EvolDir

June 1, 2016

Month in Review

Foreword

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

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

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

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Conferences

Austin 2016SSE Education Jun18

Making Evolution Work: Synthesizing research and applied practice *Evolution 2016* *Austin* *Saturday, June 18 8:30am-11:30am*

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

For more information visit: https://qubeshub.org/-groups/sseedsym2016 Apply here to participate: *http://tinyurl.com/jdb6cq6* There is no charge for this symposium, however participation is limited so registration is required. Participants will be notified by June 1. Please share this announcement with others who might be interested. Questions? Contact Louise Mead (lsmead@msu.edu) or Kristin Jenkins (kristin.jenkins@bioquest.org).

– Kristin P. Jenkins, PhD Director

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

kristin.jenkins@bioquest.org

Barcelona EvolutionMedicine Oct6-7

Recognized international scientists in the evolution and medicine will be gathered in the 15th edition of the Centre for Genomic Regulation Symposium that will take place in Barcelona on the 6-7 of October under the title “Evolution & Medicine” in Barcelona, Spain.

This open meeting will provide a unique opportunity to bring together researchers and scientists to explore topics in cancer evolution, the emergence of resistance to antibiotics and other drugs, the origin and evolution of pathogens, and the evolutionary influence on our own construction and predisposition to various diseases.

Evolutionary theory forms the basis for our understanding of the natural world. The development, behaviour and physiology of our own species has been shaped by million of years of evolution. Furthermore, the interaction of humans with species that directly affect our health and survival is constantly being modified by evolutionary forces through natural or artificial selection.

Registration is now open to the scientific community and can be done through the CRG Symposium website until September 16th. Participants are invited to submit their abstracts, a number of which will be selected for short talks.

You cannot miss this 15th edition of the CRG Symposium! Capacity is limited, so secure your place early!

Confirmed speakers:

Yegor BAZYKIN, Skolkovo Institute of Science and Technology, Moscow RU

Arturo CASADEVALL, Albert Einstein College of Medicine, New York USA Inaki COMAS, Centre for Public Health Research, Genomics and Health, University of Valencia ES Nicole MIDEO, Department of Ecology & Evolutionary Biology, University of Toronto CA Randolph NESSE, The Center for Evolution & Medicine, Arizona State University USA Anna PANCHENKO, National Center for Biotechnology Information, National Institutes of Health, Bethesda USA David ROOS, Department of Biology, University of Pennsylvania USA Shamil SUNYAEV, Division of Genetics, Department of Medicine, Brigham & Women's Hospital and Harvard Medical School, Boston USA Erdal TOPRAK, UT Southwestern Medical Center, Texas USA

Timing and Location of the Meeting: The Symposium starts on October 6 and finalize October 7. The meeting will take place at the PRR Auditorium (c/ Aiguader, 88, Barcelona Spain)

Registration and Costs: Registration is free and Now Open. Capacity is limit so first come - first served basis

Abstract submission: Symposium Organisers invite the submission of abstracts before 15 July 2016. Just authors of selected abstracts will be assigned slot to give a short talk during the CRG 2016 Symposium

See CRG website for more information: http://www.crg.eu/en/content/events/15th-crg-symposium-evolution-and-me dicine-6-7-october-2016-barcelona-spain

Please contact Laura Prat: laura.prat@crg.eu in case of any doubt.

Laura Prat Busquets <laura.prat@crg.eu>

Barcelona GeneticsEvolution Oct3-5 RegistrationOpen

XXI Seminario de Genetica de Poblaciones y Evolucion

Sitges, October 3-5, 2016

REGISTRATION OPEN

We are pleased to announce that the registration period for the XXI Seminario de Genetica de Poblaciones y Evolucion (XXISGPE) is already open. This workshop will be held October 3-5, 2016 at the Hotel Calipolis in Sitges (Barcelona, Spain).

All the information about registration fees and types of accommodation can be found in the workshop webpage

http://XXISGPE.uab.es/ To register for the workshop, please follow the link.

http://xxisgpe.uab.es/base/base3.asp?sitio=XXISGPE&anar=inscri The XXISGPE will comprise only invited talks (45 min presentation + 15 min discussion) and oral contributions (25 min presentation + 5 min discussion). Speakers can give their talks in English or Spanish.

For those wishing to present an oral contribution, we inform that abstract submission will be open from February 1 to June 30, 2016. In order to submit or present an oral contribution you must be registered for the workshop. Please don't delay your response, space is limited. We look forward to your participation!

Organizing Committee

Alfredo Ruiz Mauro Santos Antonio Barbadilla Mario Caceres

Isaac Salazar-Ciudad

Contact

Alfredo Ruiz Departament de Genetica i de Microbiologia Facultat de Biociencies, Edifici C Universitat Aut0noma de Barcelona Tel. +34 93 581 2729 sgpe.sitges@uab.es

Alfredo Ruíz Panadero <Alfredo.Ruiz@uab.cat>

Belgrad ProgrammingForEvolutionaryBiology
Sep7-12

Conference related to the Programming for Evolutionary Biology course

When: September 9th - 12th 2016 Location: Belgrad, Serbia

Registration now open

Detailed information about the conference content and how to register: http://pebconference.info/ The Programming for Evolutionary Biology (PEB) conference brings together scientists broadly interested in applying bioinformatic tools to answer evolutionary and ecological questions. It aims to serve as a platform for discussing common programming pitfalls encountered during research and features workshops to further develop participants' bioinformatic abilities. This year, we are fortunate to be joined by an outstanding list of Plenary Speakers.

The conference is an offshoot of the Programming for Evolutionary Biology course held annually at the University of Leipzig. The course teaches the essential background skills required to perform computational analyses using next-generation sequencing (NGS) data with a focus on solving research questions related to genomics and evolution. Alumni from the Class of 2014 organized the inaugural PEB conference in May 2015 at CIBIO (Vila do Conde, Portugal) in order to discuss their research and overcoming technical challenges. The conference was a spectacular success and so this year the PEB community is pleased to announce that we will be accepting applications from the broader public! We welcome all speakers interested in the application of NGS methods in ecological and evolutionary studies. The second PEB conference will be held from September 7th to 12th, 2016 in Belgrad, Serbia.

Katja Nowick <nowick@bioinf.uni-leipzig.de>

Cambridge UK PlantEvolution
Sep15-16

Dear all,

Registration is now open for the second UK Plant Evolution meeting, to be held at Cambridge University Botanic Garden on 15 and 16 September 2016.

We have a great line-up of invited speakers including Doug Soltis, Sandy Knapp, Chiara Airoldi, Robert Scotland, Vincent Savolainen, Minsung Kim, Kirsten Bomblies, and Dmitry Filatov.

Registration is only 40 (student) or 60 (standard), including lunches and all tea/coffee breaks, and the opportunity to tour the Cambridge University Botanic Garden and/or herbarium.

To register or submit an abstract see: http://www.plantsci.cam.ac.uk/research/sambrockington/uk-plant-evolution-2016 or email bjg26@cam.ac.uk or sb771@cam.ac.uk with any questions,

Please do circulate this amongst friends and colleagues who may be interested,

best wishes,

Sam Brockington and Beverley Glover

1 Brookside | Cambridge University Botanic Gardens | Cambridge | CB21JE

"sb771@cam.ac.uk" <sb771@cam.ac.uk>

DukeU MadagascarEvolution
Sep21-23

September 21 - 23, 2016: This symposium will cover topics from the evolution of cognition, One Health, disease transmission, comparative genomics, biogeography, evolutionary conservation genetics, and more!

Details and registration information can be found at: http://lemur.duke.edu/50/ Register by June 1, 2016 to secure discounted rates.

September 21: Welcome reception for speakers and attendees

September 22: Morning Session: Cognition & Behavior 9:00 - 9:25: Brian Hare: "Lemurs have gone from ignored to adored in cognitive research thanks to the Duke Lemur Center" 9:30 - 9:55: Elizabeth M. Brannon: "Counting on lemurs to uncover the evolutionary origins of quantitative cognition" 10:00 - 10:25: Evan MacLean: "Lemur Diversity as a Natural Experiment in Cognitive Evolution" 10:30 - 11:00 (break) 11:00 - 11:25: Christine Drea: "Female Lemurs Rule! Gaining Proximate and Ultimate Understanding of Social Dominance via Comparative Studies" 11:30 - 11:55: Peter Kappeler: "The evolution of lemur social systems" Afternoon Session: Evolution & One Health 1:00 - 1:25: Anne-Claire Fabre: "The evolution of prehensile behaviour and forelimb morphology in prosimians" 1:30 - 1:55: David Weisrock: "What do we really know about mouse lemur species diversity?" 2:00 - 2:30: Marina B. Blanco: "Dwarf lemur biodiversity through the lens of hibernation" 2:30 - 2:55 (break) 3:00 - 3:25: Sheena Faherty: "Gene expression and physiological extremes in primate hibernation" 3:30 - 3:55: Erin McKenney: "Gut Instincts: Lemur microbial community dynamics in health and disease" 4:00 - 4:25: Fidy Rasambainarivo: "One island, one health: transmission of pathogens between species at the human-wildlife interface" 4:30 - 4:55: Meredith Barrett: "Impacts of environmental change on lemur health" 5:00 - 5:25: Peter Larsen: "Pathogen discovery in Madagascar: the utility of next-generation disease surveillance for lemur conservation"

September 23: Morning Session: Cognition & Biomedicine 9:00 - 9:25: Michael Platt: "The Evolution of Visual Decision Making in Primates" 9:30 - 9:55: Laurie Santos: "Lemur Cognition: Some Insights and Open Questions" 10:00 - 10:25: Jeffrey Rogers: "Decoding mouse lemurs: DNA sequencing, comparative genomics and the remarkable biology of an emerging research model" 10:30 - 11:00 (break) 11:00 - 11:25: Fabienne Aujard: "The mouse lemur as a model for research on aging" 11:30 - 11:55: Steven N. Austad: "Small bodied primates: a critical need for aging research" Afternoon Session: Conservation & Biogeography 1:00 - 1:25: Alex Dehgan: "Conservation 3.0 - The Future of Conservation and Madagascar" 1:30 - 1:55: Charlie Nunn: "Cookstoves, Respiratory Health, and Conservation of Lemur Biodiversity in SAVA, Madagascar" 2:00 - 2:30: Kathleen Muldoon: "Biogeographic Evolution of Madagascar's Primate Communities: Endemism, Elevation, and the Fossil Record" 2:30 - 2:55 (break) 3:00 - 3:25: Jason L. Brown: "Predicting the genetic consequences of future climate change: the power of coupling spatial demography, the coalescent, and historical landscape changes" 3:30 - 3:55: Jorg U. Ganzhorn: "Tipping points in lemur ecology and conservation" 4:00 - 4:25: Jonah Ratsimbazafy: "Lemur conservation in Madagascar: Good news in bad times" 4:30 - 4:55: Patricia Wright: "Lemur Conservation in Madagascar-the next ten years" Friday Evening Events: Washington Duke Inn 6:00 - 7:00 p.m.: Cocktail reception 7:00 - 8:30 p.m.: Plated dinner with Plenary Speaker, Dame Alison Richard 8:30 - 9:30 p.m.: Music and dancing with Malagasy world beat musician, Razia Said

For questions and further information, please email: anne.yoder@duke.edu

Anne D. Yoder, Professor Department of Biology Duke University, Box 90338 BioSci 315 Science Drive Durham, NC 27708 anne.yoder@duke.edu http://yoderlab.org Director, Duke Lemur Center http://lemur.duke.edu/50/ Anne Yoder <adyoder@duke.edu>

Gotland PhdStudentsEvolBiol Sep11-15

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

September 2016!

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

Helsinki WildPlantPathoSystems Aug29-31

Dear colleagues,

We are pleased to announce the 2nd international meeting on

WILD PLANT PATHOSYSTEMS

29-31 August 2016, Helsinki

Please remember to secure your place as the number of participants is limited!

Conference registration & welcome reception take place on Sunday evening 28 August. For those interested, we will organize a post-conference excursion to the Ãland Islands to visit the classic metapopulation study system 1-3 September.

Research carried out on plant-pathogen interactions has provided breakthroughs in how ecological, molecular and evolutionary dynamics are coupled to produce the patterns on infection we observe in nature. This conference brings together scientists working in cutting edge areas of plant-pathogen interactions including coevolution, epidemiology, evolutionary genomics, pathogen movement across the agro-ecological interface and community level processes.

Registration opens on 14 March and closes on 31 May 2016. Please note that number of participants is limited and slots will be allocated on a first-come first-served basis. The registration fee is 250 euros (150 euros MSc and PhD students).

Conference website: http://allaine.it.helsinki.fi/?p=-244 Contact: krista.raveala@helsinki.fi and anna-liisa.laine@helsinki.fi

Confirmed speakers include Janis Antonovics (University of Virginia) Joy Bergelson (University of Chicago) Jeremy Burdon (CSIRO Canberra) Pascal Frey (INRA, University of Lorraine) Greg Gilbert (University of California, Santa Cruz) Eric Holub (University of Warwick) Michael Hood (Amherst College) Anna-Liisa Laine (University of Helsinki) Ales Lebeda (Palacky University, Olomouc) Marie-Laure Desprez-Loustau (INRA) Bruce McDonald (ETH Zurich) Erin Mordecai (Stanford University) Alison G. Power (Cornell University) Laura Rose (Heinrich-Heine-Universität) Michael Shaw (University of Reading) Samuel Soubeyrand (INRA) Eva Stukenbrock (Kiel University & MPI for Evolutionary Biology) Peter Thrall (CSIRO Canberra) John Walsh (University of Warwick)

– Professor Anna-Liisa Laine

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Anna-Liisa Laine <anna-liisa.laine@helsinki.fi>

IndianaU Galaxy Jun25-29 DeadlineMay20

This is just a reminder that the Galaxy Community Community Conference early registration (gcc2016.iu.edu/registration/), and poster and demo (gcc2016.iu.edu/abstracts/) deadlines are MAY 20.

A draft schedule of conference talks is also now available at gcc16.sched.org/type/Conference

Please pass this news along to anyone who might be interested in participating. The conference announcement is below

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2016 Galaxy Community Conference (GCC2016) gcc2016.iu.edu June 25 - 29, 2016 Indiana University Bloomington, Indiana United States

The 2016 Galaxy Community Conference (GCC2016, gcc2016.iu.edu) features two days of presentations, discussions, poster sessions, lightning talks, computer demos, keynotes, and birds-of-a-feather meetups, all about data-intensive biology and the tools that support it. Keynote speaker Yoav Gilad, a professor of human genetics at the University of Chicago, will kick-start the main conference with a discussion on the analysis of large gene regulatory data sets. Pre-conference events include data and coding hackathons, and two days of training in five concurrent tracks covering 26 topics.

GCC2016 will be held at Indiana University in Bloomington, Indiana, June 25-29, 2016. Since it started seven years ago, GCC has been a well-attended gathering of biologists, genome researchers, bioinformaticians, and others in data-intensive biomedical research around the world.

Galaxy is an open, web-based platform for data-intensive biomedical research and enables easy interactive analysis through the web on arbitrarily large data sets. The Galaxy framework is a major resource in achieving key research goals within the biological field. It provides next-generation sequencing (NGS) tools and workflows for short-read mapping, ChIP-seq, RNA-seq, metagenomics, variant analysis, visualization, and support for Galaxy in the cloud. There are hundreds of local installs, and over 80 publicly accessible servers around the world.

Abstract submission for posters and computer demonstrations closes May 20.

Early registration also ends May 20. Registration starts at less than $45/day for post-docs and students. Registering early assures you a place at the conference and also a spot in the training workshops you want to attend. You can also book conference housing when you register.

Thanks, and we hope to see you in Bloomington!

The GCC2016 Exec

Dave Clements <clements@galaxyproject.org>

KansasCity EcolGenomics Oct28-30

Save the dates; and plan to attend the 14^th Annual Ecological Genomics Symposium on October 28-30, 2016, in Kansas City at the Marriott Country Club Plaza. The symposium will convene on Friday evening and conclude on Sunday, October 30^th at noon. Registration will be opening soon!

FEATUED SPEAKERS:

- Hans Hofmann, University of Texas at Austin
- Kirsten Hofmockel, Iowa State University
- Robin Hopkins, Harvard University
- Christian Landry, Universite Laval
- Blake Matthews, Swiss Federal Institute of Freshwater Science and Technology
- Suzanne McGaugh, University of Minnesota
- Geoffrey Morris, Kansas State University
- Kenneth Olsen, Washington University in St. Louis
- Amy Toth, Iowa State University
- Jamie Walters, University of Kansas

POSTER SESSIONS: Poster sessions will be held on Friday evening and Saturday afternoon. Poster topics should be related the field of Ecological Genomics. A LIMITED NUMBER OF SUBMITTED POSTER ABSTRACTS WILL BE SELECTED FOR ORAL PRESENTATIONS.

Please share this announcement with colleagues and students who are interested in the field of Ecological Genomics.

Watch our website - http://ecogen.k-state.edu/-symposia/2016/2016.html - for more details.

Jennifer Rhodes <jenniferrhodes@ksu.edu>

LakeArrowhead California MicrobialGenomes Sep18-22

21st Annual International Meeting on Microbial Genomes - September 18-22, 2016 at Lake Arrowhead, CA

This conference is part of a yearly meeting initiated in 1991 to bring together genome sequencers, bioinformatics specialists, biologists, and geneticists, to forge interactions that would result in meaningful functional genomics. The goal of the meeting is to translate the influx of new genome sequencing information into useful biological studies.

The Lake Arrowhead 2016 meeting will have a major focus on microbial communities, the human microbiome, pathogens, and genome evolution. The field of genomics has reached the point where deriving the sequence of an organisms entire genome is now seen as a beginning rather than an endpoint. The sequence itself is a powerful tool to guide further studies to achieve an understanding of the organisms biology. This understanding requires either a detailed genetic analysis, or more rapid methods for developing functional genomics.

Therefore, this years meeting will cover micro-organisms for which extensive analyses exist, and those for which new biological and technical strategies are being developed. The focus on biodiversity, the human microbiome, pathogenic organisms, and bioenergetics adds special significance to this meeting. This meeting is designed to have a mix of invited presentations and poster sessions. The meeting will have approximately 150 participants. Since attendance is limited, please register now at http://www.lamg.info/ . Ashlee Earl <aearl@broadinstitute.org>

London EvolutionaryConflict Jun8

posting Reply-To: "Hill, Mark" <mark.hill.13@ucl.ac.uk>

London_evolutionary_conflict_June_8th

Dear colleagues,

Registration for 2016 CEE (Centre for Ecology & Evolution - https://www.ucl.ac.uk/cee) Summer Symposium 2016 entitled: "War and peace: the dynamics of evolutionary conflict" is open and there are still spaces remaining.

