students will be accepted through March 15, 2015. African students should apply for the course by contacting Dr. Eric Fokam (efokam@daad-alumni.de), a professor at the University of Buea, Cameroon.

Please contact Katy Gonder (gonder@drexel.edu) or Matt Mitchell (mwmitchell@drexel.edu) for more information.

katy.gonder@gmail.com

CostaRica Coleoptera Jun5-24

Hello all,

I am writing to ask a favor of you in distributing the following information. We are currently offering a Specialty Course titled Ecology and Evolution of Coleoptera. Although the deadline has passed, we are still have some spaces available.

Ecology and Evolution of Coleoptera (Beetles)

This three week course is oriented towards graduate students interested in intense training in the collection, identification and inquiry-based research on the largest order of insects, Coleoptera. Single site diversity in tropical rain forests, such as those in Costa Rica, has been estimated to be as high as 14,000 species. The study of beetles (including some of the largest and most beautiful of all insects) is not only fascinating, but economically important because the order includes numerous harmful as well as beneficial species that affect agriculture, forestry and man.

Coordinators: Christopher Carlton < http://www.lsuagcenter.com/en/communications/authors/ccarlton.htm >, Richard Leschen < http://www.landcareresearch.co.nz/home >, Nathan Lord, and Victoria Bayless.

Course duration: 3 weeks (June 5-24, 2015)

Credits: 2.0

Application Deadline: February 3, 2015 for priority consideration, followed by rolling admission until fully enrolled.

Thank you,

Andrés Santana Graduate Program Coordinator Organization for Tropical Studies San Pedro, Costa Rica. 676-2050 (506) 2524-0607 ext. 1511 Skype: andres.santana_otscro www.ots.ac.cr twitter: @ots_tropicaledu < https://twitter.com/ots_tropicaledu >

andres.santana@ots.cr

FloridaKeys GenomicAnalysisMethods Jun30-Jul14

Dear colleagues -

We are pleased to announce the next year of our hands-on intensive workshops in ecological genomics. We will be teaching RAD and RNA-seq in the first two weeks of July. For now, please email us (all three of us) to indicate your interest (RAD, RNAseq, or both) and how likely you are to attend. Please respond by March 25, putting "MEGA2015" (Methods in Ecological Genomics Analysis 2015) in the subject. First come - first served, classes are limited to 12 students each.

For additional general info, please see the last year's workshop's website: http://www.bio.utexas.edu/research/matz_lab/matzlab/MEGA2014.html cheers

Mikhail Matz, matz@utexas.edu Groves Dixon, grovesdixon@gmail.com Marie Strader, stradermarie@gmail.com

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Methods in Ecological Genomics Analysis (MEGA) 2015

Intensive workshops for the uninitiated at the Mote Tropical Research Laboratory, Florida Keys

Instructor-in-chief: Mikhail V. Matz, TAs: Groves Dixon and Marie Strader

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Whole-genome genotyping with 2bRAD (June 30 - July 7)

2bRAD is the flavor of Restriction site Associated DNA genotyping methods. It is one of the easiest RADs to implement due to a very streamlined protocol, initially published in Nature Methods. The current protocol allows for simultaneous processing of hundreds of samples and removal of PCR duplicates prior to the analysis. Bioinformatics pipelines for 2bRAD offer genotyping quality assessment based on replicates and advanced variant call filtering adopted from the GATK pipeline used in human genetics. The class has four parts: (1) DNA isolation and library preparation (wet lab), (2) data processing and variant calling using LINUX-based high performance computing (HPC) cluster, (3) population genetic analysis including population structure and demographic modeling, and (4) population genomic analysis to identify loci under selection.

2bRAD paper: http://www.bio.utexas.edu/research/matz_lab/matzlab/Papers_files/wang12%202b-RAD.pdf

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Global gene expression profiling with tag-based RNA-seq (July 7 - July 14)

Tag-based RNA-seq is a low-cost alternative ($50/sample) to conventional RNA-seq for quantifying the abundances of polyadenylated (protein-coding) transcripts. Low cost and ease of implementation allows for experimental designs involving extensive biological replication, leading to very high power and possibility to apply network-based approaches of gene expression analysis. The class has five parts: (1) RNA isolations and library preparation (wet lab), (2) initial data processing using LINUX-based high performance computing (HPC) cluster, (3) identifying differentially expressed genes using generalized linear models (DESeq2 package) and network approach (WGCNA package), (4) summarizing the data in terms of biological functions involved, (5) de novo assembly and annotation of transcriptomes.

Tag-based RNA-seq paper: http://www.bio.utexas.edu/research/matz_lab/matzlab/Papers_files/Meyer11%20budget%20coral%20rnaseq.pdf

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Cost: $2,000 each, $3,700 both. Class size: 12

stradermarie@gmail.com

Florida SpongeBiodiversity Aug9-16

Dear Colleagues,

I am happy to announce an opportunity for training in sponge biodiversity. Please distribute this announcement to individuals that you think will benefit from this course.

Thanks, Bob thacker@uab.edu

Sponge Biodiversity in a Changing Ocean: Species, Ecosystems, Processes August 9-16, 2015 Mote Marine Laboratory, Summerland Key, Florida

A 7-day intensive course consisting of lectures, fieldwork, and laboratory experiments will be offered at Mote Marine Laboratory, Tropical Research Lab, Summerland Key, Florida, from August 9 to 16, 2015. The course is organized by Cristina Diaz, Shirley Pomponi, and Bob

Thacker; other instructors include Janie Wulff, Thierry Perez, John Stevely, and Charles Bigger.

The course is open to graduate students, researchers, and resource managers who have a primary interest in the role of sponges as key components of tropical ecosystems in a changing ocean.

Sponges constitute an essential component of coral reefs, mangroves, and seagrass beds. Their high diversity and biomass in most benthic marine ecosystems and their unique physiology makes them important targets to understand, manage, and protect those ecosystems.