We are delighted to welcome 9 fantastic speakers from leading UK research institutions: Max Reuter - University College London Judith Mank - University College London Rebecca Dean - University College London Ted Morrow - University of Sussex Rhonda Snook - University of Sheffield Stu Wigby - University of Oxford Nina Wedell - University of Exeter Tom Price - University of Liverpool Susan Johnston - University of Edinburgh The speakers will cover 4 main themes:

- Intralocus and interlocus sexual conflicts - Intragenomic conflicts - Genomics of sexual dimorphism

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

As well as these 9 invited talks we also invite applications from PhD students to give 3 short talks during the conference, and present posters as well. The focussed nature of this conference provides an excellent opportunity for younger researchers to present and discuss their work with leaders of the field. Indeed, it also serves as a good practice run for much larger international conferences.

To register please visit the registration page linked below, and for more info visit the event website.

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

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

On behalf of the CEE Summer Symposium organisation committee.

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

Registration page: http://onlinestore.ucl.ac.uk/browse/extra_info.asp?compid=1&modid=2&deptid=128&catid%6&prodid=1400 Event website: http://ceesymposium2016.weebly.com/ Twitter updates: #ceess2016

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

Manchester MolGenomeEvolution Jun20

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

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

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

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

Hope to see you in June!

MaGE 2016 Organisers

dannagifford@gmail.com

Marseilles 20thEvolBiol Sep20-23 DeadlineJun30

The dead line for the 20th Evolutionary Biology Meeting at Marseilles (September 20-23 2016), is June 30 2016

The following subjects will be discussed:

Transposon and evolution ;

Evolutionary biology concepts and modeling;

Biodiversity and Systematics;

Comparative genomics ans post-genomics (at all taxomic levels);

Environment and biological evolution;

Origin of life and exobiology;

Non-adaptative versus adaptative evolution;

The "minor" phyla: their usefulness in evolutionary biology knowledge;

Convergent evolution;

Evolution of complex traits (Evo-Devo);

more info: http://sites.univ-provence.fr/evol-cgr/- or http://aeeb.fr/?page_id=333 or contact Marie-Helene.rome@univ-amu.fr

best regards Pierre Pontarotti

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

Paris HumanPolymorphisms Dec7-10 DeadlineMay27

CONFERENCE ANNOUNCEMENT - CALL FOR ABSTRACTS CLOSING IN TWO WEEKS

The 6th international conference of the series DNA POLYMORPHISMS IN HUMAN POPULATIONS

will be held in Paris (France), 7-10 December 2016 at the Musee de l'Homme.

The conference has a general topic: (Cross-Disciplinary) Human Population Genetics.

The conference will be hybrid, allying plenary sessions and four specialized workshops.

A *call for abstracts* is now open until the *27^th of May, 2016*.

Registrations will start in September.

You can submit abstracts concerning posters, talks in plenary sessions or talks in the frame of the workshops.

Multiple abstracts are accepted.

To submit, just send an abstract through the conference website.

There is room for one more workshop. If you want to organize it (scientifically), please send a proposal.

Conference website:

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

dnaparis2016@gmail.com

Franz MANNI <fmanni@mnhn.fr>

Paris Mutualism May30-31

Dear Evoldir community,

We would like to announce a fast-approaching symposium "EXPLOITATION AND CHEATING IN MUTUALISM: SYNTHESES, CHALLENGES, & NEW DIRECTIONS" that is open to the public in Paris, France, May 30 & 31st 2016. Our goal is to look ahead into the future of cheating: diverse perspectives are welcome!

The website is: https://cheatinginparis.wordpress.com/ and we have a form where you can sign-up to get updates before and (especially) after the meeting: http://-goo.gl/forms/8oLPE02L9Y This small symposium will be held May 30-31, 2016 at the Oceanographic Institute (Maison des Océans et de la Biodiversité). This meeting is part of the 2016 program of Pépinière interdisciplinaire CNRS "Eco-Evo-Devo" hosted at Paris-Sciences-Lettres Research University. The meeting is also supported by a grant from the Partner University Fund (France-America Cultural Exchange) to Ãcole Normale Supérieure and the University of Arizona.

Very best wishes, Judie Bronstein, Megan Frederickson, Maren Friesen

Maren L. Friesen Assistant Professor, Department of Plant Biology Program in Ecology, Evolutionary Biology and Behavior Michigan State University 612 Wilson Rd, East Lansing, MI USA 48824-6481 phone: +1 (323) 454-3023 || office: +1 (517) 844-6947 || fax: +1 (517) 353-1926 http://friesen.plantbiology.msu.edu/ maren.l.friesen@gmail.com

Roscoff EvolutionaryGenomicsSystemsBiol Oct10-14

Dear all,

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

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

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

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

Programme and confirmed invited speakers: Session EVOLUTIONARY SYSTEM BIOLOGY AND NETWORK EVOLUTION: Marie-Anne FELIX; Christian LANDRY; Ben LEHNER; Benjamin PRUD'HOMME; Sarah TEICHMAN; Trisha WITTKOPP Session EXPERIMENTAL EVOLUTION: Irene CHEN; Michael DESAI; Sinead COLLINS; Duncan GREIG; Caroline KNIBBE; Olivier TENAILLON Session GENOME EVOLUTION: Doris BACHTROG; Laurent DURET; Tatiana GIRAUD; Henrik KAESSMANN; Aoife Mc LYSAGHT; Maud TENAILLON Session THEORETICAL AND METHODOLOGICAL DEVELOPMENTS IN POPULATION GENOMICS: Mark BEAUMONT; Michael BLUM; Richard DURBIN; Asger HOBOLT; Renaud VITALIS Session ECOLOGICAL AND EVOLUTIONARY GENOMICS: Juliette DE MEAUX; Nicolas GALTIER; Dmitri PETROV; Molly PRZEWORSKI; Christian SCHLOTTERER; Xavier VEKEMANS

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

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UGoettingen Networks Oct12-13

Dear colleagues and friends, we are happy and proud to announce that the interdisciplinary symposium 'NETWORKS IN BIOLOGY' will take place October, 12th-13th 2016 at the Georg-August-University Göttingen, Germany.

Networks are a common theme in all biological processes. Since the organization and structure and thus the function of biological networks can rarely be studied directly, different specialized approaches such as mathematical modelling, empirical studies or the combination of those are being developed in various biological disciplines. The main aim of the 'NETWORKS IN BIOLOGY' symposium is to bring researchers of different research fields together to reveal commonalities of different biological networks and overlaps in the used methodology.

Invited Speakers: DAMIEN FARINE (MPI for Ornithology, Konstanz, Germany) MARC TIMME (MPI for Dynamics & Self-Organization, Göttingen, Germany) JOHANNES JAEGER (Konrad-Lorenz Institute, Vienna, Austria) STEFAN SCHEU (Department Animal Ecology, Göttingen, Germany) ARNE TRAULSEN (MPI for Evolutionary Biology, Plön, Germany) LAUREN BRENT (Centre Research Animal Behaviour, Uni Exeter, UK)

Please find the program as well as travel information here: http://goevol.uni-goettingen.de/index.php?id=meeting2016 The registration will be open until August, 5th 2016: http://goevol.uni-goettingen.de/index.php?id=addgroup0 Since the interdisciplinary nature of this meeting profits from extensive exchange among all participants, we encourage all of you to submit an abstract for a contributed oral or a poster presentation. Please specify your choice during the registration process.

This conference is organized by the GOEvol network. For more information about us, visit: http://goevol.uni-goettingen.de If you have any question, please feel free to contact us at any time via: goevolnetwork@gmail.com

We are looking forward to meeting you in Göttingen!

The GOEvol Team http://www.goevol.uni-goettingen.de/ goevolnetwork@gmail.com Twitter: @GOEEvolution Facebook: http://alturl.com/qom8b "Posnien, Nico" <Nico.Posnien@biologie.uni-goettingen.de>

UMontreal RECOMB Oct11-14

RECOMB COMPARATIVE GENOMICS 2016, SECOND CALL FOR PAPERS

http://www.crm.umontreal.ca/2016/Genomics16/index_e.php SCOPE The annual RECOMB Comparative Genomics Satellite Conference (RECOMB-CG) brings together leading researchers in the mathematical, computational and life sciences to discuss cutting edge research in comparative genomics, with an emphasis on computational approaches and the analysis of novel experimental results. The program will include keynote talks, contributed talks, and a poster session.

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

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

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

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

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

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

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

Authors will need to indicate upon submission their preferred publication option (BMC Genomics, BMC Bioinformatics, Bioinformatics). This preference should be stated in the Abstract section of the Easychair submission page.

However, the final decision about the journal for each paper will be taken by the RECOMB-CG PC chairs and communicated to the authors upon acceptance.

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

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

KEYNOTE SPEAKERS Guillaume Bourque (McGill University and Genome Quebec) Josee Dostie (McGill University) Edward Marcotte (University of Texas at Austin) Rebekah Rogers (University of California at Berkeley) Sohrab Shah (University of British Columbia and BC Cancer Agency) PROGRAM COMMITTEE Max Alekseyev (George Washington University) Lars Arvestad (Stockholm University) Anne Bergeron (UQAM) Marilia Braga (Bielefeld University) Cedric Chauve (Simon Fraser University, co-chair) Leonid Chindelevitch (Simon Fraser University) Miklos Csuros (University of Montreal) Ingo Ebersberger (Goethe University Frankfurt) Nadia El-Mabrouk (University of Montreal, co-chair)

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Vienna PopulationGenetics Oct31-Nov1

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

Bridging the gap between theoretical and empirical population genetics

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

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

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

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

Several invited speakers have already confirmed their attendance: Nick Barton (IST Austria, A) Alan Bergland (Univ. of Virginia, USA) Luis-Miguel Chevin (CEFE/CNRS, FR) Oscar Gaggiotti (Univ. of St. Andrews, UK) Anna-Sapfo Malaspinas (University of Bern, CH) Fernando Racimo (Univ. of California, Berkeley, USA) Wolfgang Stephan (LMU Munich, GER) Lev Yampolsky (East Tennessee State Univ., USA)

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

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

http://www.vetmeduni.ac.at/en/population-genetics/ https://twitter.com/PopGenVienna Julia Hosp <Julia.Hosp@vetmeduni.ac.at>

Villars sur Ollon Switzerland EvolNoncodingRNA Sept12-14

Symposium on Non-coding RNAs: Function and Evolution

Villars-sur-Ollon, Switzerland

September 12-14, 2016

The aim of the 2016 Villars Symposium on "Non-coding RNAs: function and evolution" is to provide an interdisciplinary look at the roles and evolution of non-coding RNAs in both prokaryotes and eukaryotes. An outstanding list of speakers will be discussing the latest advancement in the evolution and roles of various non-coding RNAs, including microRNAs, piRNAs, long-non-coding RNAs and circular RNAs, in both prokaryotes, animal and plants.

Registration deadline: June 15, 2016

http://www.cuso.ch/activity/?p=2392&uid=2703 Information: yves.poirier@unil.ch

Yves Poirier <Yves.Poirier@unil.ch>

GradStudentPositions

BielefeldU GalapagosSeaLions

Graduate position, Bielefeld University, Galapagos Sea lions

A PhD position to study individual behaviour and the ensuing consequences at the population level in Galapagos sea lions (Zalophus wollebaeki) is available in the Department of Animal Behaviour at Bielefeld University from August 1st 2016 or soon thereafter. The position is available for three years and is funded by Departmental funds with a gross salary of ca. 1300 €per month.

We seek a bright and highly motivated student who has a proven record of field experience studying wild animals. A very good Master degree or equivalent in a relevant topic (e.g. animal behaviour, behavioural ecology, population ecology, evolutionary ecology) is expected. The ideal candidate will be able to work both independently and as part of a multidisciplinary team, will have experience with both statistics and genetic techniques and, in addition to excellent spoken and written English, will be able to speak Spanish.

The study will take place on Caamaño, a small islet in the Galapagos archipelago. We have studied Galapagos sea lions there since 2003 and most sea lions are individually marked (www.uni- bielefeld.de/biologie/animalbehaviour/trillmich/sealions.html). Field seasons on Caamaño last from September-December and February-March each year. Caamaño is a small island and there are no facilities at all, so an ability to work in truly primitive conditions is essential.

The successful candidate will be based at the Department of Animal Behaviour at Bielefeld University (www.uni-bielefeld.de/biologie/animalbehaviour/-home.html) and will be supervised by Oliver Krüger, Fritz Trillmich and Joe Hoffman. The department is the oldest of its kind in Germany and currently hosts five principal investigators, five postdocs and fifteen PhD students. It offers a stimulating international environment and an excellent research infrastructure including a brand new molecular laboratory. The working language of the Department is English. Together with the Evolution and Animal Ecology research groups housed in the same building, there are some 50 scientists and PhD students from over ten different countries working on related topics in behaviour, ecology and evolution.

Bielefeld is a city of 325,000 inhabitants with all expected amenities and easy access to the Teutoburger Wald for hiking and other outdoor pursuits. It offers a high standard of living and is well connected to most major European cities.

To apply for the position, please provide: (i) a letter of motivation including a 1-2-page statement of your research experience; (ii) a CV including publication list; (iii) names and contact details of three referees willing to write confidential letters of recommendation. All materials should be emailed as a single PDF file to: oliver.krueger@uni-bielefeld.de.

The application deadline is June 5th 2016 and interviews will take place shortly thereafter. The preferred start date is August 1st 2016 but is flexible and will depend on the timeframe of the most qualified applicant. For further information, please see http://www.uni- bielefeld.de/biologie/animalbehaviour/home.html or contact Oliver Krüger via email (oliver.krueger@uni-bielefeld.de) with any informal inquiries.

The University of Bielefeld is an equal opportunity employer. We particularly welcome applications from women and handicapped people. Given equal suitability, qualifications and professional achievement, women and handicapped people will be given preference, unless particular circumstances apply.

Stephanie Kalberer

Stephanie Kalberer <stephanie.kalberer@uni-bielefeld.de>

CNRSFrance UrochordateRegeneration

A three years Ph.D. position is available at the Observatoire Océanologique de Villefranche-sur-Mer -LBDV (UPMC - Sorbonne Universités).

We are seeking a highly motivated student to join an international project, DEVODIVERSITY, funded by the French Agence Nationale de la Recherché (ANR) and the SÃ£o Paulo Research Foundation (FAPESP).

By using molecular and cell biology, NGS transcriptomic, genomic, and ecological approaches, a multidisciplinary consortium led by two teams, the Tiozzo Lab at the Villefranche-sur-Mer Developmental Biology Laboratory in France (CNRS-UPMC) and the Brown Lab at the Istituto de Biociências in Brazil (USP), will study the evolution of regeneration, asexual reproduction, and clonality in several species of ascidians (Urochordata), and examine how ecological factors affect distribution ranges, evolution of life cycles and developmental strategies.

The Ph.D. will be mainly based at the LBDV (Villefranche sur Mer, France) with the possibility to spend few months at the USP (Sao Paulo, Brazil).

The applicant should contact directly Dr. Stefano Tiozzo (tiozzo@obs-vlfr.fr) providing a letter of interest, a CV and the contact of three potential referees.

Start date will be October 2016.

For more details about the project please contact Dr. Stefano Tiozzo.

Stefano Tiozzo, PhD Regeneration Team

Sorbonne Universités, UPMC Univ Paris 06, CNRS, Laboratoire de Biologie du Développement de Villefranche-sur-mer (LBDV), 06230 Villefranche sur-mer, France

Ph:+33 4 93 76 39 78 Fax:+33 4 93 76 37 92 web: http://biodev.obs-vlfr.fr/ ˜ tiozzo/tiozzo-lab/ "tiozzo@obs-vlfr.fr" <tiozzo@obs-vlfr.fr>

Copenhagen ComputationalPalaeogenomicsMicrobiomics

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

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

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

Please direct any questions to

Tom Gilbert Professor of Palaeogenomics Centre for GeoGenetics Section for Evolutionary Genomics Natural History Museum of Denmark University of Copenhagen Øster Voldgade 5-7 1350 Copenhagen tgilbert@snm.ku.dk

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

ETHZurich HostParasiteCoevolution

dearcolleagues,

searchforthis PhD student is closing in 2 weeks. Thisis heads up forthe last minute applicants. pleasedo not hesitate to ask for more information.

bestwishes jukkajokela

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

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

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

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

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

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

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KielU ComputationalEvolutionaryGenomics

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

PhD position in computational evolutionary genomics

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

Research topic: Contribution of recombination and lateral DNA transfer to the genome evolution of pathogenic bacteria associated with lung disease. The advance in sequencing technologies now allows a deeper than ever sampling of the genomic space of pathogenic bacteria. This data can be utilized to study the evolutionary dynamics of pathogenic bacteria in the host. The project is planned to have two main objectives: (1) quantifying the relative impact of recombination and point mutations during the evolution of host-associated bacteria, and (2) characterizing the repertoire of mobile genetic elements (e.g., phages and plasmids) in lung associated strains and studying their role in lateral DNA transfer.

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

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

Research environment Kiel University (http://www.uni-kiel.de/) has a strong focus on life sciences (http://www.kls.uni-kiel.de/) and is maintaining an active bioinformatics network (http://www.bioinf.uni-kiel.de/). Together with the Max Planck institute for Evolutionary Biology in Plön, the Kiel area is a center for evolutionary research. The position is part of collaboration on “Evolutionary Medicine of the Lung” and will entail the opportunity for a close collaboration with experimental biologists. Everyday life in Kiel is strongly influenced by the large proportion of students and the vicinity to the Baltic Sea. The Kiel area is a center for aquatic sport including sailing, windsurfing and kiting.

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

Application deadline: July 10 2016 or until the position is filled. Interviews will take place as soon as applications are submitted. The position is available from August 2016 and the starting date is flexible.

The University strives for a high proportion of women in research and teaching. Applications from qualified female scientists are therefore particularly encouraged. Applications from candidates with migration background are welcome. Disabled persons will be given preference in filling vacancies within the existing legal provisions if equally qualified.

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

LMU Munich GeobiologyPaleobiology

Applications invited for the Master's program "Geobiology and Paleobiology" (MGAP) at the Ludwig-Maximilians-Universität (LMU) Munich (Germany) for EU students until 31 May 2016

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

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

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

Why come to Munich and study at LMU? The LMU Munich is the leading research university in Germany, with a more than 500-year-long tradition, and builds upon its success in the Excellence Initiative, a Germany-wide competition promoting top-level university research. Munich has also been repeatedly voted Germany's most livable city, only about one hour train ride away from the Alps, with a vibrant international student student community and many cultural attractions such as the (real) Oktoberfest.

More information about MGAP Visit the program's website: < http://www.mgap.geo.uni-muenchen.de > or < https://www.daad.de/deutschland/studienangebote/international-programs/en/?p=d&s=kr&id=4227 >

How to apply? Applications have to be submitted via our online submission portal: < https://www.efv.verwaltung.uni-muenchen.de/mageopal >

For the winter semester 2016-2017 (courses start mid-October) the application period ends on May 31, 2016!

"woerheide@lmu.de" <woerheide@lmu.de>

LundU MaternalEffectsEvolution

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

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

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

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

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

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

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

MonashU MarineEvolutionaryEcology

A PhD position is available to join Keyne Monro's research group in the School of Biological Sciences at Monash University, in Melbourne, Australia. We are looking for creative and motivated students who wish to do research on the evolutionary ecology of sessile marine organisms. Our general interests include adaptation to changing environments, life history evolution and quantitative genetics. Candidates with strong interests in evolutionary biology and ecology, a good grasp of experimental design and strong quantitative skills are encouraged to apply. Specific projects are flexible and will be developed in collaboration with the successful applicant.

The PhD stipend is fully-funded for 3 years with the possibility of 6 months extension. It includes all course fees plus ~$26,288 per annum tax-free. Additional expenses for research, coursework, and conference attendance will also be covered. Both Australian/NZ domestic and international students are eligible to apply.

Monash University is a member of the Group of Eight, a coalition of top Australian universities recognized for their excellence in research and teaching. The School of Biological Sciences is a dynamic unit with world-class strengths in evolutionary biology, ecology and genetics, and the nexus between these disciplines (http://monash.edu/science/about/schools/biological-sciences/). The University is located in Melbourne, one of the most liveable cities in the world and a cultural and recreational hub.

To apply, please send a CV, academic transcript, and cover letter with a brief outline of research interests to keyne.monro@monash.edu. Applicants must hold a Bachelor's or equivalent degree with first-class Honours, MSc or MPhil degree in a relevant field. Short-listed candidates will be contacted for further information and to organise interviews. Initial applications should be received before Tuesday 14th June, 2016.

Keyne Monro ARC Future Fellow School of Biological Sciences Monash University

Victoria 3800, Australia keyne.monro@monash.edu +61 3 9905-5608

"keyne.monro@monash.edu"
<keyne.monro@monash.edu>

NorthDakotaStateU ConservationGenetics

CONSERVATION GENETICS PH.D. GRADUATE ASSISTANTSHIP

NORTH DAKOTA STATE UNIVERSITY

Conservation Genetics Ph.D. Graduate Student Assistantship to conduct research on landscape genetics of northern leopard frogs. The project will analyze an existing dataset to evaluate gene flow among isolated wetlands, as means of assessing biotic connectedness. Additional sampling and possible development of additional molecular markers will be pursued as warranted. This project is funded through an EPA grant and is a collaborative project between Craig Stockwell (NDSU) and David Mushet (USGS Northern Prairie Wildlife Research Center). Field work will take place in the upper Great Plains.

Position to start as early as July 1, 2016

Requirements: BS or MS in ecology, aquatic ecology, fisheries biology, conservation biology or related field; Experience analyzing population genetics data, quantitative skills, and ability to work independently and as part of a research team.

Preferred: M.S., experience with amphibians, experience with landscape-genetic landscape-resistance models, field research experience.

Salary: $22,000/year + full tuition waiver

Contact: Craig Stockwell, Professor, Biological Sciences, 201 Stevens Hall, Box 6050, North Dakota State University, Fargo, ND 58108-6050; http://www.ndsu.edu/stockwell_lab/ e-mail: Craig.Stockwell@ndsu.edu

Please send application materials to Craig.Sockwell@ndsu.edu and include the following: 1) cover letter, 2) curriculum vitae / resume, 3) all college-level transcripts and 4) names and contact information for three references.

Craig Stockwell Professor Department of Biological Sciences Stevens 201, NDSU Box 6050 North Dakota State University Fargo, ND 58108-6050 Phone 701-231-8449 http://www.ndsu.edu/stockwell_lab/ Craig Stockwell <craig.stockwell@ndsu.edu>

OklahomaStateU PlantPhylogenomics

I am seeking a PhD student to join my lab at Oklahoma State University, Department of Plant Biology, Ecology & Evolution (http://plantbio.okstate.edu), to participate in a phylogenomic study of the milkweed genus, Asclepias, and develop an independent project of the student's choice, either with milkweeds or a different taxon. In particular, the student will employ genomic datasets to evaluate sources of gene tree discordance, such as introgression and incomplete lineage sorting, in order to obtain a robust species-level phylogeny for a rapidly diversifying clade. The ideal candidate will have a strong background in phylogenetics, population genetics, or bioinformatics. This is a collaborative project with Shannon Straub at Hobart & William Smith Colleges. The student will receive training in botanical fieldwork, molecular systematic techniques including next generation sequencing, and bioinformatics including phylogenomic analysis. Support with be through a combination of research and teaching assistantships.

Applicants should contact me directly with a statement of interest or questions about the position, and may apply online at http://gradcollege.okstate.edu/apply Review of applications will begin immediately for admission in August 2016 or January 2017.

MarkFishbein PlantBiology, Ecology & Evolution, Oklahoma State University http://plantbio.okstate.edu/people_research/Fishbein/ http://milkweedgenome.org mark.fishbein@okstate.edu

mark.fishbein@okstate.edu

QueenMaryU EvolBacterialSymbiosis

The evolution of bacterial symbiosis with eukaryotic hosts

Background

Over the past 2 billion years, symbiotic unions with microbes have resulted in key innovations that have largely shaped the evolution of complex organisms. Host-microbe symbioses have produced some of the most important evolutionary transitions, including the origins of the eukaryotic cell, the mitochondria and chloroplast. In addition to these ancient symbiotic events, beneficial microbes play important roles in many aspects of host biology, such as in development, defence against pathogens and in nutrition.

The aim of this PhD project is to use the symbiotic bacteria of aphids to understand how beneficial relationships with microbes form and what causes them to transition from being non-essential, or facultative symbioses, to permanent obligate associations where both symbiont and host depend on each other for survival. The research will combine experiments with modern molecular techniques to test fundamental questions on how bacterial symbioses evolve.

First we will explore the role of beneficial microbes in insect adaptation. We previously demonstrated that the facultative symbionts of the pea aphid have helped this insect colonize new ecological niches, such as food-plants and climatic regions. These same facultative symbionts are horizontally transferred between many different insect species and we currently do not know what insect species share symbionts between them and how communities of insects use symbionts as a resource when adapting to new environments. This project will specifically address: i) which insect species share symbiont isolates between them, and ii) test if hosts equally benefit from access to adaptations carried by different bacteria. This has important implications for the horizontal transfer of adaptive traits between host species that could allow for rapid evolution to new environments.

The second project will investigate the evolution of obligate symbioses. This is where symbionts transition from being non-essential to the host to becoming obligate permanent associations where the host and bacteria rely on each other for survival. We have identified several facultative symbionts that we hypothesize have transitioned to permanent obligate associations in many different aphid species. Using genomics and comparative methods we will test several key hypotheses on what conditions facilitate these evolutionary transitions and determine how symbiont and host genomes respond to the early stages of forming permanent symbiotic bonds. This project will reveal the ecological conditions that stabilize host-microbe symbioses and establish this system as a model for studying this important evolutionary process.

Based on outcomes of the above research the student will be encouraged to develop and test her or his own ideas and hypotheses on the evolution of bacterial symbiosis.

Skills required

- Past experience with either molecular biology and/or genomics is essential

- Strong understanding of evolutionary theory

- Experience cultivating plants and herbivorous insects is an asset

- Basic statistical knowledge

Funding Notes

The student will have a strong 1st class degree, or a MSc degree (or about to finish a MSc degree). The studentship will cover tuition fees and provide an annual tax-free maintenance allowance for 3 years at Research Councils UK rates (Â£16,054 in 2016/17). Interviews will take place at Queen Mary and will be announced in July.

References

Henry LM, Maiden MJC, Ferrari J and Godfray HCJ (2015). Insect life history and the evolution of bacterial mutualism. Ecology Letters 18:516-25.

Lukasik P, Guo H, van Asch M, Henry LM, Godfray HCJ and Ferrari J (2015) Horizontal transfer of beneficial symbionts is limited by host relatedness. Evolution 69:2757-2766.

Henry LM, Peccoud J, Simon J-C, Hadfield J, Maiden MC, Ferrari J and Godfray HCJ (2013). Horizontally transmitted symbionts and host colonization of ecological niches. Current Biology 23:1713-1717.

Ailsa HC McLean, Benjamin J Parker, Jan HrcÌek, Lee M Henry, H Charles J Godfray (In Press) Insect symbionts in food webs. Philosophical Transactions of the Royal Society of London.

Supervisor Information

Dr. Lee Henry

Senior Lecturer

Queen Mary University of London

Email: l.henry@qmul.ac.uk

Websites:

http://zoo-godfray.zoo.ox.ac.uk/people/dr-lee-henry/ http://www.falw.vu.nl/en/research/ecological-sciences/animal-ecology/st aff/henry-lee.aspx

Lee Henry Senior Lecturer Queen Mary University of London School of Biological and Chemical sciences Mile End Rd London E1 4NS

lee henry <leehenrym@gmail.com>

UAlabama InvertebrateSystematics

The newly formed Kocot lab in the Department of Biological Sciences at The University of Alabama seeks a highly motivated and enthusiastic PhD student interested in invertebrate systematics.

The successful applicant is expected to have an interest in combining traditional morphological approaches (e.g., scanning electron microscopy and histology) and cutting-edge molecular approaches (e.g., transcriptome and whole genome sequencing, anchored hybrid enrichment, and bioinformatics) in the study of the diversity and evolutionary history of invertebrates. Significant experience with at least some of the aforementioned approaches and a passion for invertebrate zoology are required.

Ongoing projects in the lab primarily seek to improve understanding of the phylogeny and evolutionary genomics of Mollusca. Research by the incumbent may leverage the PI's extensive collections of aplacophoran and scaphopod molluscs (among other taxa) and newly sequenced draft mollusc genomes to address questions ranging from alpha taxonomy to phylogeny to comparative and evolutionary genomics. I also welcome students with their own invertebrate systematics-related research questions, which may or may not involve molluscs, to pursue joining the lab.

Details on the University of Alabama Department of Biological Sciences graduate program can be found here: http://bsc.ua.edu/graduate-program/ More details on the Kocot lab can be found here: http://www.kocotlab.com Kevin M. Kocot Assistant Professor, Department of Biological Sciences Curator of Invertebrates, Alabama Museum of Natural History The University of Alabama < https://www.ua.edu/ > 307 Mary Harmon Bryant Hall, Tuscaloosa, AL 35487 office 205-348-4052 <tel:205-348-4052> kmkocot@ua.edu | http://bsc.ua.edu/ [Facebook] < https://www.facebook.com/kmkocot > [Twitter] < https://twitter.com/kmkocot >

kmkocot@ua.edu

UBritishColumbia LandscapeGenomics

I am looking for a PhD student to join my research team at The University of British Columbia (Okanagan Campus) that will broadly explore ways in which insights from landscape genomics can inform conservation unit designation and prioritization. This opportunity recently emerged and I am hoping to find a highly motivated graduate student to join the project in September 2016, although I will consider applicants that require a January 2017 start date. Individuals with a population genetics background and strong analytical skills are especially encouraged to apply. Expertise with RADseq and bioinformatics experience is desirable.

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

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

michael.russello@ubc.ca

UGeneva BotanicalSystematics

PhD position at the Botanical Garden of Geneva/University of Geneva, Switzerland Systematics, species delimitation and conservation in a Madagascar endemic genus of Sapotaceae

We are seeking a highly motivated candidate for a PhD project at the Plant Systematics and Biodiversity Laboratory, Conservatoire & Jardin botaniques de Genève and University of Geneva, Switzerland. The project is supported by the Swiss National Science Foundation for three years (2016-2019) and includes species delimitation, phylogenomic diversity and species distribution modelling and their application to the conservation of Capurodendron, an endemic genus of ca. 30 species of valuable trees in the family Sapotaceae.

The ideal candidates should be a botanist who enjoys working in the laboratory (targeted gene capture) as well as in the field (at least one trip scheduled to Madagascar), and should have good basic knowledge of taxonomy, phylogenetics, population genetics and bioinformatics. We are particularly interested in students that already have experience with Next Generation Sequencing techniques. Good writing skills in English is a must and familiarity with French is a plus.

Applications (motivation letter, CV, email address of 2/3 reference persons) should be sent before May 31st, 2016 to: Yamama Naciri (yamama.naciri@ville-ge.ch / yamama.naciri@unige.ch).

Project starting October 2016.

Yamama Naciri Conservatrice T. +41 22 418 5165 F. +41 22 418 5101 yamama.naciri@ville-ge.ch Conservatoire et Jardin botaniques (CJB) Département de la culture et du sport chemin de l'Impératrice 1 1292 Chambésy www.ville-geneve.ch

Yamama.Naciri@ville-ge.ch

UGothenburg Speciation

PhD studentship on speciation in Littorina

Applications are invited for a fully-funded, four year studentship based at the Sven Lovén Centre - Tjärnö, Department of Marine Science, University of Gothenburg and supervised by Roger Butlin and Kerstin Johannesson. You will be part of the Linnaeus Centre of Excellence in Marine Evolutionary Biology (CeMEB: http://cemeb.science.gu.se/) which provides a highly stimulating research environment. You will join a team studying contact zones between locally-adapted ecotypes of the coastal snail, Littorina saxatilis. We are interested in the genetic basis of local adaptation and the ways in which it might lead to the evolution of further barriers to gene flow, including the reinforcement of pre-zygotic barriers. You will be responsible for experiments aimed at measuring components of reproductive isolation and determining the roles of gene flow, selection and assortative mating in generating associations amongst traits and genes. There will be a mix of fieldwork, snail husbandry, behavioural and other phenotypic measurement and genetic analysis.

We seek a highly motivated evolutionary biologist with a Masters in a biological discipline, willingness to work in a team, flexibility in learning new tasks, and excellent data handling and communication skills. The expected start date is September 2016. The position will be based at the Sven Lovén Centre - Tjärnö, on the Swedish west coast, north of Gothenburg, but you will be expected to visit Sheffield, U.K., for research discussion and training and Spain for fieldwork. Applications should be submitted at http://www.gu.se/omuniversitetet/aktuellt/-ledigaanstallningar/?id=19144&Dnr=767272&Type=E and should include a curriculum vitae and a statement of research interests (maximum one A4 page). Further details are available online, from Roger Butlin (r.k.butlin@shef.ac.uk) or from Kerstin Johannesson (Kerstin.johannesson@marine.gu.se). The closing date for applications is Thursday 30 June 2016.

– Roger K Butlin

Professor of Evolutionary Biology Animal and Plant Sciences The University of Sheffield Western Bank Sheffield S10 2TN UK

r.k.butlin@shef.ac.uk

+44(0)114 2220097

“r.k.butlin@sheffield.ac.uk” <r.k.butlin@sheffield.ac.uk>

UMontpellier France MammalConvergentEvolution

Hi,

We invite applications for a PhD position funded by the European Research Council (ERC) for 36 months at the University of Montpellier (France).

The ConvergeAnt project: morphological convergence and dental simplification in ant-eating placentals.

Co-supervisors. Dr. Lionel Hautier (lionel.hautier@univ-montp2.fr) and Dr. Frédéric Delsuc (frederic.delsuc@univ-montp2.fr)

Research Unit. Institut des Sciences de l'Evolution de Montpellier, Université Montpellier, CNRS, IRD, EPHE.

Host Laboratory. Form and Genome Departments Teams “Paleontology” and “Phylogeny and Molecular Evolution”

Background. Despite its widespread occurrence across the tree of life, many questions still remain unanswered concerning the fascinating phenomenon of convergent evolution. Our objectives with this project are to provide new insights on a textbook example of adaptive evolutionary convergence represented by mammalian myrmecophagous species, in which similar phenotypes evolved independently in several lineages. The acquisition of a myrmecophagous diet almost exclusively composed of ants and/or termites has indeed evolved independently in five placental lineages with armadillos (Cingulata), anteaters (Pilosa), aardvarks (Tubulidentata), pangolins (Pholidota) and aardwolves (Carnivora). The skull of myrmecophages has attracted considerable attention because they show an extreme dental reduction, reaching its paroxysm in anteaters and pangolins that totally lack teeth. The selective constraints imposed by this highly specific diet have driven the convergent evolution of numerous morphological, anatomical, and physiological characters resulting in similar morphologies in these animals. We propose taking advantage of the unique set of convergently evolved characters associated with the ant-eating diet to investigate the developmental mechanisms underlying phenotypical adaptation.

Tasks. The main objectives of this PhD are to reveal the details of the morphological convergence towards skull elongation and dental reduction observed among independent myrmecophagous lineages. The successful candidate will address the following questions: (i) How is the skull variation shaped by convergent evolution towards myrmecophagy? (ii) Can we characterize the developmental origin of dental reduction? (iii) Can we identify a set of convergently evolved characters defining the myrmecophagous phenotype?

Candidate profile. Mandatory requirements include a master's degree in evolutionary biology, experience in working with vertebrate collections, a high degree of initiative and motivation, capacity for teamwork, good English skills, and good knowledge of statistics applied to geometric morphometrics. Skills and experience with CT scanning and 3D reconstruction techniques will be useful. Desirable is a background in vertebrate comparative anatomy and evolution, especially in mammals. Skills in myology would also be useful. The successful candidate will have a genuine interest to interact with molecular biologists. S/he should also be keen to travel to visit international museum collections for data collection during the course of the Ph.D.

Applications. Candidates must send electronically their application before June 20th, 2016 in the form of a single PDF file including a cover letter, a CV, eventually a copy of their Master thesis, and contact information (not supporting letters) of two persons of reference to lionel.hautier@univ-montp2.fr and frederic.delsuc@univ-montp2.fr. We will review applications upon receipt. Short-listed candidates will be interviewed the last week of June.

This PhD position forms part of the ConvergeAnt project funded by the European Research Council (ERC), which aims at investigating the complex interplay between the mammalian genome, phenome, and associated microbiome in a classical case of adaptive convergence driven by a highly specialized diet.

Starting date: 01/10/2016

Duration: 3 years

For further information, please contact Lionel Hautier (lionel.hautier@univ-montp2.fr) and/or Frédéric Delsuc (frederic.delsuc@univ-montp2.fr).

–

Frédéric DELSUC (Chargé de Recherche CNRS) Case Courier 64 Institut des Sciences de l'Evolution UMR5554-CNRS-IRD-EPHE Université de Montpellier Place Eugène Bataillon 34095 Montpellier Cedex 05 France Tel: (+33) 4 67 14 39 64 FAX: (+33) 4 67 14 36 10

"Frederic.Delsuc@univ-montp2.fr"
<Frederic.Delsuc@univ-montp2.fr>

UNewBrunswick EvolutionGreenAlgae

Graduate student position - Evolution in green algae; UNB, CANADA

A graduate student position is available in the laboratory of Aurora Nedelcu (http://www2.unb.ca/-vip/amnedelcu/), in the Department of Biology (http://www2.unb.ca/biology/) at the University of New Brunswick (http://www.unb.ca/), Fredericton, CANADA. Research in our laboratory is directed towards understanding general, fundamental issues in evolution - such as the evolution of multicellularity, development, cell differentiation, sex, programmed cell death, altruism. Our research is rooted in the framework of transitions in individuality and evolution of complexity (at a conceptual level), and of cellular responses to stress (at a more mechanistic level). The experimental model-system we are currently using is the green algal group, Volvocales (see our Volvocales Information Project; http://www.unbf.ca/vip). Highly motivated students with interests in either theoretical/genomics or experimental/molecular approaches, and previous research experience are encouraged to apply. Interested applicants should e-mail a CV, summary of research experience and interests, unofficial transcripts, and contact information for three referees to anedelcu@unb.ca. Applicants should meet the minimum requirements for acceptance in the Biology Department Graduate Program (see http://www2.unb.ca/biology/Degree_Info/-Graduate.html).