Through this course, students will learn how to identify and describe common sponge species from Florida Keys seagrass, mangrove, and coral reef ecosystems. They will also gain experience using sponges as models to address questions related to biodiversity, biotechnology, and climate change.

Apply by mailing a letter of intent, your CV, and a letter of recommendation (sent separately) to taxochica@gmail.com. Your letter should state why it is important for you to participate in this course, and how your work, education, and/or research will benefit from it. The deadline for applications is March 31, 2015. Applicants will be notified of acceptance by April 30, 2015. Space is limited to 12-14 students.

Tuition is $1000 and includes accommodation, breakfast/lunch, field trips (scuba and snorkeling), and laboratory fees. Tuition assistance may be available.

Participants planning to scuba dive must meet the certification and training requirements of Mote Marine Laboratory: https://mote.org/locations/details/tropical-research-laboratory/tropical-research-laboratory-scuba-requirements-training Application instructions are available at: http://thackerlab.weebly.com/-spongecourse2015.html Information that must be included in the application:

Name Address Phone number Email

CV (should include education, research and field experience)

One letter of recommendation

Brief description of why you want to take the course and how you intend to use what youve learned

Dive experience: - Are you a scuba diver? - Do you intend to scuba dive? Participants planning to scuba dive must meet the certification and training requirements of Mote Marine Laboratory: https://mote.org/locations/-details/tropical-research-laboratory/tropical-research-laboratory-scuba-requirements-training - Current diving certification - Indicate if you are currently certified to dive under the auspices of an AAUS-affiliated institution.

Bob Thacker <thacker@uab.edu>

FridayHarborLabs UWashington ComparativeInvertEmbryology Jun15-Jul17

Course: Comparative Invertebrate Embryology

Location: Friday Harbor Laboratories, University of Washington

Dates: June 15 - July 17, 2015 (5 weeks)

Comparative Invertebrate Embryology will use hands-on lab experience to introduce students to the great diversity of developmental modes and processes found among marine invertebrates. The course will bridge cell and molecular approaches with ecological and evolutionary approaches to provide an integrated view of animal development. The course is intended to serve both biologists who wish to understand diversity in modes of development for ecological and evolutionary studies, and cell and developmental biologists who wish to broaden their knowledge of embryos beyond the standard model systems.

This course provides extensive laboratory experience with fertilization, embryonic and larval development, and metamorphosis of diverse animals. Phyla represented usually include the Porifera, Cnidaria, Ctenophora, Platyhelminthes, Nemertea, Mollusca, Annelida, Brachiopoda, Phoronida, Bryozoa, Echinodermata, Chordata, Chaetognatha, and Arthropoda.

In addition to the basics of invertebrate reproduction and development, lectures will also include analysis of morphogenetic processes, evolutionary changes in development, and functional consequences of different modes of development.

Lab time will be devoted to obtaining, observing and documenting stages of embryogenesis. Lecture and lab practice will also introduce various techniques including (but not limited to) time-lapse microscopy, immunofluorescence, confocal microscopy or in situ hybridization, and biomechanical methods. Field collecting trips to diverse habitats will acquaint students with the environments in which reproduction and development occur and diverse sources of embryos.

The application deadline for this course has been extended to March 1, 2015.

For application procedures please see:

http://depts.washington.edu/fhl/studentApplicationInfo.html Additional information is available here:

http://depts.washington.edu/fhl/studentSummer2015.html#SumA-4 Yale Passamaneck, PhD Kewalo Marine Laboratory Pacific Biosciences Research Center University of Hawaii Honolulu, HI 96813 yale_at_hawaii.edu

yale@hawaii.edu

HarvardU PhenotypicPlasticity May1-3

Dear Colleagues,

microMORPH is pleased to announce our second interdisciplinary workshop, "Phenotypic Plasticity: evolution at the intersection of ecology, genetics, and development" to be held at the Arnold Arboretum of Harvard University in Boston, MA on May 1st - 3rd, 2015.

We are soliciting participation of graduate students and post docs interested in exploring plant phenotypic plasticity from the perspective of development and microevolution. microMOPRH is an NSF funded Research Coordination Network (RCN). The goal of the RCN is to promote interdisciplinary interactions in evolutionary developmental biology at the emerging interface between developmental biology and the study of natural intraspecific and interspecific variation.

microMORPH INTERDISCIPLINARY WORKSHOPS bring together small groups of graduate students, post docs, and faculty with very different interests and expertise to interact and discuss critical concepts, intellectual objectives, emerging technologies, and analytical approaches that have the potential to advance our understanding of the evolution of plant form. All participants give presentations on their research and there is extensive discussion following each presentation. These workshops provide students and faculty with unique opportunities to explore new and challenging frontiers of knowledge.

SPEAKERS AND FACULTY PARTICIPANTS INCLUDE: Sally Assmann (Pennsylvania State University), Ben Blackman (University of Virginia), David Des Marais (Harvard University, Arnold Arboretum), Michael Donoghue (Yale University), Lisa Donovan (University of Georgia), Andrew Doust (Oklahoma State University), Cynthia Jones (University of Connecticut), Neelima Sinha (Univeristy of California, Davis), Mark van Kleunen (Universität Konstanz), John Stinchcombe (University of Toronto), Sonia Sultan (Wesleyan University), William (Ned) Friedman (Harvard University, Arnold Arboretum), and Pamela Diggle (Univeristy of Connecticut).

APPLICANT INFORMATION: We encourage applications from graduate students (at all stages of their dissertation research) and post doctoral researchers now through February 28th, 2015. Eight student or post doctoral participants will be chosen to attend and give presentations on their research. microMORPH will fund travel, accommodations, and meals for selected participants who are US-citizens or currently at US institutions (although non-US citizens not currently associated with US institutions are encouraged to apply, we cannot supply funding for them).