Aurora M. Nedelcu University of New Brunswick Department of Biology PO Box 4400 Fredericton, NB Canada E3B 5A3 phone: (506) 458-7463

Aurora Nedelcu <anedelcu@unb.ca>

UOslo EvolutinaryMycology

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

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

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

UPadova Italy PenguinAdaptationGenomics

PhD position in population genomics and adaptation in penguins

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

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

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

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

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

For further information on the application submission, please contact lorenzo.zane@unipd.it

Emiliano Trucchi <emi.trucchi@gmail.com>

UQueensland EvolutionaryTheory

The Engelstädter Lab at The University of Queensland, Brisbane, Australia, invites applications for a PhD position in theoretical evolutionary biology. We are interested in the evolution of sex and recombination, host-parasite coevolution and the evolution of drug resistance. Different PhD projects from these research areas and involving mathematical modelling are available or can be developed together with the successful candidate. For details about our research and recent publications, see our website at http://engelstaedterlab.org/ . We are looking for a highly motivated student with a background in evolutionary biology and/or strong quantitative skills. Applicants should possess a Bachelor's degree with Honours, Master of Science, MPhil or equivalent. Candidates with a non-biology degree (mathematics, physics, computer science) are also encouraged to apply. Good communication skills, scientific curiosity and enthusiasm for research in evolutionary biology are essential.

Acceptance for this PhD is contingent on a successful application for PhD funding. Overseas applications are encouraged, as the School of Biological Sciences at The University of Queensland has made available a number of competitive international PhD scholarships. The next deadline for international scholarships is on the 8th of July for programs starting in January 2017; applicants with at least one publication have particularly good chances of being accepted. International applicants can apply before conferal of their degree if the degree is conferred by the end of August. Students within Australia can apply for an Australian Postgraduate Award (APA). Note also that UK applicants need to have a Master's degree. For further information and conditions of employment, please visit http://www.biology.uq.edu.au/scholarships . Interested applicants should send a CV, academic transcript, and a brief outline of their research interests to j.engelstaedter@uq.edu.au.

— Dr Jan Engelstädter ARC Future Fellow & Senior Lecturer School of Biological Sciences The University of Queensland Brisbane QLD 4072 Australia

phone: +61 7 336 57959 fax: +61 7 336 51655 http://engelstaedterlab.org/? Jan Engelstaedter <j.engelstaedter@uq.edu.au>

UQueensland MammalianBrainEvoDevo

The Weisbecker Lab at the University of Queensland, Brisbane, Australia, is looking for a motivated PhD student to work on a project on the development and evolution of gross morphology and cellular infrastructure of the mammalian brain.

This projects targets an exciting intersection between large-scale brain evolution and the constraints governing brain development. In particular, this project will look at brain anatomy development using innovative soft-tissue micro-CT protocols, microscopic serial sectioning, and cell structure assessments using an in-lab flow cytometer. The work will be carried out mostly on marsupial brains, which are easy to access. Within this framework, the project allows a substantial degree of intellectual freedom , and can be conducted in a series of high-profile publications as chapters.

Good spoken and written English is essential. A good track record and interest in this study is sufficient, but knowledge in the following is an advantage: comparative/veterinary anatomy, histology, digital 3D visualization, antibody labelling, developmental biology of vertebrates, brain anatomy/structure.

Acceptance for this PhD is contingent on a successful application for PhD funding. OVERSEAS APPLICATIONS ARE ENCOURAGED, as the School of Biological Sciences at The University of Queensland has made available a number of competitive international PhD scholarships. The next deadline for international scholarships is in on July the 8ˆth for starting in January 2017; applicants with at least one publication have particularly good chances of being accepted. International applicants can apply before conferal of their degree if the degree is conferred by the end of August. Students within Australia can apply for an Australian Postgraduate Award (APA). Note also that UK applicants need to have a Master's degree. For further information and conditions of employment, please visit http://www.biology.uq.edu.au/scholarships . Please send expressions of interest, along with a CV, to Vera Weisbecker: v.weisbecker@uq.edu.au

Dr Vera Weisbecker

Lecturer University of Queensland School of Biological Sciences Goddard Building 8 St. Lucia 4072 Australia

Ph.: +61 7 336 57071

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www.weisbeckerlab.com.au Vera Weisbecker <v.weisbecker@uq.edu.au>

UTexas Tyler LabManager MSstudents AntSymbiosis

The Ant Symbiosis Laboratory at the University of Texas at Tyler is seeking a laboratory manager and graduate students (MS level) to work on a new NSF-funded project (IOS-1552822, http://nsf.gov/awardsearch/showAward?AWD_ID=1552822&HistoricalAwards=false) on ant-fungal interactions in North American Trachymyrmex ants.

* Laboratory Manager Position in Symbiosis Research*

Responsibilities: oversee laboratory operations; assist with experiments, data collection, data management, collection of colonies from nearby and remote field sites and maintenance of colonies in the laboratory. This is a full-time benefits-eligible position. Salary would be commensurate with experience.

Qualifications: BS or MS in biology, entomology or related field, preferably with experience and/or interest in ants, molecular and microbial ecology, mycology, experimentation and bioinformatics.

Start Date: Preferably 15 January 2017 but negotiable. Appointment would be for one year initially, which may be renewed for up to two additional years.

Application Deadline: Please send letter of interest, names of 2-3 individuals who could write a letter of reference and CV to Jon Seal, University of Texas at Tyler (jseal@uttyler.edu) by September 1, 2016.

MS Positions in Symbiosis Research

Research focus: 1-2 highly motivated graduate students (MS-level) are sought to conduct research on the biology of ants and their symbionts. We employ a variety of methods including descriptive and experimental approaches, along with biochemical, physiological, bioinformatics, molecular and microbial techniques. Projects could range from phylogeography/population genetics to functional ecology and experimental studies.

There is considerable flexibility for projects within this broad theme.

Preferred applicants will have earned a Bachelor's degree and exhibit equal enthusiasm for field-based work, experimentation, molecular ecology and bioinformatics.

Support: Graduate Students will be supported by a combination of Research and Teaching Assistantships. Tuition remission scholarships are available on a competitive basis. Accepted students can expect support for two years.

Teaching assistants in our program typically teach introductory biology or upper division laboratory courses (e.g., ecology or entomology).

Qualifications: Bachelor's degree and qualifying GPA and GRE scores. It is useful to have prior research experience, but not necessary. Most important is identifying your own research interests that are consistent with the ongoing research in our lab. Further information regarding our graduate program and admission requirements can be found at

http://www.uttyler.edu/biology/graduate/master-science-degree.php Start Date: Flexible but must coincide with academic calendar: January 2017 (Winter semester), May (2017) (Summer term) or Fall 2017 (fall semester).

Application deadline: September 1st, 2016; 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 jseal@uttyler.edu by the deadline to be considered for this position.

Part of the University of Texas System, UT Tyler is located in northeastern Texas at the ecotone between two state and federally designated ecoregions, southeastern pine forests (the âWoods') and post oak savannas. As a result, the area contains a mixture of eastern, western and southern species. We have a number of field sites established nearby and many others within driving distance in central and southeastern Texas. Additional field sites are in Florida and Arizona.

Tyler has a regional airport, and is approximately a 90 minute drive to either Dallas, Texas or Shreveport, Louisiana.

Departmental strengths include bioinformatics, microbial and molecular ecology, aquatic ecology, conservation biology, genomics and landscape ecology. Please see full departmental requirements and details at:http:/-/www.uttyler.edu/biology/ .

Dr. Jon Seal

Department of Biology

3900 University Blvd.

Tyler, TX 75799

Office: (903)565-7126

Lab: (903)565-7151

Email: jseal@uttyler.edu

Website:

http://www.uttyler.edu/biology/research/seal/-index.php Jon Seal <jon.seal@utexas.edu>

UToulouse PollinationNetwork

Hi,

We invite applications for a PhD position funded by the federal university of Toulouse and the region Languedoc-Roussillon/Midi-Pyrénées for 36 months at the University of Toulouse (France). To apply send before June 20th, 2016a cover letter, a CV, and contact information (not supporting letters) of two persons of reference who are in a position to judge your potential and your aptitude to conduct research and to exceed expectations of the post-graduate program to André Pornon (andre.pornon@univ-tlse3.fr). We will review applications upon receipt.

PhD title: Analysis of pollination network through environmental genomics approaches (GENOPOLI) Co-supervisors: Dr. Andre Pornon (EDB)/ Dr. Didier Galop (GEODE) Host Laboratory: Laboratoire Evolution et Diversite Biologique EDB - Universite Paul Sabatier, Toulouse and Laboratoire Geographie de l'Environnement GEODE - Universite Toulouse Jean Jaures

Summary: Insect pollinators are currently facing a strong decline that threatens agricultural productions, ecosystem functioning and overall biodiversity. Its major causes are well understood but its consequences remain largely unknown, mainly because of the high complexity of the plant-pollination interaction networks and of several methodological difficulties. The aim of this project is to use NGS techniques and metabarcoding tools to study plant pollinator interactions in several more or less anthropized environments. The objectives are: - To describe in details (in terms of quantity and composition) the pollen loads on the insects and on stigmas in order to infer the sign, the strength and the symmetry of the pollination links in both the plant and the insect communities (direct interactions) but also between the different plant species (indirect interactions) within the community, by using metabarcoding and NGS; - To reconstruct and to model pollination interactions at different levels (infra-specific, functional groups) in order to understand how they vary in structure and in functioning.

This study was started in the EDB lab in 2013/2014 (POLLIBAR, Labex TULIP-Toulouse/: /ANR-10-LABX41; ERESA, APEGE 2013-2014: DJ/ST/IP/2013/D-112).

*Candidate * *Background, knowledge, skills://*MSc or MRes with good academic*//*records; good skills and qualifications in molecular biology and bioinformatics *//**Personal skills://*high naturalist motivation in flora and fauna; interest in combining field and lab work; well organized; very good communication skills. Good level in English (spoken, written).

Starting date: 01/10/2016 Duration: 3 years

For further information, please contact Andre Pornon (andre.pornon@univ-tlse3.fr)

– *Nathalie ESCARAVAGE* ***Enseignant-Chercheur*

UNIVERSITÃ TOULOUSE III - Paul Sabatier Laboratoire Evolution & Diversite Biologique CNRS UMR 5174 Batiment 4R1 118 route de Narbonne 31062 Toulouse cedex 09

Tél. +33 5 61 55 67 52

*www.edb.ups-tlse.fr * < http://www.univ-tlse3.fr >

Nathalie Escaravage <nathalie.escaravage@univ-tlse3.fr>

UTours BarcodingForestBiodiversity

*PhD studentship on the ecological impact of climate-induced tree diebacks on highland forest biodiversity** ***

Applications are invited for a fully funded; three-year studentship based at the Institut de Recherche sur la Biologie de l'Insecte (IRBI), at University François Rabelais, Tours (France) and co-supervised by Elisabeth Herniou and Carlos Lopez-Vaamonde. You will be part of an international project (CLIMTREE) funded by the French National Research Agency (ANR) and BELMONT FORUM. https://www.belmontforum.org/-funded-projects/climtree-ecological-and-socioeconomic-impacts-climate-induced-tree-diebacks-highland This international project involving French, German, Italian and Chinese teams aims to investigate the ecological and socioeconomic impacts of climate-induced forest die-offs in several mountain ranges. The student will visit other labs for training and will benefit from interaction with three other newly recruited PhD students within the consortium.

Background Climate change affects mountain forests by increasing the intensity and frequency of disturbances such as drought, insect and pathogen outbreaks, fire, wind and ice storms. As a result widespread tree mortality has been reported in recent decades. Most mountain forests support a rich community of organisms, so the loss or replacement of any tree species implies a change in species composition and a financial and economic cost. Understanding which species are lost and which are resilient to these environmental changes is crucial in order to take reasoned management decisions for mitigation.

Objectives To study the impact of climate change and forest management (Thorn et al 2014) on the biodiversity of highland forests, you will quantify changes in taxonomic, phylogenetic and functional structure of communities of a wide range of invertebrates (with a focus on saproxylic beetles, Rougerie et 2015) and fungi along gradients of tree dieback and replacement of Silver fir (Abies alba) in the French Pyrenees, using cutting-edge molecular and bioinformatics techniques (Ji et al 2013; Tang et al 2015). The student will develop a monitoring pipeline that uses high-throughput DNA sequencing and conducts taxonomic assignment against reference DNA barcode libraries to streamline species identification. The metabarcoding pipeline will generate "operational taxonomic units" (OTUs), which will be used to describe community richness and structure. This approach will allow the processing of large numbers of specimens and permit an efficient sampling of communities of a wide range of taxa across a large geographical scale.

Ji, Y. et al. (2013) Reliable, verifiable and efficient monitoring of biodiversity via metabarcoding. Ecology letters 16, 1245J1257, doi:10.1111/ele.12162 . Rougerie, R. et al. (2015) PASSIFOR: A reference library of DNA barcodes for French saproxylic beetles (Insecta, Coleoptera). Biodiversity Data Journal 3, e4078, doi:10.3897/BDJ.3.e4078. Tang, M. et al. (2015) High throughput monitoring of wild bee diversity and abundance via mitogenomics. Methods in Ecology and Evolution 1 doi: 10.1093/nar/gku917. Thorn, S. et al. (2014) New insights into the consequences of post windthrow salvage logging revealed by functional structure of saproxylic beetles assemblages. PloS one 9, e101757 .

Candidate Profile We seek a highly motivated biologist with a Masters in biological sciences, willingness to work in a team, flexibility in learning new tasks, excellent data handling and communication skills. Good command of English both spoken and written is required for communication within the international CLIMTREE consortium. An interest and some experience in next generation sequencing, including sample preparation and data analyses, such as required for meta/DNA-barcoding would be advantageous. The studentship is open to all nationalities. * **Conditions of employment * We offer a fully funded, three-year studentship of 1700 euros/month (gross salary, health insurance included). For further information: http://www.phdinfrance.net/affpage.php?name=faq http://www.phdportal.eu/countries/10/france.html *How to apply* Please send a Curriculum Vitae, contact names and emails for two reference letters, and a cover letter describing your background, interest as well as a description of previous research experience (such as bachelor/master research projects) via email to Carlos Lopez-Vaamonde Email: Carlos.lopez-vaamonde@orleans.inra.fr with ≪ CLIMTREE PhD Application ≫ as subject. The closing date for applications is Thursday the 30th June 2016.

– Carlos Lopez-Vaamonde, PhD Research Scientist

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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

UZurich ComputEvolutionaryBiol

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

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

To be considered, please send a single (!) PDF file merged from the following parts to annette.schmid@ieu.uzh.ch: CV including publication list, academic transcripts, a statement of research interests not exceeding three pages, and three academic references. Please include the word "PEVOLPHD16" in the subject line. Applications will be considered until June 3, 2016, or until the position is filled, whichever comes first. The position is available from the fall of 2016.

Annette Schmid

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

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

Vienna PopulationGenetics

Reminder: Call for PhD applications at the Vienna Graduate School of Population Genetics is now open: Apply by May 22, 2016

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

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

Topics include:

§Convergent and adaptive evolution during ecotype formation

§Wolbachia infection dynamics in evolving Drosophila populations

§Optimizing novel, NGS-based, approaches for dissecting the genetic basis of complex traits

§Evolution of the transposable element landscape in Drosophila

§Inferring evolutionary trajectories from time series data

§Functional characterization of beneficial alleles in Drosophila

§Modified evolve and re-sequence design

§Statistical inference for experimental evolution using pooled NGS data

Only complete applications (application form, CV, motivation letter, university certificates, indication of the two preferred topics in a single pdf) received by May 22, 2016 will be considered. Two letters of recommendation need to be sent directly by the referees.

Monthly salary of a successful candidate will be according to the regulations of the Austrian Science Fund FWF. All information about the about available topics, the training program and the application procedure can be found at www.popgen-vienna.at Julia Hosp <julia.hosp@gmail.com>

Jobs

BangorU ResAssist SpeciesMonitoring

Part-time Research Project Support Officer (0.4 FTE)

Invasive species monitoring - mobile phone application - tilapia cichlid fishes

The School of Biological Sciences seeks a Research Project Support Officer to work within the Turner cichlid research group. The role is a fixed-term (6 month), part-time (40% FTE) post, working on an ESRC funded project to develop a mobile phone application for the monitoring and tracking of introduced cichlid fishes in Tanzania.

Duties will include oversight of an online content management system, monitoring the output and data collection from the mobile app, and liaison with external project partners.

Candidates should be educated to degree standard (or equivalent) and have previous experience working on collaborative projects, and data input/management.

The successful candidate will be expected to commence in August 2016.

Informal enquiries may be sent to Antonia Ford, email a.ford@bangor.ac.uk.

Applications will only be accepted via the on-line recruitment website, jobs.bangor.ac.uk. However, in cases of access issues due to disability, paper application forms are available by telephoning 01248 383865.

Committed To Equal Opportunities

Job Number: BU01158 Starting Salary: 25,023 (Grade 6) p.a. pro rata Contract Duration: 6 months Responsible to: Prof. G. Turner Closing Date: 01-06-2016

For a full project and job description, please visit the recruitment website: jobs.bangor.ac.uk.

Rhif Elusen Gofrestredig 1141565 - Registered Charity No. 1141565

CaliforniaDeptFoodAgriculture PlantTaxonomist

TheCalifornia Department of Food and Agriculture (CDFA), Plant Pest Diagnostics Branch (PPD) (https://www.cdfa.ca.gov/plant/ppd/) is seeking a full time Senior Plant Taxonomist to fill the vacancy left by the retirement of Dr. Fred Hrusa. A general description of the job can be seen at http://www.calhr.ca.gov/state-hr-professionals/pages/0486.aspx. The online Examination posting, with links, is at https://jobs.ca.gov/Public/Bulletin.aspx?examCD=6FA17 . THEOFFICIAL BULLETIN WHICH INDICATES THE INSTRUCTIONS FOR FILING THIS EXAMINATION is found here: https://jobs.ca.gov/JOBSGEN/6FA17.PDF (note, this document also contains the Supplemental Examination). Note, the final filing date for applications in June 17, 2016.

Pleasecontact me (Dr. Steve Gaimari: stephen.gaimari@cdfa.ca.gov) if you have any questions about the position. Do NOT send application materials to me!

Forquestions about the examination, please contact Darlene Hayashi (Examinations Unit, darlene.hayashi@cdfa.ca.gov; (916)403-6584).

The“application package” consists of two items: 1)the Application Form (STD678 - https://jobs.ca.gov/pdf/std678.pdf) 2)the Supplemental Exam (https://jobs.ca.gov/JOBSGEN/6FA17.PDF)

Theapplication package must be completely filled out and delivered to CDFA in one of the following ways:

Bymail/In person: CaliforniaDepartment of Food and Agriculture ExaminationUnit, Attn: Darlene Hayashi 1220N Street, Room 242 Sacramento,CA 95814 (916)403-6584

Bye-mail: exams@cdfa.ca.gov

NOTE:Facsimiles (FAX) applications will not be accepted under any circumstances.

THEFINAL FILING DATE FOR APPLICATIONS IS FRIDAY, JUNE 17, 2016! So time is short!

Dr.Stephen D. Gaimari EnvironmentalProgram Manager I (Entomology & Botany)

PlantPest Diagnostics Center CaliforniaDepartment of Food and Agriculture 3294Meadowview Road Sacramento,CA 95832, USA

Tel.916-262-1131, Fax 916-262-1190 E-mail stephen.gaimari@cdfa.ca.gov http://www.cdfa.ca.gov/-plant/ppd/staff/sgaimari.html 20May 2016

diggle@colorado.edu

Dupont Summer Internships

DuPont Industrial Biosciences has several summer internship positions for undergrads available. We are looking for driven and creative interns to conduct research in the following areas:

§Enzyme immobilization supports for select enzyme systems.

§New tools for microbial strain and genome engineering using state-of-the-art methodologies.

§Rapid high throughput assays to screen microorganisms from various sources for enzymatic activities of interest.

§High throughput combinatorial approaches to the formulation of growth media in support of microbial enrichments, strain isolations and growth optimization.

§Meta-transcriptomics for the discovery of new enzymes.

§Strain adaptation techniques in defined chemostat environments for microbial strain development.

The internships are based at the Experimental Station R&D Center in Wilmington, DE.

If interested, apply fast!

For more information and to apply, go to:

http://careers.dupont.com/jobsearch/job-details/-industrial-biosciences-summer-internship/008549W-10/ Gerda Saxer Gerda.Saxer@dupont.com

"Gerda.Saxer@dupont.com" <Gerda.Saxer@dupont.com> "Gerda.Saxer@dupont.com" <Gerda.Saxer@dupont.com>

FloridaAtlanticU ResTech MarineGenomics

Florida Atlantic University 's (FAU) Harbor Branch Oceanographic Institute Position: Senior Research Technician #01005164

Job Description : Under general supervision assists Principal Investigator on research projects that involve laboratory (molecular genetics) and field work.

* Applies standard molecular biology techniques to the study of marine organisms, including cloning, DNA and RNA preparation, PCR, qPCR, and DNA sequencing. * Participates in the development of new OMICs techniques for HBOI - FAU, including high throughput SNP genotyping and transcriptome profiling. * Participates in the development of methylation next generation sequencing (NGS) methods in the study of epigenetics. * Assists with running and maintenance of the Molecular Genetics Laboratory at HBOI - FAU * Assists in training of volunteers, interns and student RAs * Conducts research on a range of marine species, including project design and execution, data analysis and publication of research findings.

MINIMUM REQUIREMENTS:

1. Master's degree in Science or closely related field and six months experience in molecular genetics, or B.Sc. or B.A. degree in Science or a closely related field and 30 months of applicable laboratory or research e xperience in molecular genetics required. 2. Experience working in molecular ecology lab with cloning, PCR and automated sequence and fragment analysis systems required. 3. Experience in RNA extraction, cDNA preparation and qPCR preferred. 4. Experience with methylation sequencing preferred. 5. Experience in data analysis and writeup preferred. 6. Must be able to work flexible hours, including weekend work. 7. Must be able to communicate effectively with all levels of employees and managers.

Salary range: $35,000 - $ 41,000 per annum

Term: Grant funded, current end date 12/31/16, eligible but not guaranteed for additional funding

Special Instructions to Applicant:

* This position is location at FAU's Harbor Branch in Fort Pierce Florida. * Final candidate will be required to have official, sealed transcripts and original NACES evaluation, if applicable, sent from their educational institution to Human Resources prior to the start of employment. * Successful completion of a background and motor vehicle check is required for the selected candidate prior to the start date. * Applicants must apply electronically on the website https://jobs.fau.edu by completing Support Personnel (SP) and Temporary Positions Application, position number 01005164. * Florida Atlantic University is an equal opportunity/affirmative action/equal access institution and all qualified applicants will receive consideration for employment without regard to race, color, religion, sex, sexual orientation, gender identity, national origin, disability status, protected veterans status or any other characteristic protected by law. Individuals with disabilities requiring accommodation, please call 561 - 297 - 3057. 711. * FAU is committed to the principles of engaged teaching, research and service, and reflects this commitment as a key Platform in its 2015 - 2025 Strategic Plan. All persons aspiring to achieve excellence in the practice of these principles are encouraged to apply.

"jbrusini@fau.edu" <jbrusini@fau.edu>

FloridaStateU JavaProgrammer

We have NSF funding to hire a Java programmer to develop image analysis and measurement software. Experience in Java and image analysis desired. The goal is image segmentation and object recognition of specific insect body parts as a precursor to morphometric analysis. Later development will generalize the application to accommodate images of a variety of objects. A first generation application is online at http://bio.fsu.edu/~dhoule/wings.html. To apply, please contact David Houle <dhoule@bio.fsu.edu>.

– David Houle Phone: 850-645-0388 FAX: 850-645-8447 http://bio.fsu.edu/~dhoule/ Department of Biological Science Florida State University 319 Stadium Drive Tallahassee, FL 32306-4295

"David C. Houle" <dhoule@bio.fsu.edu>

GeorgiaInstTech TeachingEvolution

BIOLOGY TEACHING FACULTY POSITIONS

The *Georgia Institute of Technology* is one of the top ranked institutions in the country and ranks as one of the best places to work. *The School of Biology in the College of Sciences* invites applications for two full-time, non-tenure-track *Academic Professional faculty positions* beginning August 2016. Candidates must have a Ph.D. in a biological science.

(1) Academic Professional: Director of Introductory Biology Laboratories

Ideal candidates should have experience teaching undergraduate biology courses and an interest in innovative undergraduate laboratory instruction. This position will require teaching, laboratory curriculum development, and supervision and professional development of teaching assistants in biology laboratory courses. Preferred candidates will have expertise in one or more of the following subject areas: cell & molecular biology, genetics, ecology, or evolution. In addition to overseeing the introductory biology labs, the successful candidate may also teach in core biology courses in his/her area of expertise, depending on curricular needs.

(2) Academic Professional: Teaching Faculty and Academic Advisor

Ideal candidates should have experience teaching undergraduate biology courses and an interest in innovative undergraduate instruction. This position requires expertise in some combination of ecology, evolution, population biology, organismal biology, cell & molecular biology, statistics, anatomy, or physiology. In addition to teaching 5 biology courses per year and contributing to curriculum development, the successful candidate will also be responsible for academic advising of undergraduate biology majors, as a member of a team of academic advisors in the School of Biology. The primary teaching responsibilities in this position will be in freshman and sophomore level courses. The successful candidate may also teach upper-level biology and TA development courses depending on his/her expertise and on curricular needs.

Salary and rank for both positions will be commensurate with experience and qualifications.These positions are renewable, 12-month, non-tenure-track appointments. Candidates should submit their application as a single

PDF that contains: a letter of application designating the position(s) of interest, a statement of teaching philosophy, summary of teaching experiences, sample course syllabus, a curriculum vitae, and names and contact information of three professional references. Submit applications at http://searches.biology.gatech.edu. An applicant interested in both positions need only submit a single application. Review of applications will begin May 18th, 2016 and continue until the positions are filled. Send questions to Dr. Chrissy Spencer, Academic Professional Search Chair, chrissy.spencer@biology.gatech.edu <mailto:chrissy.spencer@biology.gatech.edu>. Georgia Tech is an affirmative action, equal opportunity employer and requires compliance with the Immigration Control and Reform Act of 1986.

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Chrissy Spencer, PhD School of Biology Georgia Institute of Technology 950 Atlantic Drive Atlanta, GA 30332

office 404 385 0539 fax 404 894 0519 chrissy.spencer@biology.gatech.edu

Chrissy Spencer <chrissy.spencer@biology.gatech.edu>

Glasgow Tech FishEvoDevo

We are seeking a technician to start the summer of 2016, as part of a project entitled 'The predictability and limits of evolution in response to increased temperature: insights from a natural 'experiment", funded by a Highlight Topic Grant from the Natural Environment Research Council (NERC) and led by Kevin J. Parsons, Neil B. Metcalfe, Jan Lindström and Shaun S. Killen. The wider focus of the lab involves an emerging eco-evo-devo view with this project examining both intra and intergenerational changes (developmental, physiological, genetic and epigenetic) that occur in in fish in response to warmer environments. Specifically we will use freshwater populations of stickleback fish inhabiting geothermally warmed habitats as a study system.

The holder of this research technician position will be a key player in the experimental work on fish, and will be responsible for running a stickleback breeding programme (in which adults from different wild populations of sticklebacks will be used as the parents for our lab populations), providing in-depth technical expertise on experimental protocols, arranging logistics, helping to run the experiments, and collating the resulting data. The person will be part of a team funded by this NERC grant, and so will work closely with a fish biology postdoctoral scientist and animal care technicians, as well as a second postdoctoral scientist that will focus on molecular analyses.

You will have experience with the rearing and handling of fish in a laboratory setting and have the ability to set up, conduct, and record data from various assays. You would also oversee and monitor the project's consumables budget in conjunction with the Principal Investigator, and coordinate the purchasing of materials required for the experiments.

Previous experience as a technician would be desirable. Some experience with the measuring of metabolic rates in fish, or lab experience with molecular assays such as WISH, immunohistochemistry, or general histology is also desirable but not necessary.

This fulltime position is funded for 40 months. Closing date for applications is May 30th, 2016

For further information and formal application search reference # 013153 at:

http://www.gla.ac.uk/about/jobs/vacancies/ For informal inquiries contact:

Kevin.Parsons@glasgow.ac.uk

Dr. Kevin Parsons Lecturer, Institute of Biodiversity, Animal Health, and Comparative Medicine University of Glasgow

http://www.gla.ac.uk/researchinstitutes/-bahcm/staff/kevinparsons/ Kevin Parsons <Kevin.Parsons@glasgow.ac.uk>

InvernessCollege BiodiversityGenomics

University of the Highlands and Islands / Inverness College Rivers and Lochs Institute 3 year Fixed Term contract; Full-time (35 hours per week) Salary Range H: £31,011 - £35,787 Start date: 1 September 2016 Closing date Sunday 26 June 2016

The Rivers and Lochs Institute, Inverness College UHI has an opening for a Researcher in Molecular Genomics. The RLI is filling an important niche in the freshwater biodiversity and fisheries research, education and management support sector in Scotland and has an existing international reputation for research excellence.

The position will be based at Inverness College UHI on the new Inverness Campus, and will focus on research projects utilising the Institute's recently opened state-of-the-art Biodiversity Management Applied Genomics (BioMAG) facility. The laboratory is equipped for both the development of molecular genomic methodologies, supported by NexGen sequencing capacity, and for high-throughput genetic typing in support of field studies of molecular biodiversity. The successful candidate will take day-to-day charge of the facility and be part of a small dynamic team of researchers delivering a programme of fundamental and applied research in molecular genomic methods and applying these to the management of aquatic biodiversity. The focus for the new position will be to lead in bringing on board new molecular tools as part of research projects using eDNA, DNA barcoding, metabarcoding and population genetics, collaborating on the development of field studies, and using these methods to screen samples. The position is, in the first instance, for a term of 3 years, with work focused on a secured EU Horizon2020 project, but will also involve advising on new project applications as part of internal and external collaborations, with the objective to secure further funding to extend the position. The successful candidate will have a record of publication in the field of molecular genomics, experience in molecular genetic methodologies and the use of molecular genomics platforms, ideally, including experience in the NexGen Sequencing.

Informal enquiries about this opportunity may be made to Professor Eric Verspoor (Eric.Verspoor.ic@uhi.ac.uk) or Dr Melanie Smith (Melanie.Smith.ic@uhi.ac.uk).

Visit http://www.inverness.uhi.ac.uk/staff/vacancies for the full job description and to apply.

Please note the post holder will be subject to a PVG Disclosure Scotland and other background checks.

Joanne Russell <Joanne.Russell.ic@uhi.ac.uk>

MichiganStateU LabTech PlantEvolBiol

Michigan State University Lab Tech: Plant Evolutionary Ecology

The Schemske lab (Department of Plant Biology) is seeking a full time lab technician for a research project investigating the genetic basis of adaptation in. plants. Primary duties will include some combination of the following: Plant propagation, maintenance, and phenotypic data collection associated with conducting large-scale greenhouse and growth chamber experiments; supervision of several undergraduate assistants; high throughput DNA extractions; genotyping samples with SNP assays, CAPs markers, and RADseq.

Experience with molecular techniques, DNA extraction, and genotyping is preferred. Applicants with prior lab managerial experience and experience working with the model plant Arabidopsis thaliana are strongly encouraged to apply.

This is a temporary full time position for 9 months (starting July 5, 2016), with benefits after 90 days. Salary will be commensurate with experience. A bachelor's degree is required, and a minimum of 1 year of experience working in a research lab is strongly preferred.

Applications should include a cover letter describing previous experience and fit to the position, CV, and the names and contact information of two references. Review of applications will begin immediately, and continue until the position is filled. Applications should be sent to:

MSU is an affirmative action, equal opportunity employer and is committed to achieving excellence through cultural diversity. The university actively encourages applications and/or nominations of women, persons of color, veterans and persons with disabilities. Job applicants are considered for employment opportunities and employees are treated without regard to their race, color, religion, sex, sexual orientation, gender identity, national origin, disability or veteran status.

coakley at msu dot edu

Monsanto QuantGenomics

Sustainable agriculture is at the core of Monsanto. We develop technologies that enable farmers to produce more crops while conserving natural resources. Monsanto scientists are conducting research and development (R&D) to revolutionize plant breeding and biotechnology.

Monsanto is seeking a very talentedGenomics Scientistto become an integral member of our Global Pipeline Analytics team with a focus on quantitative genetics. The ideal candidate will have familiarity with modeling and analysis of genetic data sets using a variety of statistical techniques.

Major Responsibilities: - Provide guidance on experimental design for genomic-related experiments - Familiarity with analysis of the following methods: GWS, QTL, eQTL, RNA-Seq - Provide written and oral presentations of methods, results, conclusions, and recommendations to peer and management groups. - Ensure timely delivery and clear communication of results - Develop strong and successful collaborations among various Monsanto enabling teams.

Required Skills:

- PhD degree in Statistics, Biostatistics, Statistical Genetics, Quantitative Genetics, Breeding, Bioinformatics or a related field with 2 years of experience - Working knowledge and experience with one of the following quantitative languages:R, Python, Perl, SAS - Background in Windows and Linux operating systems - Very strong problem solving skills will be required to work well as a member of a dynamic team - Strong verbal and written communication skills. - Demonstrated ability to deliver timely results and be results oriented. - Extensive knowledge of quantitative genetics and experimental design. - Demonstrated track record of solving challenging and complex problems.

Desired Skills/Experience:

- Excellent communication skills, with the ability to summarize complex concepts in language understandable by scientists from a variety of disciplines. - Experience in agronomy and/or plant breeding in vegetables or row crops.

Please apply to https://jobs.monsanto.com/job/st-louis/genomics-scientist/769/2081771 Anne C. Moise Account Executive 2990 Ponce de Leon Blvd, Suite 400 Coral Gables, FL 33134

p) 305-704 4795 anne.moise@tmp.com

"Moise, Anne Capucine" <anne.moise@tmp.com>
"Moise, Anne Capucine" <anne.moise@tmp.com>

Monsanto VegetableGenomics

Job Title is : Vegetable Genomics Scientist

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

Responsibilities:

1. Leverage world-class genomic datasets to perform statistical genetic analyses and develop scripts that will support Monsanto's vegetable trait discovery pipeline. 2. Implement statistical methods to identify associations between trait phenotypes and genetic markers in structured and unstructured populations (e.g. linear regression, ANOVA, mixed effects models, QTL mapping, genome-wide association mapping, genomic selection). 3. Combine phenotypic and genotypic data to assess diversity and structure in vegetable germplasm. 4. Generate and update consensus genetic linkage maps for various types of mapping populations. Construct reference maps that successfully integrate both genetic and bioinformatics data. 5. Conduct analyses to support evaluation and improvement of genotyping platforms. 6. Communicate results concisely and accurately in written and oral form to stakeholders. 7. Provide statistical training and consulting with scientists and research associates. 8. Direct research associates to meet business goals and identify development opportunities. 9. Pursue intellectual property opportunities around project responsibilities, in collaboration with patent science and legal functions.

Required Skills/Experience:

* Master's degree or higher in population genetics, statistical genetics, biostatistics, computational biology, bioinformatics, breeding or related field of study. * Broad and extensive knowledge of theoretical and applied statistics, with strong skills in statistical modeling, data quality control and data mining. * Experience constructing genetic linkage maps. * Proficiency with one or more common statistical analysis software environments (e.g. R, SAS). * Experience with at least one scripting language commonly used in genomics research (e.g. Python, Perl) * Self-motivation and strong initiative. * Ability to balance workloads from multiple competing tasks, excellent organization and time management skills. * Outstanding written and verbal communication skills.

Desired skills:

* PhD degree in population genetics, statistical genetics, biostatistics, computational biology, bioinformatics,

breeding or related field of study. * Applied knowledge of plant breeding * Experience developing interactive interfaces for data analysis and visualizations (e.g. R Shiny, JavaScript) * Proficiency querying enterprise level databases

"Moise, Anne Capucine" <anne.moise@tmp.com>

NHM London ResAssist PlantEvol

Research Assistant Natural History Museum, London

Job details: This is part-time position for 30 months. You will join the laboratory of Dr Silvia Pressel in the Department of Life Sciences and will be mainly responsible for the in vitro cultivation and manipulation of plants and associated fungi and microscopy analyses of these, including light, scanning and transmission electron microscopy, as well as facilitating the smooth running of the laboratory. You will be expected to collaborate with and contribute to the effective communication of results to all members of the research group. You will have a BSc (or equivalent) in biological sciences and have experience of working in a laboratory. A MSc or MRes in ecology, evolution, plants or fungi would be desirable. Experience in in vitro cultivation of plants and/or fungi and in microscopy techniques would be appreciated, but full training will be available in all aspects of the work. Deadline: 31 May 2016.

"m.bidartondo@imperial.ac.uk"
<m.bidartondo@imperial.ac.uk>

PacificU LabCoordinator TeachingEvolution

The biology department of Pacific University invites applications for a continuing 0.85 (10.2 month full time) lab coordinator position, starting in early August 2016. Bachelor's or higher in biological science with at least one year of experience in laboratory management or laboratory preparations is required. Potential for teaching opportunities with master's degree or higher in biology.