HOW TO APPLY: Please visit the microMORPH website (http://projects.iq.harvard.edu/micromorph) for full instructions on how to submit applications. Applicants are asked to submit a CV, research statement that includes a description of the proposed talk, and letter of endorsement from their major advisor or supervising principle investigator.

For additional information, contact Becky Povilus at (RCNmicromorph@gmail.com)

Sincerely,

Pamela Diggle (University of Connecticut) (microMORPH CO-PI)

William (Ned) Friedman (Harvard University, Arnold Arboretum) (microMORPH CO-PI)

Becky Povilus (Ph.D. Candidate, Harvard University) (microMORPH RA)

microMORPH Contact information: email: RCNmicromorph@gmail.com website: http://projects.iq.harvard.edu/micromorph Pamela Diggle

Professor Department of Ecology and Evolutionary Biology University of Connecticut

860-486-4788

"Diggle, Pamela" <pamela.diggle@uconn.edu>

HarvardU PlantBiologyEvolution Jun22-Jul3

Short Course in Organismic Plant Biology 2015 Plant Anatomy: Development, Function, and Evolution At the Arnold Arboretum of Harvard University June 22 ñ July 3, 2015

The NSF-sponsored Research Coordination Network (RCN) microMORPH and the Arnold Arboretum of Harvard University are pleased to announce our third summer short course, Plant Anatomy (with an emphasis on woody plants), June 22 ñ July 3, 2015. This short course will be taught by experts from around the world as an intense, two-week lecture, laboratory, and living collections learning experience. The course will be based at the Weld Hill Research Building at the Arnold Arboretum, which offers a state-of-the-art microscopy laboratory for teaching and sits amid the 15,000+ living specimens of more than 2,200 species at the Arnold Arboretum. We invite applications from graduate students and postdoctoral researchers who wish to gain a solid foundation in plant anatomy from an organismic perspective, with a special focus on wood anatomy.

COURSE INSTRUCTORS: Pieter Baas (Naturalis Biodiversity Center) William (Ned) Friedman (Harvard University) Peter Gasson (Royal Botanic Gardens, Kew) Elisabeth Wheeler (North Carolina State University)

COURSE SYLLABUS: Week 1: Basics of Plant Anatomy, Primary Tissues Week 2: Anatomy of Woody Plants

APPLICATION INFORMATION: Applications from graduate students and postdoctoral researchers must be received by March 31, 2015 at 11:30 pm. Undergraduates in their final year of study, who have been admitted to a graduate or professional program for the fall of 2015, may also apply. Twelve participants will be chosen to attend. Funding for travel, accommodations, and meals will be provided by the microMORPH RCN and the Arnold Arboretum. Non-US participants are welcome!

HOW TO APPLY: Please visit the microMORPH website (http://projects.iq.harvard.edu/micromorph/summer-course-2015) for full instructions on how to submit an online application. Applicants will need to submit a short essay detailing their interest in the course and in plant biology, and two letters of recommendation.

microMORPH is an NSF funded Research Coordination Network (RCN). The goal of this RCN is to promote interdisciplinary interactions in evolutionary developmental biology at the emerging interface between developmental biology and the study of intraspecific and interspecific variation.

For additional information, contact Becky Povilus at (RCNmicromorph@gmail.com)

Pamela Diggle

Professor Department of Ecology and Evolutionary Biology University of Connecticut

860-486-4788

“Diggle, Pamela” <pamela.diggle@uconn.edu>

InstGenomeSciences UMaryland 5omics

The Institute for Genome Sciences (IGS) is an internationally known research center located at the University of Maryland School of Medicine in Baltimore. IGS offers five different workshops as part of a professional development program organized by Dr. Michelle Giglio, a faculty member at IGS with over 17 years of experience in genomics and bioinformatics. Dr. Giglio has recruited IGS faculty and staff to form a highly experienced instruction team to provide workshop participants with the knowledge and skills needed to engage in numerous ‘omics applications. All IGS workshops are hands-on, providing attendees with real-world challenges and experience.

Please see our workshop dates listed below.

IMPORTANT DATES:

Metagenome Analysis * March 3rd - 6th, 2015 (Open Enrollment Ends February, 27, 2015) * October 13th - 16th, 2015

Introduction to Programming for Bioinformatics * March 16th - 20th, 2015

Transcriptome Analysis * May 18th - 20th, 2015

Prokaryotic Comparative Genomics * September 29th - October 1st, 2015

Introduction to Genomics and Bioinformatics * November 2nd - 6th, 2015

FOR MORE INFORMATION & REGISTRATION: www.igs.umaryland.edu/workshops EMAIL: Renée

Nathaniel Workshop Administrative Coordinator rnathaniel@som.umaryland.edu

"Nathaniel, Renee" <rnathaniel@som.umaryland.edu>

LakeheadU PracticalDNA Apr-Jun

Practical DNA Training Program:

A two-week (9 business days) intensive laboratory-based training program designed to teach participants the fundamentals of molecular techniques including DNA extraction, amplification (using PCR), sequencing and interpretation.

This training program is offered at various times throughout the year and we will work with you to find a suitable time for training.

The next scheduled times for the Practical DNA Training Program are: April 14 - 24, 2015, May 5 - 15, 2015, May 25 - June 4, 2015, June 15 - 25, 2015

For more information please contact us at 807-343-8877 or email paleodna@lakeheadu.ca or visit our website at www.ancientdna.com and click on 'Training Programs'.

Thank you.

Karen.