The full job description can be found here: http://www.pacificu.edu/about-us/offices/human-resources/employment/available-positions/1435-biology-lab-coordinator Application materials - A cover letter addressing your experiences and qualifications as outlined in the Essential Functions and Required Knowledge, Skills, Abilities, and Behaviors sections of the job description. - A resume - Names and contact information for 3 references who can speak to your professional preparation or skills.

Review of applications begins May 20th and will continue until the position is filled. Submit applications electronically to: Patty Larkins, plarkins@pacificu.edu Administrative Assistant, School of Natural Sciences, Pacific University

The subject line of your e-mail submission should be Biol Lab Coordinator; e-mails without this subject may not be reviewed.

Please contact Dr. David Scholnick, david.scholnick@pacificu.edu (Biology Department Chair) with questions.

"Chan, Lauren M." <lchan@pacificu.edu>

TelAvivU EvolutionaryBiology

The Department of Zoology, Tel Aviv University, invites applications from exceptional candidates for a tenure-track position.

Basic Qualifications: Applicants are expected to have a PhD and postdoctoral experience in one of the following fields: ecology, biogeography, comparative physiology, conservation, neuroethology, animal behavior, behavioral ecology, evolution, systematics, taxonomy. They should have strong and substantive training and an active zoologically-oriented research agenda, as evidenced by their publications in first-class international, peer-reviewed journals. Candidates should be committed to graduate and undergraduate teaching and to be able to teach undergraduate and graduate courses in Hebrew within 3 years of obtaining the position.

Application Procedure: Submit electronically a letter of application, CV and short research and teaching statements TO: zoologyh@tauex.tau.ac.il

Review of applications will begin immediately and will continue until September 1 as deadline or until the position is filled.

shai meiri <uncshai@post.tau.ac.il>

UKansas ResAsst Drosophila ComplexTraits

A research assistant position is available in the Macdonald lab in the Department of Molecular Biosciences at KU. The Macdonald group explores the genetic basis of complex phenotypic variation using Drosophila as a model system. The successful candidate will help maintain a panel of fly lines, supervise and carry out large-scale phenotyping screens, and generate next-generation sequencing libraries for various genomics applications. We are looking for an enthusiastic and organized individual who is willing to learn new skills, and has excellent oral and written communication skills. Previous research assistants in the Macdonald group have undertaken independent research projects and been authors on research publications from the lab. The position is funded through a recently-renewed multi-year NIH grant and has an anticipated start date of 1 August 2016 (although this is negotiable).

For a complete announcement and to apply online, go to https://employment.ku.edu/staff/6269BR Please direct any questions about the position to Stuart Macdonald (sjmac@ku.edu).

A complete online application includes the following materials: CV/resume, cover letter outlining relevant experience, and contact information (phone/email/address) for three referees. Initial review of applications begins 2 June 2016 and will continue until the position is filled.

The University of Kansas prohibits discrimination on the basis of race, color, ethnicity, religion, sex, national origin, age, ancestry, disability, status as a veteran, sexual orientation, marital status, parental status, gender identity, gender expression, genetic information and retaliation in the University's programs and activities. Access to information regarding equal opportunity and diversity worksite posters is available at http://www.humanresources.ku.edu/policies_procedures/category_details/index.aspx?category=8 or you may contact 785-864-4946 or employ@ku.edu for alternate access options. Any inquiries regarding the nondiscrimination policies should be directed to: Executive Director of the Office of Institutional Opportunity and Access, IOA@ku.edu, 1246 W. Campus Road, Room 153A, Lawrence, KS, 66045, (785)864-6414, 711 TTY.

Dr. Stuart J. Macdonald Department of Molecular Biosciences 4043 Haworth Hall 1200 Sunnyside Avenue University of Kansas Lawrence KS 66045

office: 785-864-5362 lab: 785-864-5777 fax: 785-864-5321 email: sjmac@ku.edu web: FlyRILs.org

"sjmac@ku.edu" <sjmac@ku.edu>

UmeaU MathematicalEcolEvolution

The Department of Mathematics and Mathematical Statistics at Umeå University, Sweden, invites applicants for a research-oriented permanent position as senior lecturer in mathematical modelling and analysis. Current research at the department include mathematical evolutionary ecology, in particular using adaptive dynamics methods.

The successful applicant is expected to sustain active research within mathematical modelling and analysis with connections to the department's current activities in this area and to neighboring departments and units. Examples of relevant research areas are population dynamics, frequency-dependent evolution, structured population models, and optimal switching. The holder of the position will primarily be based at Umeå University's creative research environment IceLab (www.org.umu.se/icelab/english), which currently houses about 20 young scientists conducting interdisciplinary research, training, and education at the intersection of physics, mathematics, social sciences, and the life sciences.

For full application details, please see

https://umu.mynetworkglobal.com/en/what:job/jobID:99557 Applications must be submitted through Umeå University's web-based recruitment system linked above. Last application date is 2016-05-30.

ake.brannstrom@gmail.com

UNevada LasVegas HawaiianDrosophila

I am moving my lab to the School of Life Sciences at the University of Nevada, Las Vegas. (http://www.unlv.edu/lifesciences/). I will be advertising a Research Technician position to start in August 2016 or as soon after that as possible. The position will be funded for up to three years by UNLV. The primary responsibility of the person in this position will be to maintain several species and 50+ recombinant inbred lines of Hawaiian picture-winged *Drosophila* in the laboratory. In addition, the research technician will coordinate the measurement of several phenotypic traits, prepare samples for genetic analysis and assist with the statistical and bioinformatic analyses. There will also be occasions to conduct field research in Hawaii. The position will be officially posted soon. Anyone interested in this position please contact me via email (donaldp@hawaii.edu). Research associated with this position will be conducted in collaboration with faculty at the University of Hawaii, Virginia Tech University, and Janelia Research Campus, HHMI. The research technician will have the opportunity to develop semi-independent studies on related themes.

I am also accepting new graduate students who are interested in conducting research on Hawaiian *Drosophila*. There are several funding opportunities for graduate students. Please see my website for additional information and projects of current and recent graduate students. https://sites.google.com/a/hawaii.edu/price-lab-at-university-of-hawaii/ My lab group investigates the local adaptation and divergence of species with a focus on Hawaiian *Drosophila* and other winged animals. We are most interested in the evolution of behavioral and associated morphological and physiological traits that facilitate local adaptation and speciation, and have recently sequenced and begun the annotation of the genomes of several species of Hawaiian picture-winged *Drosophila*.

Donald Price

Professor and Director, School of Life Sciences (starting August 2016)

University of Nevada, Las Vegas

donaldp@hawaii.edu

UNewBrunswick PlantEvolutionaryEcol DeadlineMay20

Plant Evolutionary Ecology

The University of New Brunswick, Department of Biology (Fredericton) invites applications for a tenure track position in Plant Evolutionary Ecology at the rank of Assistant Professor. We seek candidates asking questions in evolutionary ecology, broadly defined, including ecological genetics. Examples of research interests include (but are not limited to) plant-insect/microbial/fungal interactions, mating system evolution, stable isotopes in plant-based food webs, or invasive species. We welcome applications from candidates who could build research collaborations within and outside the Department. The Department of Biology houses the Connell Memorial Herbarium, Microscopy and Microanalysis Facility, Stable Isotopes in Nature Laboratory, a climate-controlled greenhouse, and has access to the Atlantic Computational Excellence Network (ACEnet). Potential opportunities for external collaborations in Fredericton include UNBs Faculty of Forestry and Environmental Management, the Canadian Rivers Institute, the Canadian Forest Services Atlantic Forestry Centre, and Agriculture and Agri-Foods Canadas Fredericton Research and Development Centre.

The successful candidate will contribute to teaching of plant-related modules in our 1st and 2nd-year core, and contribute to upper-level courses as appropriate.

Qualifications: The successful candidate must hold a PhD in a relevant discipline and a minimum of 1 year postdoctoral experience. Candidates should demonstrate a record of, or potential for, excellence in teaching and in research.

This position will begin in September 2016 or as mutually negotiated. Application packages should be received by May 20, 2016 and include a current CV, a statement of research interests, a statement of teaching philosophy, samples of up to three research publications, and a cover letter outlining reasons for seeking the position and listing names and contact information for three references.

Applications should be sent to: Dept. of Biology, UNB 10 Bailey Drive, Fredericton, NB E3B 5A3 c/o: Melanie Lawson

This position is subject to budgetary approval.

All qualified candidates are encouraged to apply: however, Canadians and permanent residents will be given priority. Applicants should indicate current citizenship status. The University of New Brunswick is committed to the principle of employment equity.

Jason Addison <ja.addison@gmail.com>

UParis13 Research TeachingFellow Ethology

Research/teaching fellow in Ethology (non-permanent); University of Paris 13, France

General profile: This position (Attaché Temporaire d'Enseignement et de Recherche, ATER) includes research and teaching, and will be on a full-time basis for 1 year (non-permanent). There might be the possibility of renewal for a maximum of one more year. The person recruited for this position (usually with a PhD) will be attached to two different structures of the University of Paris 13: to the Laboratoire d'Ethologie Expérimentale et Comparée (LEEC, EA 4443) to carry out the research activities and to the Departement de Psychophysiologie for teaching. These two structures administratively belong to the UFR LLSHS of the Universite Paris 13 and are situated at the Villetaneuse campus.

Research on mechanisms, function and evolution of social behaviour: Candidates should have a strong scientific background in a field closely related to ethology / behavioural sciences, and an adequate publication record in international peer-reviewed journals. The applicant is expected to present a project outline of his/her planned research at the LEEC, feasible during the contractual period of one year and well-integrated into our general line of research on the study of the mechanisms, function and evolution of social behaviour. Please include the contact information of two referees within your application. More information about the research carried out at our laboratory can be found on our website: http://leec.univ-paris13.fr Teaching: The teaching activities of the recruited person will be within the fields of neuroscience and of ethology, at the Bachelor's level (bachelor in psychology) and Master's level (master in ethology; 1st and second year). A qualification of the candidate in ethology or in a closely related field is desired. The successful candidate should be francophone as the teaching will be in French.

Contacts: More information on this position can be received from the following contact persons: Research : Prof. Dr. Heiko G. Rodel, Head of the Laboratoire d'Ethologie Expérimentale et Comparée, University of Paris 13, France; email : heiko.rodel@leec.univ-paris13.fr ; phone : +33 1 49 40 32 18 Teaching : Dr. Fabrice Savarit, Head of the Teaching Unit on Psychophysiology, University of Paris 13, France; email : fabrice.savarit@leec.univ-paris13.fr ; phone : +33 1 49 40 32 29

Application: Applications are only possible via the online portal GALAXIE (application ALTAIR), where this position is posted in the section neuroscience (section 69) for the University of Paris 13. https://www.galaxie.enseignementsup-recherche.gouv.fr/ensup/cand_recrutement_ATER.htm Direct applications to the persons and structures mentioned above cannot be considered. The application deadline is the 12 May 2016; see details in GALAXIE.

* Prof. Heiko G. Rödel *** Directeur * Laboratoire d'Ethologie Expérimentale et Comparée-EA 4443* Institut Galilée, bâtiment C, 4ème étage +33(0)14940 3218

* Université Paris 13 - Sorbonne Paris Cité * 99 av. Jean-Baptiste Clément ***fb-avrile < http://leec.univ-paris13.fr >* * *** F-93430 Villetaneuse, France***

Heiko Rödel <heiko.rodel@leec.univ-paris13.fr>

UPittsburgh EvolutionaryMicrobiology Genomics Education

We seek multiple researchers in evolutionary biology also interested in microbiology, ecology, genomics, or education. This is part of a broader effort at the University of Pittsburgh to build in evolutionary biology and microbiome research (see http://1.usa.gov/1rJUV11). We are currently seeking applicants for the following positions.

1) Postdoctoral Researcher, Experimental Evolution of Antimicrobial Resistance. The aim of this project is to identify antibiotic-specific evolutionary pathways that lead to resistance under distinctive growth and immune-system pressures. This project focuses on how S. pneumoniae, A. baumanii, and P. aeruginosa evolve under various antibiotic and host immune constraints, using genomics, transcriptomics, and state-

of-the-immune-system profiling to identify selective forces on genetic and physiological targets. This multi-investigator NIH U01 project is described here: http://1.usa.gov/1ZNCS4S. We're looking for candidates with expertise in evolutionary biology, microbiology, and/or genetics/genomics.

2) Postdoctoral researcher, Mechanisms of Adaptation in Biofilms. This project seeks to disentangle eco-evolutionary dynamics in experimental biofilms and to define the precise targets of selection, which ultimately produce synergistic mixed communities. This work is supported by NIH and a NASA Astrobiology Institute (http://nai.nasa.gov/teams/can-7/umt/) and builds upon research reported in Traverse et al PNAS 2013 (http://www.pnas.org/content/110/3/E250) and Ellis et al Evolution (http://www.ncbi.nlm.nih.gov/pubmed/25494960).

3) Bioinformatics Research Staff, apply here https://www.pittsource.com/hr/postings/117344: The Cooper lab generates and analyzes a wide range of genomic data related to bacterial evolution during infections or model systems. Applicants must be proficient in one or more scripting languages (e.g. Python, Ruby, Perl) and familiar with Unix environments. This position provides an outstanding opportunity to gain expertise in high-throughput genomics and make intellectual contributions to projects supported by NIH, NSF, and NASA. Minimum requirements include a bachelors's degree in computational biology, bioinformatics, biological science, or equivalent work experience.

4) Evolution Curriculum Outreach Coordinator. We are expanding a curriculum, EvolvingSTEM (http://evolvingstem.org), that enables 9th-grade students to learn principles of evolution and heredity with a week-long evolution experiment in biofilms. We seek a student or staff member to help us refine and distribute this curriculum in greater Pittsburgh and beyond. This position will require both hands-on teaching and contribution to fundraising.

5) Ph.D. positions will be available for students interested in bacterial population genetics, sources of variation in the mutation rate, or evolution during infections. Please apply through the graduate program that best suits you: a. Biology (http://biology.pitt.edu/graduate) b. Carnegie Mellon-Pitt Computational Biology (http://www.compbio.cmu.edu/) c. Molecular Virology and Microbiology (http://www.mvm.pitt.edu/).

For more information, please email or visit http://micropopbio.org/opportunities/ Vaughn Cooper, Ph.D. < http://www.mmg.pitt.edu/person/vaughn-s-cooper > Associate Professor Microbiology and Molecular Genetics University of Pittsburgh School of Medicine 425 Bridgeside Point II, 450 Technology Drive Pittsburgh, PA 15219 m: 603.988.7590 o: 412-624-1265 CooperLab < http://micropopbio.org/ > EvolvingSTEM < http://evolvingstem.org/ >

"Vaughn S. Cooper" <vaughn.cooper@pitt.edu>

Other

ApplicationsPhDGrant Hybridization

Call for expression of interest: applications for 'FundaçÃ£o para a Ciência e a Tecnologia' PhD grants 2016: the role of hybridization on evolutionary rescue through an experimental evolution approach

We are looking for students interested in applying for a PhD grant for the next 'FundaçÃ£o para a Ciência e a Tecnologia' (FCT) call (June 15^th-July 15^th)

We are a dynamic team at the Centre for Ecology, Evolution and Environmental Changes (cE3c: Reseacrh Grupo 'Evolutionary Ecology, subgroup 'Local Adaptation in Drosophila), analysing the real-time evolution (by experimental evolution) of Drosophila subobscura populations adapting to a novel (laboratory) environment, since foundation from natural populations - see details of our research at

http://ce3c.ciencias.ulisboa.pt/teams/profile/-sub.php?idT The research plan will involve the role of hybridization in the evolutionary dynamics of populations derived from contrasting natural locations (extremes of the European cline), when a adapting to a novel (laboratory) environment. Previous studies of our team have shown that populations adapt fast. Moreover we showed that populations highly differentiated at the start clearly converge at the phenotypic level, particularly for fitness-related traits (Fragata el al. PLoS One 2014, Evolution 2016), though not at the karyotypic (chromosomal inversions, Fragata et al Journal of Evolutionary Biology 2014) or the genome-wide level (manuscript in preparation).

Building on this knowledge, we will now question whether hybridization between populations with contrasting biogeographic history affects the adaptive dynamics, during evolution to a similar, new environment. Particularly, will hybrids adapt faster than parental populations, contributing to evolutionary rescue, a hot topic both in evolutionary and conservation terms? Will hybridization lead to the evolution to a different adaptive peak, suggesting a complex, rugged landscape? Preference (though not being a necessary condition) will be given to candidates with some experience in Experimental Evolution, as well as the maintenance of laboratory populations of Drosophila The details of the research plan that will be submitted to the FCT call will be discussed with the chosen candidate.

The grant involves in general a monthly payment of 980 EUR plus social security (125 EUR); if part of the project is developed abroad (involving a foreign co-supervisor, with details to discuss) some of the monthly payments will be 1710 EUR.

If you are interested in the topic, please send an email to mmatos@fc.ul.pt, including a short cv and a motivation letter until May 31 2016.

If you already have a PhD degree and you are interested in the topic you may also express your interest, and an application for a Post-doc grant will be discussed.

Best,

Margarida Matos

Margarida Matos, PhD Centro de Ecologia, EvoluçÃ£o e AlteraçÃµes Ambientais (cE3c - Centre for Ecology, Evolution and Environmental Changes)

Faculdade de Ciências da Universidade de Lisboa Campo Grande, Edificio C2 - 5Âº Piso Phone: +351 217500000 ext. 22141 1749-016 Lisboa Portugal

Margarida Matos <mmmatos@fc.ul.pt>

ExtractingDNA from RNAlater answers

Dear All,

I posted the following question on EvolDir about a week ago:

'Dear Colleagues,

I am attempting to extract DNA from RNAlater stored tissue samples for downstream DNA methylation sequencing (MS-AFLP, MeDIP-seq).

I have tried several different extraction protocols: Qiagen DNeasy blood & tissue, Promega Wizard, Phenol/Chloroform and a spooling protocol from ThermoFisher specifically intended for this type of DNA extraction. All of these extraction protocols I followed-up with isopropanol precipitation to clean the extracts further.

Whilst I successfully extracted some relatively high quality DNA (when visualized on a gel), yields were lower than expected. More worryingly the 260/230 ratios were low (<1.2) suggesting that a lot of salts were being co-extracted alongside DNA. My main concern here is that these salts could impede enzyme action during restriction-ligation or PCR leading to problems with reproducibility.

Has anyone had some success extracting DNA from RNAlater stored tissue and would be willing to share some tips/advice on how to carry these extractions out successfully and cleanly?'