Karen Maa Administrative Assistant Paleo-DNA Laboratory 1294 Balmoral Street, 3rd Floor Thunder Bay, Ontario P7B 5Z5 Telephone: 1-866-DNA-LABS or 1-807-343-8616

Karen Maa <kmaa@lakeheadu.ca>

Leipzig NGSDataAnalysis Mar9-13

A Beginner's Guide to NGS Data Analysis Quality Control, Read Mapping, Visualization and Downstream Analyses

Scope and Topic

The purpose of this workshop is to get a deeper understanding in Next-Generation Sequencing (NGS) with a special focus on bioinformatics issues. Additionally, all workshop participants should be enabled to perform important tasks of NGS data analysis tasks themselves. The first workshop module is an introduction to data analysis using Linux, assuring that all participants are able to follow the practical parts. The second module dicusses advantages and disadvantages of current sequencing technologies and their implications on data analysis. The most important NGS file formats (fastq, sam/bam, bigWig, etc.) are introduced and one proceeds with first hands-on analyses (QC, mapping, visualization). You will learn how to read and interprete QC plots, clip adapter sequences and/or trim bad quality read ends, get bioinformatics backgrounds about the read mapping and understand its problems (dynamic programming, alignment visualization, NGS mapping heuristics, etc.), perform your own mapping statistics and visualize your data in different ways (IGV, UCSC, etc.). The last two modules adress two specific applications of NGS: RNA-seq of model organisms and RNA-seq of non-model organisms.

Key Dates

Opening Date of Registration: November 10th 2014 Closing Date of Registration: March 1st 2015 Workshops: March 9-13 2015 (8am - 5pm)

Attendance

Location: iad Pc-Pool, Rosa-Luxemburg-Straße 23, Leipzig, Germany Language: English Available seats: 24 (first-come, first-served)

Registration fees:

Industry rate: 900-1,950 EUR Academic rate: 700-1,450 EUR

Contact

ecSeq Bioinformatics Brandvorwerkstr.43 04275 Leipzig Germany Email: events@ecSeq.com

David Langenberger <david.langenberger@ecseq.com>

MichiganStateU EvolutionSoftware Jun4-6

Active LENS Train-the-Trainers Workshop on Digital Evolution Educational Software: We invite applications for an intensive residence workshop at Michigan State University on teaching evolution and the nature of science using the software package Avida-ED to be held June 4-6, 2015 in East Lansing, MI. Avida-ED is an award-winning, free, user-friendly version of the Avida research platform that was developed specifically for educational purposes, with a graphical user interface and visualizations that allow students to observe evolution in action and conduct their own evolutionary experiments. Teams of two will learn to use Avida-ED in their own classrooms and how to train other educators.Travel and expenses will be covered as part of an NSF-funded IUSE grant for the 20 applicants selected for the workshop and funds are available for subsequent training projects.For further information see the Avida-ED home page: http://avida-ed.msu.edu/.Application deadline: March 2, 2015.If you have any questions or difficulties with the application, contact Michael Wiser (mwiser@msu.edu).

Louise S. Mead, PhD Education Director BEACON Center for the Study of Evolution in Action 567 Wilson Ave, BPS 1441 East Lansing, MI 517-884-2560

Louise Mead <lsmead@msu.edu>

Montreal GeometricMorphometrics

Drs. Clint Kelly and Pedro Peres-Neto (Département des sciences biologiques, UQÀM) are pleased to announce that they will be hosting a Geometric Morphometrics Workshop at the Université du Québec à Montréal through the Canada Research Chairs program. Please see below or visit our website for further details: http://uqamgreca.weebly.com/-geometric-morphometrics-workshop-2015.html KELLY.CLINT@uqam.ca

Portal Arizona AntEvolution Aug6-16

ANT COURSE 2015 August 6-16, 2015 Southwestern Research Station (SWRS), Portal, AZ, USA http://www.calacademy.org/scientists/ant-course . DEADLINE FOR APPLICATION: April 1, 2015. Application form: https://docs.google.com/forms/d/-1Z5Fu8DHxqW5EGFkiLbxi4mHWpnc2Tn0vzmN5ctvXj1g/viewform?c=0&w=1 . ANT COURSE will be taught at the Southwestern Research Station (SWRS) in Portal Arizona (http://research.amnh.org/swrs/). The Station is centered amid the richest ant fauna in North America.

PARTICIPANT ACCEPTANCE CRITERIA. - ANT COURSE is open to all interested individuals. Priority will be given to those students for whom the course will have a significant impact on their research with ants. An entomological background is not required. We aim to include students with a diverse interest in biology, including ant systematics, ecology, behavioral biology, genetics, and conservation. The high instructor to student ratio will allow students to receive individual attention. ANT COURSE is presented in English and limited to 30 participants.

COSTS. - Tuition for the 10-day COURSE is $475 for current students and $675 for non-students (including postdocs). In addition, the Southwestern Research Station (SWRS) fee for this period, covering dormitory room and board, is $670. Transportation costs between home and Tucson (air) or SWRS (auto) are to be borne by all participants.

SPONSORS. - California Academy of Sciences and Museum of Comparative Zoology.

2015 INSTRUCTORS: Brian Fisher (Coordinator), California Academy of Sciences; Stefan Cover, Museum of Comparative Zoology; Bob Johnson, Arizona State University, Tempe; Josh King, University of Central Florida; John LaPolla, Towson University; Jack Longino, University of Utah; Corrie Moreau, Field Museum of Natural History; Scott Powell, George Washington University; Andrew Suarez, University of Illinois; James Trager, Shaw Nature Reserve; Walter Tschinkel Florida State University Tallahassee; Phil Ward, University of California Davis; Special Guests: Raymond Mendez, Howard Topoff.

bpescador@gmail.com

Raleigh Bioinformatics May18-22

Spring workshop in Bioinformatics

Raleigh, North Carolina May 18 - 22, 2015

The handling of large datasets has become intractable without some level of bioinformatic literacy. Many biologists find that there is a steep learning curve to develop the confidence required to explore their genomics datasets effectively. This bioinformatics short course includes a rich collection of hands-on instruction and lectures specifically intended to help novice users become comfortable with a range of tools currently used to analyze next-generation data. There is no prerequisite for this course other than a willingness to learn and to work hard throughout the week. All workshop exercises will be implemented via VirtualBox and focus on Illumina data.