I received some excellent replies and also several requests to post the replies. Please find below the collated responses to my query in rough chronological order. Many thanks to all those who took the time to help me with my problem

Best wishes

Alan (alan.hudson@bristol.ac.uk)

Hi Alan,

I was asked this question recently by a colleague. As was the case then, I have not actually tried to do this myself, but came across the following when looking for Chelex-based extraction protocols.

https://www.researchgate.net/post/-Is_that_possible_to_extract_DNA_using_Chelex_from_RNALater_preserved_samples Maybe this is of help? Or maybe is just another version of what you've already tried.

Anyways, good luck!

David Garfield

Hi Alan,

WE had some issues before with RNAlater-preserved samples. What we did was we washed our samples with 1x PBS to get rid of the salts. Our DNA quality and PCR amplification was better afterwards.

Best,

Marilou Sison-Mangus

Dear Alan,

We used a kit that should be analogous to the Qiagen kit (silica based column), but we did not purify it further (just followed the instructions of the kit). You can see our results in the attached paper (gel in Figure 3- NAP turns out to be the same as RNA later).

Good luck!

Jennifer Leonard

Dear Alan,

we have had a very good experience rinsing RNA-Later fixed samples in PBS (1X) before homogenization. We do this for RNA extraction. If we use CTAB instead of Trizol, we always recover very high quality DNA from RNA-Later fixed specimens and clean the DNA using the Zymo Duet kit (this usually cause the DNA to break, but we are only interested in RNA...).

How long, this we never tested. We ussually transfer the sample from RNA-Later into PBS and wait for, say, no longer than 5 mins before transfering the sample to lysis buffer.

Long ago, I read this PBS wash step helps getting better RIN values, likely due to salt removal. Maybe it does the trick.

cheers

Sergio Vargas

Dear Dr. Hudson,

I have extracted DNA from tissues stored in RNAlater using the classic Phenol/Choroform/Isoamyl alcohol (PCI 25:24:1) protocol without any modification. After extraction, there were huge white precipitates in the tubes as I guess happens to you. Therefore, I performed an extra step of cleaning-up with magnetic beads (AMPure beads). After this clean-up I have used these samples for RRBS and also specific PCRs after bisulfite conversion and everything worked fine.

If you need further details on the clean-up step, please let me know.

Best regards,

Dafni Anastasiadi

Hi Alan,

re your evoldir question - Isopropanol tends to leave more salts. I would use >95% ethanol to precipitate then wash pellet with 70% ethanol to remove even more salts. Personally I've never had a problem with RNAlater preserved tissue. Though I've only ever PCRed it, nothing fancier. Secondly I've never been a big fan of 260:280 as a measure of quality. DNA not cleaned of salts can both PCR and restrict just fine. Though you need to check for yourself if it is in your experiment.

Cheers

Dave Lunt

Hey Dr. Hudson,

We extract DNA from microbes on filters stored in RNAlater (or a homemade equivalent, anyway) all the time. For us, the key is to rinse the filters thoroughly before starting the extractions. I don't know how easy this would be for you if you have tissue samples, but we just put the filters back in our filtering apparatus and run a few hundred milliliters of ultrapure H2O through... Hope you get your problem solved. Good luck!

Mattias Johansson

—

Hi Alan,

I have had great success extracting DNA from tissues stored in

— / —

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

JagiellonianU EvolutionaryBiolDegree

Master studies in Ecology and Evolution

EcoEvo is a two year Master of Science programme for students interested in the functionning and evolution of the biosphere, offered by the Institute of Environmental Sciences at Jagiellonian University in Krakow, Poland. The participants investigate the mechanisms underlying ecological and evolutionary processes and develop practical skills related to carrying out research and conservation projects. They undertake a range of multidisciplinary courses (consisting of lectures, seminars, laboratory work and field classes) as well as carry out group and individual research projects.

Tuition fees: free for EU/EFTA/Swiss citizens and other countries' citizens with documented Polish nationality; otherwise 2200 for the 1st and 2000 for the 2nd year.

Website: www.ecoevo.uj.edu.pl Facebook profile: https://www.facebook.com/ecolevoluj/ – Dr. Zofia Prokop Molecular and Behavioral Ecology Group Jagiellonian University Gronostajowa 7 30-387 Krakow, Poland tel. +48 12 664 5151 e-mail: zofia.prokop@uj.edu.pl *Google Scholar profile < http://scholar.google.co.nz/citations?user=-3D58lKo7IAAAAJ&hl=3Den&oi=3Dao >*

"zofia.prokop@uj.edu.pl" <zofia.prokop@uj.edu.pl>

Lactobacillus strain

Dear list members,

for an in vitro study we would urgently need thefollowing bacterial strain: Lactobacillus acidophilus ATCC 314.

In case you have it in your collection, we would verymuch appreciate receiving a subculture.

Please contact us (Melissah Rowe: melissah.rowe@nhm.uio.no and Gábor Czirják: czirjakgabor@yahoo.com) to discuss the details of the shipment.

Thank you very much in advance!

Best wishes,Melissah and Gábor

czirjakgabor@yahoo.com

RNALater extractions

Dear Colleagues,

I am attempting to extract DNA from RNAlater stored tissue samples for downstream DNA methylation sequencing (MS-AFLP, MeDIP-seq).

I have tried several different extraction protocols: Qiagen DNeasy blood & tissue, Promega Wizard, Phenol/Chloroform and a spooling protocol from ThermoFisher specifically intended for this type of DNA extraction. All of these extraction protocols I followed-up with isopropanol precipitation to clean the extracts further.

Whilst I successfully extracted some relatively high quality DNA (when visualized on a gel), yields were lower than expected. More worryingly the 260/230 ratios were low (<1.2) suggesting that a lot of salts were being co-extracted alongside DNA. My main concern here is that these salts could impede enzyme action during restriction-ligation or PCR leading to problems with reproducibility.

Has anyone had some success extracting DNA from RNAlater stored tissue and would be willing to share some tips/advice on how to carry these extractions out successfully and cleanly?

Best wishes and thanks in advance

Alan Hudson (alan.hudson@bristol.ac.uk)

– Dr Alan G. Hudson School of Biological Sciences University of Bristol Life Sciences Building 24 Tyndall Avenue Bristol BS8 1TQ

Alan Hudson <alan.hudson@bristol.ac.uk>

Saskatchewan VolAssist PrairieDogConservation

Field Assistants Required - Black-tailed prairie dogs Grasslands National Park, Saskatchewan, Canada

We are looking for 3 volunteers to assist with fieldwork beginning June 15 and continuing until August 31 (preference may be given to applicants who can start earlier in June). The project investigates the ecology, conservation and evolution of Black-tailed prairie dogs and will involve live-trapping, handling and monitoring of individuals. Prairie dog towns are home to (among others): burrowing owls, swift fox and, the recently reintroduced, black-footed ferret. Assistants will have the opportunity of seeing all of these iconic grassland species, plus the many more resident in the Park.

This is an excellent opportunity to gain experience working with a population of wild mammals in a spectacular setting and in collaboration with university, park and zoo researchers. All fieldwork is carried out in Grasslands National Park, southern Saskatchewan, one of the largest remaining tracts of native prairie in Canada. We will be staying in Parks Canada housing in the heart of the park. Food and accommodation are provided. Volunteers are required to provide for their own travel to Saskatoon, Saskatchewan. Travel between the field station and Saskatoon is provided.

Training will be provided and no experience is necessary, but candidates should have an interest in the following (the more the better!): ecology, evolutionary biology, wildlife, field biology, and conservation biology. The field house and study population is isolated (the nearest town is approx. 45 min away) and, as such, successful applicants need to be able to cope under these conditions, 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) ASAP. Applications will be evaluated as they are received. While we thank all applicants for their interest in these positions, due to Canadian Immigration law, we are only able to consider Canadian applicants. Only applicants chosen for interview will be contacted.

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

SouthAfrica VolFieldAssist PlantPollination

A two month research assistant position is available in the Biological Interactions Lab (www.biointeractionslab.com; http://www.biointeractionslab.com/jurene-kemp.html) in the Department of Botany and Zoology at Stellenbosch University, South Africa. Work will be based in the beautiful Namaqualand during the annual spring mass flowering displays where we will be conducting pollinator observations to study the evolution of floral specialization. Candidates need to be hard-working and willing to spend long hours in the field. Previous experience in pollinator observations will be an advantage. Food, accommodation, and a small stipend will be provided. Travel costs to South Africa are not included.

Please direct any questions and applications to Jurene Kemp (jurenekemp@yahoo.com or jekemp@sun.ac.za).

Deadline:15 June 2016

JureneE. Kemp PhDcandidate Departmentof Botany and Zoology StellenboschUniversity SouthAfrica http://www.biointeractionslab.com/jurene-kemp.html jekemp@sun.ac.za

Teaching Evolution videos

I am happy to report that the 3rd edition of my textbook Evolutionary Bioinformatics (Springer, New York) is now available: http://link.springer.com/book/10.1007%2F978-3-319-28755-3 . Since the second edition

(2011), accesses to the ebook have greatly increased. This parallels the growing trend towards online courses which supplement traditional educational approaches and facilitate self-directed learning. These courses can be much more than videos of formal lectures. The 'Khan Academy' is an interesting example. The pen-tablet of impresario Salman Khan captivates millions world-wide. Students see multicolored drawings, arrows, numbers and letters, moving across a black background to Khan's melodious accompaniment. With pause and rewind options, they can proceed at their own pace.

While lacking Khan's eloquence - but one has to start somewhere - I have experimented with his method, generating a series of 15 minute videos that explain evolutionary principles in everyday terms and, it is hoped, with a touch of humor. Rather than supplementing the textbook, which has been extensively updated, the videos provide an elementary introduction - primarily directed at high school students and the general reader (https://www.youtube.com/user/forsdyke1/playlists).

Donald Forsdyke, Department of Biomedical and Molecular Sciences, Queen's University, Kingston, Ontario, Canada

Donald Forsdyke <forsdyke@queensu.ca>

Teaching Statistics using Evolution

— Dear friends, — I am teaching Statistics for Biology undergraduate students and in my classes I would like to compare diferent species using genetic variables and after that calculate porcentage similarities to construct something like a dendrogram. I would like to do something realistic but I dont know what kind of variables I could simulate, maybe counting and comparing the— nitrogenous bases (A G T C) proportion among species?

Thanks for any help! —

— Prof. Dr. J. C. VOLTOLINI— Grupo de Pesquisa e Ensino em Biologia da ConservaçÃ£o - ECOTROP Universidade de Taubaté, Departamento de Biologia Taubaté, SP. 12030-010.— E-Mail: jcvoltol@uol.com.br— * Grupo de pesquisa ECOTROP CNPq: http://dgp.cnpq.br/dgp/espelhogrupo/6541980798150818 * Currículo Lattes: http://lattes.cnpq.br/8137155809735635— * Assessoria Estatística: http://assessoria-estatistica.blogspot.com.br/ * Fotos de Cursos e Projetos: http://www.facebook.com/ecotrop VOLTOLINI <jcvoltol@uol.com.br>

USussex FieldAssist EvolWaspBehaviour

VOLUNTEER FIELD ASSISTANT sought for 4-6 weeks starting immediately, to help with a study of paper wasp (Polistes) behavioural ecology in southern Spain. The work will involve helping a PhD student to census and observe colonies as part of experiments to elucidate the basis of helping behaviour in these wasps, which live in small colonies of <20 individuals. The successful applicant must be prepared to work hard and have an interest in behavioural/evolutionary biology, and have enthusiasm and fitness level suitable for fieldwork. Successful applicants will obtain excellent experience of cutting-edge insect behavioural ecology. A driving licence and any ability to speak Spanish would be advantages, but are not essential. Because the work involves recording colour marks on individual animals, the job would not be suitable for someone who is colour-blind. See our research group website for more information about the kind of work we do (http://www.sussex.ac.uk/lifesci/fieldlab/).

Air fare (from the UK or mainland Europe) and accommodation expenses will be provided, with the applicant needing to pay for only their own food/personal expenses, which are relatively cheap in Spain. A successful applicant will also receive a pounds 500 contribution towards their expenses. Accommodation will be your own room in a flat shared with the PhD student/ 1-2 other members of the research group - including shower, cooking facilities, TV etc. Accommodation is in a medium-sized coastal town with nice beach.

Please send a covering letter and CV, including contact details (including e-mail addresses/tel nos.) for the applicant and 2 or 3 referees. Please email as a single Word document to: j.field@sussex.ac.uk.

Professor Jeremy Field School of Life Sciences, John Maynard Smith Building, University of Sussex, Falmer, Brighton BN1 9QG, UK

j.field@sussex.ac.uk http://www.sussex.ac.uk/lifesci/fieldlab/ Tel 01273 877135

Jeremy Field <J.Field@sussex.ac.uk>

PostDocs

AarhusU MegafaunaEvolution

Three 2-year postdocs on megafauna ecosystem ecology and functional diversity at Aarhus University

I'm happy to announce the first set of three 2-year postdocs in our exciting new project on "Megafauna ecosystem ecology from the deep prehistory to a human-dominated future" (MegaPast2Future)".

One position is focused on building an integrative paleobiological-macroecological understanding of how megafauna functional complexity has built up across time and space, taking a macroevolutionary perspective (http://bit.ly/megaevolPD).

The others include a position on the same topic, but taking a biogeographic perspective (http://bit.ly/-megabiogPD) and a position on developing theory for megafauna ecosystem ecology (http://bit.ly/-megatheoPD).

All positions involve a strong set of international collaborators.

The application dead-line is June 20, 2016.

Professor Jens-Christian Svenning, PhD Ecoinformatics & Biodiversity, Department of Bioscience, Aarhus University Homepage < http://person.au.dk/-en/svenning@biology.au.dk > - Google Scholar profile < http://scholar.google.com/citations?user=-3Dwe7WLk8AAAAJ > - Research Gate profile < https://www.researchgate.net/profile/Jens-Christian_Svenning/ >

ArizonaState EvolutionaryGenomics

Postdoctoral Research Associate — Genomics/Bioinformatcs

URL: http://cartwrig.ht/jobs/2016/05/19/Postdoc-Opening/ PDF: http://cartwrig.ht/postdoc-2016.pdf A Postdoctoral Research Associate position is available at the Biodesign Institute at Arizona State University (ASU). This new Postdoctoral Research Assocate will be part of the Cartwright lab (http://cartwrig.ht/) located in the Biodesign Center for Personalized Diagnostics. The lab is focused on evolutionary research related to mutation and population variation, as well as developing statistical software to process large, genomic datasets to identify and study somatic and germline mutation patterns. A successful candidate will participate in two NIH funded research programs: (1) analysis of mutation accumulation lines from the ciliate, Tetrahymena thermophila, and (2) development of DeNovoGear (https://github.com/denovogear/denovogear), a general toolkit for the study of mutation rates from next-gen sequencing of related individuals and cells. Corresponding projects in the lab involve the study of somatic and germline mutations in humans, chimps, trees, bacteria, bees, mice, and cancer.

In particular, under guidance from Dr. Cartwright, the candidate is expected to:

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

Requirements

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

Desired Qualifications

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

Instructions to Apply

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

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

The Biodesign Institute Mission

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

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

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

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

ArizonaStateU EvolutionaryMedicine

Evolution& Medicine Postdoctoral Research Fellowship at Arizona State University Salary:$60,000 Reference # 11557 http://evmed.asu.edu/now-hiring-postdoctoral-fellow-evolution-medicine Initialclosing date May 1, 2016

TheCenter for Evolution & Medicine (CEM) at Arizona State University (ASU) invitesapplications from exceptional early career scientists for the Evolution& Medicine Research Fellowship. The Fellowship brings talented researcherswith a recently awarded M.D. or Ph.D. to the ASU campus to developand extend their own independent research agendas in conjunction withCEM faculty and their labs. Additionally, fellows will work with their mentorsto develop skills in the areas of outreach, education and grant writing.Possible research areas include, but are not limited to, co-evolutionand infectious diseases, regulation of inflammation and other defenses,autoimmune disorders, cancer, female reproductive health, lactation,and factors that influence disease susceptibility. The proposed researchproject is expected to potentially demonstrate the utility of evolutionarysciences for medicine or public health.

TheCenter for Evolution & Medicine is a university-wide Presidential Initiativedirected by Randolph Nesse. Its mission is to improve human healthby establishing evolutionary biology as an essential basic science formedicine, worldwide. It supports research that demonstrates the power ofevolutionary biology to advance the understanding, prevention, and treatmentof disease, as well as teaching and outreach initiatives. See http://evmed.asu.edufor details and information on the Core Faculty. As an interdisciplinaryunit, the CEM provides Fellows with opportunities collaboratewith faculty from a wide-range of disciplines including anthropology,biology, complex systems, computational informatics, genetics,infectious disease, psychology, and virology.

Fellowswill receive a salary of $60,000 and will have access to funding of upto $10,000 per annum to support their research, of which $1500 may be allocatedfor moving expenses. The initial closing date for receipt of completeapplications is May 15, 2016; applications will be reviewed weekly thereafteruntil the search is closed. The earliest anticipated start date isAugust, 2016, the latest is January, 2017. This is a fullâ(1.0 FTE)benefitsâ, fiscal year (July 1 â€June 30) appointment. The fellowshipis granted for a period of two years, with a possible third year.Renewal for the second and possible third year is contingent on satisfactoryperformance, and the availability of resources. For additional informationand policies regarding postdoctoral scholars at ASU, please see http://provost.asu.edu/postdoc . Thesuccessful fellow will be an outstanding scientist with a specific independentresearch plan, wide-ranging interests in evolutionary biology relatedto disease and health, and an appreciation for interdisciplinary research.Selections are based on academic achievement, creativity, goodnessof fit, overlap of interests with multiple CEM faculty, and the likelysuccess and impact of the research project. Fellows cannot have had morethan five years of previous postdoctoral experience, nor have been employedpreviously as an assistant professor, associate professor or professoron the tenure track. Nominees who are non-US citizens are encouragedto apply, and must show eligibility for obtaining J-1 Scholar visastatus for the duration of the Fellowship. The CEM does not support H1Bvisa status. A background check is required for employment.

ArizonaState University is a new model for American higher education, anunprecedented combination of academic excellence, energy and broad access.This New American University is a single, unified institution comprisingfour differentiated campuses positively impacting the economic,social, cultural and environmental health of the communities itserves. Its research is inspired by real world application blurring theboundaries that traditionally separate academic disciplines. ASU servesmore than 80,000 students in metropolitan Phoenix, Arizona, the nation'sfifth largest city. ASU champions intellectual and cultural diversity,and welcomes students from all fifty states and more than onehundred nations across the globe.

Bythe start date, candidates must have completed a M.D. or Ph.D. in anthropology,biology, psychology or another natural science field that providesan extensive background in evolutionary biology.