Course participation is limited to to 25 students to ensure an intimate learning environment. Course tuition is $1000 and is open to graduate students, postdocs, staff, faculty, and industry researchers on a first come basis.

Full course information, contact, instructor info and application instructions at https://biodatatraining.wordpress.com nblouin69@gmail.com

Roscoff France MarineEvolutionaryGenomics May31-Jun12

SUMMER COURSE ON MARINE GENOMICS AT THE MARINE BIOLOGICAL STATION OF ROSCOFF (F)

First announcement

>From May 31st - June 12th, 2015 the 11th Summer Course on Marine Evolutionary & Ecological Genomics takes place at the Station Biologique de Roscoff, Roscoff, France.

Aims: Genomic knowledge is crucial for understanding the marine environment and for an efficient use of its resources. State of the art NGS methods have revolutionized the field, spawning applications in basic research and environmental management. The course will give insight into population, environmental, biodiversity, comparative, evolutionary and functional genomics through lectures, case studies and computer labs. It takes place at the Biological Station, a vibrant research community of 273 scientists and support personnel, located in the old town and fishing port of Roscoff, Brittany, France.

The course includes lectures, tutorials and computer based exercises on the following topics. * Genomics - next generation sequencing, database searching, basic skills in data handling and bioinformatics * Population genomics - diversity, structure, connectivity and gene flow, assignment, effective population size, population dynamics, adaptive variation, genotyping by sequencing * Environmental genomics - environment - genome interactions, ecogenomics, metagenomics and metagenetics * Functional genomics - genome structure, molecular evolution at the functional level, genomic architecture, functional networks * Comparative genomics - whole genome comparisons, concatenated phylogenies, genome organization, annotating genomic information, co-evolution

The course covers all aspects of life in the ocean.

Target group: PhD students (at least in their second year) and junior postdocs with a solid knowledge in phylogenetics and/or population genetics. 18 participants will be selected on the following criteria: 1. Relevance of the course for their PhD or post-doc project 2. Background and experience 3. We aim at training people with different research backgrounds; not more than one person per institute will be considered. We implement a gender policy.

The selected persons will be notified by March 25th and will have to confirm attendance within 7 days. There is a waiting list in case of non-confirmations and cancellations.

Teaching staff : Jonas Collén, SB-Roscoff, FR Simon Creer, Univ. Bangor, UK Yves Desdevises, OO-Banyuls, FR Jakob Hemmer-Hansen, DTU-Aqua, DK Erica Leder, Univ. Turku, Fi Frédéric Partensky, SB-Roscoff, FR Daniel Vaulot, SB-Roscoff Filip Volckaert, Univ. Leuven, BE Mathias Wegner, AWI-Sylt, GE

Organizing committee Jonas Collén, SB-Roscoff, FR Damien Guiffant, SB-Roscoff, FR Matthias Obst, Univ. Gothenburg, SE Sarah Bourlat, Univ. Gothenburg, SE Nic Blouin, Univ. Rhode Island, USA Nathalie Turque, EMBRC-France, FR Filip Volckaert, Univ. Leuven, BE

For information, a flyer and application please check http://meeg2015.sciencesconf.org . The application deadline is March 10 2015.

Filip Volckaert <Filip.Volckaert@bio.kuleuven.be>

SCENE Glasgow RGeneticDataAnalysis Aug3-7

Genetic data analysis in R (statistics course)

Overview: This course is ideal for evolutionary biologists that deal with various types of genetic data. The course will provide an extensive overview of exploratory methods for the analysis of genetic data using the R software. It will address a number of key problems in population genetics, such as: How to examine genetic diversity using phylogenetic trees as well as multivariate methods, identify genetic clusters, and unravel spatial genetic patterns. Participants will be provided with the theoretical background and statistical methodology necessary to approach each problem from a number of different angles. Hands-on practical sessions will then provide an opportunity to highlight the pros and cons of methods introduced by the lectures, while conferring to participants advanced knowledge of the R packages adegenet, ape, and phangorn.

The course will run from 3rd - 7th of August 2015 at SCENE (the Scottish Centre for Ecology and the Natural Environment), Glasgow. The cost is Â£490 including lunches and course materials. An all-inclusive option is also available at Â£665; this includes breakfast, lunch, dinner, refreshments, accommodation, and course materials.

The course is being delivered by Dr. Thibaut Jombart who has contributed towards a number of R packages (adegenet, adephylo, geography, outbreaker, Outbreakertools, bmmix, episerve (author) and ade4 and phylobase (contributor) and Caitlin Collins (Imperial College London) who also contributes to the R packages adegenet, Outbreakertools and episerve)

Curriculum is as follows;

Day 1: Intro 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: Intro 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: Genome-Wide Association Studies (GWAS) Lecture 4: Intro to GWAS study design and statistical approaches: univariate, regression-based and multivariate analysis. Practical 4: Applying each class of methods covered in morning lecture, with emphasis on their strengths and weaknesses. Main packages: adegenet, glmnet.

Day 5: Spatial genetic structures Class 1: Discussing the origin and significance of spatial genetic patterns, and how to test for them. Practical: Visualising and analysing spatial genetic data. Topics: spatial density estimates, Moran/Mantel tests, mapping principal components in PCA, spatial PCA. Main packages: adegenet, adehabitat, ade4.

Please send inquiries to oliverhooker@prstatistics.co.uk

oliverhooker@prstatistics.co.uk

Swiss Alps EvolutionaryBiol Jun19-25 DeadlineExtended

Dear Colleagues, we still have places available for this years edition of Evolutionary Biology Workshop in the Alps (19-25 June 2015, Riederalp, Switzerland)

Target participants: PhD students, advanced Master students

We have extended application deadline until March 8.

Faculty: Judith Mank (University College London) Andrew Read (Pennsylvania State University) Tanja Schwander (University of Lausanne) John Pannell (University of Lausanne) Tadeusz Kawecki (University of Lausanne)

The main goals of this annual workshop, based on a concept developed by Stephen Stearns and John Maynard Smith, are to develop the following skills: - developing your scientific ideas through discussions in groups; - thinking critically and expressing oneself clearly; - turning a general idea into a research project; - writing a research proposal and defending it.

The workshop will take place in Villa Cassel (http://www.pronatura-aletsch.ch/home-en), at 2000 m of altitude, a >100 year old villa where Winston Churchill once stayed, amid the magnificent mountain landscape of a UNESCO World Heritage Site, walking distance from the largest glacier of the Alps.

Costs: CHF 530.- for room and board. 3 ETSC credit points

To apply, send a single file (pdf or rtf) containing a short motivation letter including a brief summary of your research interest, a cv, and the name of your scientific advisor to Caroline Betto-Colliard <ecologie-evolution@cuso.ch>, with Cc to tadeusz.kawecki@unil.ch .

– Tadeusz J. Kawecki Department of Ecology and Evolution University of Lausanne Biophore, office 3111 CH 1015 Lausanne, Switzerland

tadeusz.kawecki@unil.ch

SwissAlps PopulationGenetics Jun17-20

We are organizing a workshop in the Swiss Alps in June 2015 on the theme "Theoretical and empirical evidence of adaptation". The format of the symposium is pretty informal and the plan is to have it in a remote (but beautiful) location in the Swiss Alps called La Fouly. The aim is to allow Swiss and international PhD students and postdocs to gather, present their work, and have close interactions with internationally renowned scientists in the field, all in a relaxed atmosphere.

For further information on the workshop, including registration details, please see:

http://www.cuso.ch/activity/?p=3D1128&id=3D2243 Jeffrey D. Jensen School of Life Sciences École Polytechnique Fédérale de Lausanne (EPFL) http://-jensenlab.epfl.ch/ jeffrey.jensen@epfl.ch

Sydney Hawkesbury RNASeq May4

The Hawkesbury Institute for the Environment is pleased to announce a Next Generation Sequencing and Analysis workshop on the topic of transcriptomics for non-model species.

http://www.uws.edu.au/hie/events_and_seminars/-next_generation_sequencing_and_analysis_workshop This bioinformatics course will be delivered Brian Haas (the Broad Institute, MIT, USA; of Trinity RNA-Seq fame) and will be geared towards biologists who are working on RNASeq data from species with smaller genomic communities and are interested in further understanding how to analyse these types of data.

The course will be run over the course of one week and will be focused on hands-on exercises on transcriptome assembly, structural and functional annotation and differential expression experiments.

Everyone with an interest is encouraged to apply.Attendees are expected to have a solid understanding of the BASH command line, bring their own laptops and are strongly encouraged to bring their own data so that they can use the opportunity to discuss their analyses with the lecturers and other attendees.Registration for this course is first by Expression Of Interest to ensure that we have a small group of(ca 20)enthusiastic attendees that are on a similar level and have similar expectations.

Venue: Hawkesbury Institute for the Environment University of Western Sydney College Drive Richmond NSW 2754

Dates: Monday 4th May to Friday 8th May 2015 9.00am to 5.00pm daily Costs: $200 plus GST.Includesmorning/afternoon tea and lunch every day. Excludes travel, accommodation, hotels transfers, breakfasts and dinners.

For all inquiries please contact Dr Alexie Papanicolaou on (02) 4570 1385 or emaila.papanicolaou@uws.edu

Dr. Alexie Papanicolaou

Phone: +61(0) 2 4570 1385 | Mobile: +61 (0) 46 85 81 247 Lecturer in Bioinformatics | Hawkesbury Institute for the Environment University of Western Sydney | Hawkesbury Campus, Richmond NSW 2753, Australia Postal address:Locked Bag 1797, Penrith, NSW 2751, Australia www.uws.edu.au/hie Alexie Papanikolaou <A.Papanicolaou@uws.edu.au>

Sydney Hawkesbury RNASeq May4 Correction

Dear all Apologies my address was missing the .au bit, please resend any emails you may have sent.

NB: Feel free to send queries to a.papanicolaou@uws.edu.au but to apply fill out the Expression of interest form via the link available on the website.

thanks a

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– Dr. Alexie Papanicolaou

Phone: +61(0) 2 4570 1385 | Mobile: +61 (0) 46 85 81 247 Lecturer in Bioinformatics | Hawkesbury Institute for the Environment University of Western Sydney | Hawkesbury Campus, Richmond NSW 2753, Australia Postal address: Locked Bag 1797, Penrith, NSW 2751, Australia www.uws.edu.au/hie A.Papanicolaou@uws.edu.au

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Taormina Italy SystemsBiology Jul5-9

Call for Participation (apologies for multiple copies)

Synthetic and Systems Biology Summer School - 2nd Edition Taormina - Sicily, Italy, July 5-9, 2015

http://www.taosciences.it/ssbss2015/ ssbss.school@gmail.com

*News: New Speaker! Ron Weiss, MIT, USA

** Deadlines ** Student Application: February 15, 2015 Oral/Poster Submission: February 15, 2015

** List of Speakers ** * Adam Arkin, University of California Berkeley, USA * Jef Boeke, New York University, USA * Angela DePace, Harvard University, USA * Forbes Dewey, MIT, USA * Karmella Haynes, Arizona State University, USA * Richard Kitney, Imperial College London, UK * Timothy Lu, MIT, USA * Philip Maini, Oxford University, UK * Steve Oliver, Cambridge University, UK * Velia Siciliano, MIT, USA * Greg Stephanopoulos, MIT, USA - TBC * Ron Weiss, MIT, USA * Nicola Zamboni, ETH, Switzerland

** Industrial Panel ** * Jon D. Chesnut, Life Sciences Solutions Group -Thermo Fisher Scientific, USA * Carlos Olguin, Autodesk Inc., USA * Zach Serber, Zymergen, Inc. USA

School Directors Jef D. Boeke, New York University, USA Giuseppe Nicosia, University of Catania, Italy Mario Pavone, University of Catania, Italy Giovanni Stracquadanio, University of Oxford, UK

** Short Talk and Poster Submission ** Students may submit a research abstract for presentation. School directors will review the abstracts and will recommend for poster or short-oral presentation. Abstract should be submitted by February 15, 2015. The abstracts will be published on the electronic hands-out material of the summer school.

http://www.taosciences.it/ssbss2015/index.html#applicationForm http://www.taosciences.it/ssbss2015/ ssbss.school@gmail.com

Apologies for multiple copies. Please forward to anybody who might be interested.

cfp.ssbss@dmi.unict.it

UBirmingham EnvironmentalGenomics Mar23-27

NERC-MDIBL Environmental Genomics Course, 2015

Online Registration Site: www.birmingham.ac.uk/-EnGen Dates: March 23-27, 2015

Location: University of Birmingham, UK

Number of Places: Between 25 and 50

Open to: Participation is open to everyone.

Priority is given to NERC-funded PhD students and early-career postdocs. Confirmation to attend will be announced March 2, 2015.

Course Leaders: John Colbourne, Joseph Shaw, Mark Viant, Xin Zhou

Research Organizations Involved: University of Birmingham (UK), BGI China National GeneBank (Shenzhen, China), Mount Desert Island Biological Laboratory (USA)

Online Registration Site: www.birmingham.ac.uk/-EnGen Description This training opportunity in Environmental Genomics is the second European/UK instalment of a successful annual course originating from Mount Desert Island Biological Laboratory. It trains PhD students and early career postdoctoral scientists to investigate how gene function is influenced by environmental conditions while accounting for variation that exists within and among natural populations. The course is built on the paradigm that the multidisciplinary research field encompassing ecology, evolution, toxicology, biostatistics and informatics will most effectively grow by training early career environmental scientists to properly design comprehensive, large-scale, experiments enabled by drastically increased sample-throughput and lower costs. Most importantly, the challenges of manipulating and analysing population-level genomics (big) data must be addressed.

The course provides intensive training in seminar and laboratory formats, especially around expression profiling by RNA-Seq. Topics covered include bioinformatics using sequence analysis workflows and R statistical analysis tools, plus experimental design for environmental genomics research. For the laboratory, participants will be introduced to automated sample preparation as well as preparing their own RNA-sequencing libraries. The course provides a significant introduction and some hands-on training experience so that participants can initiate their own environmental genomics study and network with others in the field to launch Environmental Scientist careers in academia and industry.

Course Content Participants are taught using open-source analysis tools and existing OMICS data.

Course Presentations - Library construction methods and QC - Introduction to automation systems - Introduction to the sequence data workflow - Software solutions for the sequence and metabolomics data workflows & their applications for environmental research - Review of sequencing technology, its strengths and weaknesses - RNA-Seq alignment to individualize transcriptomes - Statistical considerations for analysing genome-scale data

Bioinformatics Training - Introduction to R - Visualization of sequence and metabolomics data for quality assurance - Visualization of complex data - Navigating the command line - Data analysis workshop using R to analyse Tuxedo output - Gene set enrichment analysis - Exploring genome sequence variation - Help desk to explore participants research questions

Synthesis Sessions - Models in search of ecology vs ecology in search of models - What can I extract from the sequence data for my investigations - Integrating omics data - How do I obtain funding for my Environmental Genomics project

Evening Lecture Series There will be four evening lectures designed to highlight environmental omic applications that draw on the expertise of our guest faculty.

Daphnia is used for training because of their growing use as model systems for environmental genomics and for improving environmental health protection, yet the skills learned during the course will be applicable to all study systems with mature genomics resources.

School of Biosciences, The University of Birmingham Birmingham, B15 2TT, United Kingdom

Mount Desert Island Biological Laboratory Old Bar Harbor Rd., Salisbury Cove, ME 04672

j.k.colbourne@bham.ac.uk

UBremen EvolutionStatisticsUsingR

BRESSS V BRemen Ecological Statistics Summer School 2015

Date: June 02 V 05, 2015

Place: University of Bremen, Germany

Application deadline: 17th of April, 2015

Data obtained in research in ecology and evolution are often not normally distributed. Within the workshop we will use the unifying concept of generalized linear models (GLM) to deal with such data. Besides short lectures, exercises will be offered using the open source software R.

*For further information please visit our website: * *https://sites.google.com/site/statisticsbremen/* Topics covered: Linear Models, Generalized Linear Models (Poisson, Negative binomial, Gamma and Binomial distribution), Zero-inflated/-truncated Models, Generalized Linear Mixed Models

Thanks to the funding of the *Deutsche Zoologische Gesellschaft*, registration is free for all DZG members (The course fee for non-members is 20£á/50£á for PhD students/PostDocs).

We hope to welcome you soon in Bremen!

The organizing committee,

Katharina Merkel, Mareike Koppik and Thomas Hoffmeister

Statistics Bremen <statisticworkshopbremen@gmail.com>

UTennessee Knoxville EvolutionWarfare Sep16-18

Topic: Evolutionary approaches to the understanding of decentralized warfare

Meeting dates: September 16-18, 2015

Location: NIMBioS at the University of Tennessee, Knoxville

Organizers: Biology: Michael L. Wilson < http://www.cbs.umn.edu/explore/departments/eeb/faculty-research/directory/michael-wilson >, Univ. of Minnesota Anthropology: Luke Glowacki < http://scholar.harvard.edu/glowacki >, Harvard Univ. Defense Analysis: Anna Simons < http://faculty.nps.edu/asimons/ >, Naval Postgraduate School Modeling: Sergey Gavrilets < http://www.tiem.utk.edu/%7Egavrila/ >, Univ. of Tennessee, Knoxville

Webpage: http://www.nimbios.org/workshops/WS_warfare *Application deadline:* May 17, 2015. Participation in the workshop is by application only. Individuals with a strong interest in the topic are encouraged to apply, and successful applicants will be notified within two weeks of the application deadline. If needed, financial support for travel, meals, and lodging is available for workshop attendees.

Sergey Gavrilets Department of Ecology and Evolutionary Biology Department of Mathematics National Institute for Mathematical and Biological Synthesis (NIMBioS) University of Tennessee Knoxville, TN 37996

phone: (865) 974-8136 fax: (865) 974-3067 e-mail: gavrila@tiem.utk.edu web: www.tiem.utk.edu/~gavrila NIMBioS: www.nimbios.org Sergey Gavrilets <gavrila@tiem.utk.edu>

WoodsHole Immune selection 19-22April

Workshop: Immune selection on protozoan & metazoan parasites

We invite applications to participate in our NSF-funded workshop on immune selection, to be held in conjunction with the 2015 Woods Hole Immunoparasitology (WHIP) Conference, 19-22 April in Woods Hole, Massachusetts, USA.

Natural selection operates on the ecological dynamics of parasites both within hosts and across host populations. Our NSF-funded Research Coordination Network (RCN) integrates theoretical and empirical tools to study these cross-scale dynamics and explain heterogeneities in parasite life cycles, virulence and efficacy of control.

A major challenge is to identify relevant and tractable immune parameters to inform our understanding of within-host dynamics. The main objective of this workshop is therefore to characterize dynamics of immune killing in relation to the effectors that target parasites, from vector-borne trypanosomes and malaria to directly-transmitted helminths and trophically-transmitted toxoplasmosis. By embedding ourselves in WHIP, we will tap into broad and deep immunoparasitological expertise in an informal and highly interactive setting on lovely Cape Cod.

Primary questions that we will consider during the workshop: Do parasite species that differ in mode of transmission experience differential types/strengths of immune selection? How heterogeneous are the immune responses induced by different parasite strains within species? When does cross-reactivity of immune responses lead to apparent competition versus competitive release of different parasite genotypes? What are the most relevant yet tractable metrics that predict strength and timing of immune selection? What are the appropriate functional forms for understanding and modelling immune selection?

Workshop participants are expected to present relevant data and/or theory in short formal presentations, and (even more importantly!) to participate fully in discussions and the real-time development of statistical, mathematical and experimental approaches to studying the evolution of infectious diseases. We will support WHIP registration, travel and subsistence for up to 20 workshop participants.

If you are interested in attending the 2015 workshop and WHIP conference, please apply via this link: http://ideas.princeton.edu/workshop-for-2015/ We require a 250-word (max) abstract describing the work you propose to present as a talk or poster to the WHIP audience, plus a brief justification of your interest in the workshop. Please note that WHIP especially favors oral presentations by postdoctoral and predoctoral researchers.

Workshop applications will be considered on a rolling, first-come, first-served basis until the workshop fills or 15 March 2015, whichever comes first.

For more information on this RCN, please see: http://ideas.princeton.edu/ For WHIP, please search "WHIP 2015" & follow the first Marine Biological Laboratory link.

All best, Andrea

– Andrea L. Graham Department of Ecology and Evolutionary Biology Princeton University Princeton, NJ 08544 USA

Tel: (+1) 609-258-6703 E-mail: algraham@princeton.edu

Graham Group URL: http://algraham.princeton.edu/ ISI Researcher ID: http://www.researcherid.com/rid/A-8808-2010 algraham@princeton.edu

Instructions

Instructions: To be added to the EvolDir mailing list please send an email message to Golding@McMaster.CA. At this time provide a binary six letter code that determines which messages will be mailed to you. These are listed in the same order as presented here — Conferences; Graduate Student Positions; Jobs; Other; Post-doctoral positions; WorkshopsCourses. For example to receive the listings that concern conferences and post-doctoral positions this would be 100010. Messages are categorized on the basis of their subject headings. If this subject heading is not successfully parsed, the message will be sent to me at Golding@McMaster.CA. In addition, if it originates from 'blackballed' addresses it will be sent to me at Golding@McMaster.CA. These messages will only be read and dealt with when I have time. The code 000000 has all channels turned off and hence gets only a once monthly notifcation of the availability of a monthly review pdf file.

To be removed from the EvolDir mailing list please send an email message to Golding@McMaster.CA. Note that 'on vacation', etc, style messages are automatically filtered and should not be transmitted to the list (I hope), but should you wish to avoid the e-mail's your code can be temporarily changed to 000000.

To send messages to the EvolDir direct them to the email evoldir@evol.biology.McMaster.CA. Do not include encoded attachments and do not send it as Word files, as HTML files, as LaTeX files, Excel files, etc. . . . plain old ASCII will work great and can be read by everyone. Add a subject header that contains the correct category "Conference:, Graduate position:, Job:, Other:, Postdoc:, Workshop:" and then the message stands a better chance of being correctly parsed. Note that the colon is mandatory.

The message will be stored until the middle of the night (local time). At a predetermined time, the collected messages will be captured and then processed by programs and filters. If the message is caught by one of the filters (e.g. a subject header is not correctly formated) the message will be send to me at Golding@McMaster.CA and processed later. In either case, please do not expect an instant response.

Afterword

This program is an attempt to automatically process a broad variety of e-mail messages. Most preformating is collapsed to save space. At the current time, many features may be incorrectly handled and some email messages may be positively mauled. Although this is being produced by LaTeX do not try to embed LaTeX or TeX in your message (or other formats) since my program will strip these from the message.