Toapply, please email a single pdf document to evmedsearch@asu.edu that contains:

-a one page statement explaining your interest in this position and how it couldadvance your career plans, -a one or two page statement that describes the research you will pursue

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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

ArizonaStateU EvolutionaryMedicine May15

Evolution & evoldir@evol University Salary: $60,000 Reference # 11557 http://evmed.asu.edu/now-hiring-postdoctoral-fellow-evolution-medicine Initial closing date May 15, 2016 (previous announcement incorrectly stated May 1)& Medicine Postdoctoral Research Fellowship at Arizona State

The Center for Evolution & Medicine (CEM) at Arizona State University (ASU) invites applications from exceptional early career scientists for the Evolution & Medicine Research Fellowship. The Fellowship brings talented researchers with a recently awarded M.D. or Ph.D. to the ASU campus to develop and extend their own independent research agendas in conjunction with CEM faculty and their labs. Additionally, fellows will work with their mentors to develop skills in the areas of outreach, education and grant writing. Possible research areas include, but are not limited to, co-evolution and infectious diseases, regulation of inflammation and other defenses, autoimmune disorders, cancer, female reproductive health, lactation, and factors that influence disease susceptibility. The proposed research project is expected to potentially demonstrate the utility of evolutionary sciences for medicine or public health.

The Center for Evolution & Medicine is a university-wide Presidential Initiative directed by Randolph Nesse. Its mission is to improve human health by establishing evolutionary biology as an essential basic science for medicine, worldwide. It supports research that demonstrates the power of evolutionary biology to advance the understanding, prevention, and treatment of disease, as well as teaching and outreach initiatives. See http://evmed.asu.edu for details and information on the Core Faculty. As an interdisciplinary unit, the CEM provides Fellows with opportunities collaborate with faculty from a wide-range of disciplines including anthropology, biology, complex systems, computational informatics, genetics, infectious disease, psychology, and virology.

Fellows will receive a salary of $60,000 and will have access to funding of up to $10,000 per annum to support their research, of which $1500 may be allocated for moving expenses. The initial closing date for receipt of complete applications is May 15, 2016; applications will be reviewed weekly thereafter until the search is closed. The earliest anticipated start date is August, 2016, the latest is January, 2017. This is a fulltime (1.0 FTE) benefits-eligible, fiscal year (July 1 - June 30) appointment. The fellowship is granted for a period of two years, with a possible third year. Renewal for the second and possible third year is contingent on satisfactory performance, and the availability of resources. For additional information and policies regarding postdoctoral scholars at ASU, please see http://provost.asu.edu/postdoc . The successful fellow will be an outstanding scientist with a specific independent research plan, wide-ranging interests in evolutionary biology related to disease and health, and an appreciation for interdisciplinary research. Selections are based on academic achievement, creativity, goodness of fit, overlap of interests with multiple CEM faculty, and the likely success and impact of the research project. Fellows cannot have had more than five years of previous postdoctoral experience, nor have been employed previously as an assistant professor, associate professor or professor on the tenure track. Nominees who are non-US citizens are encouraged to apply, and must show eligibility for obtaining J-1 Scholar visa status for the duration of the Fellowship. The CEM does not support H1B visa status. A background check is required for employment.

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By the start date, candidates must have completed a M.D. or Ph.D. in anthropology, biology, psychology or another natural science field that provides an extensive background in evolutionary biology.

To apply, please email a single pdf document to evmed-search@asu.edu that contains:

- a one page statement explaining your interest in this position and how it could advance your career plans,

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mcmaster.ca/~brian/evoldir.html

BroadInst ComputationalMicrobialGenomics

REQUISITION NUMBER 2627 (search by this number at Careers at www.broadinstitute.org to apply)

JOB TITLE Postdoctoral Researcher -Computational Biology

LOCATION Broad Institute, Cambridge, MA

JOB DESCRIPTION The Broad Institute is an amazing place - we apply our deep knowledge of human and microbial genetics to empower a revolution in biomedicine and accelerate the pace at which the world conquers disease. Through our partnerships with MIT, Harvard, and the Harvard teaching hospitals, we've become a worldwide hub of cutting-edge biomedical science.

Who are we? The Bacterial Genomics Group within the Genome Center for Infectious Diseases tackles pressing questions related to bacteria and their role in human health. We work in a dynamic and rich training environment, connected to groups across the Broad community and to clinical and academic researchers from around the globe.

*We solve puzzles *– We use diverse analytical approaches to understand how key pathogens evolve and interact with their host and host-associated microbiota.

We love "big data" – Our team develops data analysis strategies, writes algorithms and leverages grid computing for the integration and exploration of thousands of 'omics data sets (i.e., genomes, transcriptomes, microbiomes).

*We work as a team *– From project start to finish, we work closely with each other and with clinical and experimental researchers to design and execute studies that test critical biomedical hypotheses, including interpretation of analytical results for validation and publication.

What do we do? We devise and carry out large-scale studies that generate genomic, metagenomic and transcriptomic data sets that we use to understand human pathologies like tuberculosis, recurrent urinary tract infections and life-threatening infections caused by hospital adapted pathogens.

About the position: We are seeking a creative and highly motivated postdoctoral researcher in Computational Biology. The ideal candidate should be broadly conversant with bioinformatics techniques for genomic data analysis, and will apply their expertise to understanding the evolution and spread of bacterial pathogens and antibiotic resistance. The candidate should be proficient in at least one programming language (e.g., Perl, Python, R), familiar with statistics and have made significant contributions to their area of study.

REQUIREMENTS A Ph.D. in Computer Science, Bioinformatics, Biostatistics, Mathematics, Physics, Biological Sciences or a related field Must be proficient in working in the Unix environment. Solid coding proficiency in some combination of Python, Perl, Scala, Java, C/C++ and R. Experience with cluster computing and parallelization preferred. Comfort and experience with programming for biological data analysis Excellent ability to communicate scientific material Excellent collaborative skills and unrelenting enthusiasm for genomic science

EOE/Minorities/Females/Protected Veterans/Disabilities

aearl@broadinstitute.org

BrooklynCollege EvolutionaryBiol

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

Job ID: 14984

Location: Brooklyn College

Full/Part Time: Full-Time

Regular/Temporary: Regular

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

The post-doctoral fellow will:

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

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

- Develop, plan, and conduct new research projects.

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

- Train and supervise undergraduate and graduate researchers.

MINIMUM QUALIFICATIONS

Doctoral Degree in a related field and demonstrated research ability.

OTHER QUALIFICATIONS

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

- Published research in evolutionary biology.

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

- Experience with the mathematical analysis of models.

- Outstanding communication and writing skills.

- A history of successful collaborative work and mentoring.

COMPENSATION

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

BENEFITS

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

HOW TO APPLY

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

CLOSING DATE

June 22, 2016

EQUAL EMPLOYMENT OPPORTUNITY

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

Jennifer Tsui <JTsui@brooklyn.cuny.edu>

CIBIO Portugal PlantColoniztion

Post-Doctoral Research Fellowship (BPD)

Reference: ICETA 2016-47_

Link to the call: http://www.eracareers.pt/-opportunities/index.aspx?task=global&jobId=760 84

Scientific Area

Biological Sciences

Description

A call is open for the award of a Post-Doctoral Research Fellowship (BPD) (Reference ICETA 2016-47 Expand Tree) within the framework of a FCT-ARN funded Project “ExpandTree: SPATIO-TEMPORAL COLONIZATION PATTERNS IN EXPANDING TREE POPULATIONS: an integrated genetic and genomic approach” (FCT-ANR/BIA-BIC/0010/2013) as member of the Plant Biology Group at CIBIO/InBIO, under the following conditions:

Title

SPATIO-TEMPORAL COLONIZATION PATTERNS IN EXPANDING TREE POPULATIONS: an integrated genetic and genomic approach (BPD “ExpandTree”)

Admission requirements

Candidates will be admitted to the competition when demonstrating:

(i) A Ph.D. title in Environmental Sciences, Biological Sciences, Mathematics, Physics, or Computer Sciences;

(ii) Experience in working with molecular data (SSRs and SNPs) to address ecological questions. A strong background in data quantitative genetics analysis and spatial-explicit modelling;

(iii) Proficiency in written and spoken English; and

(iv) Autonomy to lead a scientific work, excellent oral and written communication skills.

Preference will be given to candidates with:

(i) An excellent publication record by international standards, including publications as first author;

(ii) Expertise in programing;

(iii) Participation in research projects relevant to this project;

(iv) Availability to travel among different labs involved in the project sited in Portugal, France, and Spain.

Work plan

The successful candidate will be in charge of analysing data sets containing multilocus genotypes of two study species Juniperus phoenicea subsp. turbinata and Cedrus atlantica in a spatial-explicit context to infer population demographic parameters by applying Landscape tools and ABC models.

Legislation and regulations

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

Workplace

The work will be performed at two hosting centers in collaboration with CIBI-InBIO: i) the Integrative Ecology Group (IEG, Estacion Biologica de Donana, CSIC, Spain) locally supervised by Prof. Pedro Jordano and; ii) the INRA-Avignon (France) locally supervised by Prof. Etienne Klein and Sylvie Oddou. The workplan will be supervised by Dr. Cristina GarcÃa, based in CIBIO- InBIO (Portugal).

Grant duration

The grant will be awarded for a period of 6 months, with the possibility of a 6 month extension subject to budget availability and a review of the candidate's performance, starting on June 2016.

Value of monthly maintenance allowance

Monthly allowance will be 2.245 euro according to the stipends established by FCT, I.P. for research abroad (http://alfa.fct.mctes.pt/apoios/bolsas/valores). Payment will be made by bank transfer on a monthly basis.

Selection methods

The ranking of candidates will be performed by a global evaluation based on the publication record relevant to the project (40%), and his/her experience in previous projects relevant to the work-plan and other merits (40%). The motivation of the applicant along with the statement of two reference letters (20%). The three best-ranked candidates will be invited for personal interview (via Skype if the researcher is located abroad). The jury may not award this grant, if the expected quality and requirements of the candidates are not met.

Composition of the Selection Panel

Dr. Cristina GarcÃa (Chair), Prof. Etienne Klein. (Vogal), Ana Campilho (CIBIO-InBIO), and Herlander Azevedo (substitute member, CIBIO-InBIO).

Way of advertising/notification of results

The final evaluation results will be published and the selected candidate will be notified by e-mail or telephone.

Deadline for application and presentation of applications

The call will be open from 7 June 2016 until 21 June 2016.

Presentation of applications

Application documents:

A. A motivation letter explaining why you are interested in the position;

B. A PDF of your CV, where you should include the name and contact details for two people who can provide references.

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CIBIO UPorto Biodiversity

Post-doctoral Fellowship

Reference: ICETA 2016-43

Scientific Area: Biological Sciences / Biodiversity Patterns and Conservation

Link to the call

Job description:

One post-doctoral fellowship (Reference ICETA 2016-43) is available at CIBIO-InBIO, funded by the FCT

Project PTDC/BIA-BIC/5558/2014 in the field of biodiversity patterns and conservation, under the following conditions:

Admission requirements:

The post-doc fellowship is suitable for candidates of any nationality holding a PhD degree in biology, ecology, environmental sciences or related fields but candidates from mathematics, statistics or other quantitative areas are strongly encouraged to apply. The candidate should have a strong quantitative background and programming experience. Further preferred skills include excellent verbal and written communication skills. Excellent speaking and written knowledge of English is required. A proven publication track record is required.

Project overview:

This project investigates how species diversity, with emphasis on species abundance distributions, scale as a function of area or sample size. The research will be mainly desk based and will include statistical analysis and the development of probabilistic models to describe the patterns of species diversity scaling, with emphasis on the species abundance distribution. However, practical aspects of data collection relevant to mathematical developments will also be considered and the candidate will interact with researchers from the Azorean Biodiversity Group (cE3c) based at the University of Azores on these matters. The candidate will join a dynamic teams led by LuÃs Borda de Ãï¿½gua and Henrique M. Pereira in Lisbon, and Paulo Borges in Azores working on ecological theory of biodiversity modeling.

Fellowship:

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

Salary:

Monthly stipend is euro1495 according to the stipends established by FCT, I.P. in Portugal (http://alfa.fct.mctes.pt/apoios/bolsas/valores). Payment will be made by bank transfer on a monthly basis.

Legislation applicable:

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

Work place:

Work will be conducted at CIBIO-InBIO branch located at the Tropical Research Institute, Lisbon, Portugal

Application:

The call for applications is open between 20/05/2016 and 03/06/2016 (24:00 GMT).

Applications should be submitted by email to bolsas@cibio.up.pt and will include:

a) Curriculum vitae (including a publication list and other relevant information in the context of the project research goals);

b) Motivation Letter (including a brief description of research experience and why you are suitable for the announced position);

Selection criteria:

The jury panel will select the best candidate based on his/her merit, through the analysis of:

- Overall appreciation of the Curriculum Vitae, particularly the publication record (60%);
- Specific experience in research projects related to the call (40%);

The best candidates will be invited for an interview (typically ca. 25%), in person or by videoconference, to establish the final ranking.

Jury Panel:

LuÃs Borda de Ãï¿½gua (Chair), Henrique Miguel Pereira (vowel), Paulo Borges (vowel), and Cesar Capinha (vowel).

Results announcement:

Candidates will be directly informed by email about the result of their application. The ranking of the candidates will be published at a visible and public area of ICETA facilities.

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

Campus Agrario de Vairao Rua Padre Armando Quintas 4485-661 Vairao Portugal

t: +351 252 660 411 Ext. 285 f: +351 252 661 780 e: divulgacao@cibio.up.pt w: http://cibio.up.pt | http://inbio.pt f: https://www.facebook.com/cibio.inbio CIBIO-InBIO DivulgaçÃ£o

ClarkU PlasticityLedEvolution

Clark University: Post-doctoral fellowship in Plasticity-Led Evolution

A post-doctoral position is available in the laboratory of Susan Foster and John Baker at Clark University in Worcester MA USA beginning September 1 2016 as follows:

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

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

The successful candidate will participate in research design, fieldwork, bench work and, most importantly bioinformatic analysis of Illumina sequencing data. — We thus seek applicants experienced in Illumina library construction and strengths in functional, evolutionary, and population genomics who have an interest in understanding all aspects of the research from the natural history of a remarkable adaptive radiation through analysis of the way in which plasticity of gene expression has influenced diversification in the radiation. Our intent, in addition to obtaining significant insight into the role of plasticity in evolution, is to provide the post-doctoral fellow with sufficiently broad background to carry a significant extension of this project into an independent faculty career should the fellow choose to do so. The fellow will also have the opportunity to add additional lines of inquiry related to the research.

This research is funded by, and is part of, a > $8 million multinational grant from the John Templeton Foundation involving 49 investigators and 8 leading academic institutions. The research is designed to examine the role of plasticity in evolution. The overall project is led by Kevin Laland and Tobias Uller http://synergy.st-andrews.ac.uk/ees/the-project/. Collaborators on the Clark component of the research are William Cresko (University of Oregon), John Gibbons (Clark University), Kevin Laland (St. Andrews University), Juha Merilä (University of Helsinki), and Matthew Wund (The College of New Jersey). The successful applicant will have the opportunity to participate in workshops associated with the research at Clark University http://www.clarku.edu/articles/clark-university-biologist-co-lead-87-million-grant-evolutionary-biology, and also in the larger workshops associated with Templeton Grant.

The position is available as early as September 1, 2016, initially for a 2 year period. Salary is commensurate with experience relative to NIH guidelines.

To apply, please submit a letter of application, a CV, a statement of research interests and contact information for three references to sfoster@clarku.edu. Review of applications will begin immediately and will continue until the position is filled. Inquiries can be directed to sfoster@clarku.edu Additional information about our lab can be found at http://wordpress.clarku.edu/foster-baker-lab/ AA/EOE Clark values diversity.

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

CNRSFrance EcoEvoDevoTunicates

A 15 months postdoctoral position is available at the Observatoire Océanologique de Villefranche-sur-Mer - LBDV (UPMC - Sorbonne Universités). We are seeking a highly motivated and passionate researcher to join a 5-years international project, DEVODIVERSITY, funded by the French Agence Nationale de la Recherché (ANR) and the SÃ£o Paulo Research Foundation (FAPESP).

By using molecular and cell biology, NGS transcriptomic, genomic, and ecological approaches, a multidisciplinary consortium led by two teams, the Tiozzo Lab at the Villefranche-sur-Mer Developmental Biology Laboratory in France (CNRS-UPMC), and the Brown Lab at the Istituto de Biociências in Brazil (USP), will study the evolution of regeneration, asexual reproduction, and clonality in several species of ascidians (Urochordata), and examine how ecological factors affect distribution ranges, evolution of life cycles and developmental strategies. DEVODIVERSITY has the following main aims:

1. To resolve the phylogenetic relationships and evolutionary transitions between strict sexual reproduction to budding and high regenerative abilities among Styelidae (Ascidiacea). 2. To provide a coupled morphological and ecological understanding of asexual propagation (budding). We will generate detailed anatomical and developmental descriptions of budding processes, and explore if and which environmental conditions are associated with the use of particular budding modes. 3. To compare gene pathways involved in stem cell functions or trans/de-differentiation of budding and regenerative processes by the generation and in silico analyses of transcriptomic data. 4. To launch a comparative genomic approach study in order to better understand the evolution of a major life history transition in marine chordates, in particular the evolutionary transition from sexual to asexual propagation.

The candidate will be mainly based at the LBDV (Villefranche sur Mer, France) and may have the opportunity to do laboratory and fieldwork in both countries.

It is ESSENTIAL:

- A doctoral degree in animal biology, evolutionary biology or related disciplines. - Demonstrated experience in molecular biology, organismal biology and at least bases of bioinformatics and biostatistics. - Enthusiasm and genuine commitment to research work. - Demonstrated ability to undertake independent research, flexibility and problem solving skills. - Excellent communication skills in English spoken/written. - Ability to collaboratively work on a team.

Expertise in phylogenomics and transcriptomics is highly desirable but not mandatory. The LBDV has an international working environment, speaking French is not required but it would be a plus.

The applicant should contact directly Dr. Stefano Tiozzo (tiozzo@obs-vlfr.fr) providing a letter of interest, a CV and the contact of three potential referees. Please, add “DD_postdoc” on the subject of your email. Applications review will continue until the position is filled. Starting data could be any time from September 2016.

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Stefano Tiozzo, PhD Regeneration Team

Sorbonne Universités, UPMC Univ Paris 06, CNRS, Laboratoire de Biologie du Développement de Villefranche-sur-mer (LBDV), 06230 Villefranche sur-mer, France

Ph:+33 4 93 76 39 78 Fax:+33 4 93 76 37 92 web: http://biodev.obs-vlfr.fr/ ˜ tiozzo/tiozzo-lab/ “tiozzo@obs-vlfr.fr” <tiozzo@obs-vlfr.fr>

DalhousieU ProtistGenomics

Research Associate (in Comparative and Functional Genomics of Anaerobic Protists), Department of Biochemistry and Molecular Biology, Faculty of Medicine, Dalhousie University, Halifax, Nova Scotia

Position Overview

The Department of Biochemistry and Molecular Biology at Dalhousie University invites applications for a Research Associate in the laboratory of Dr. Andrew Roger. This full-time fixed term (grant-funded) position is for two years, subject to availability of grant funds.

Reporting to the Principal Investigator (PI), the primary purpose of this position is to work under the supervision of the PI on a project aimed at comparative and evolutionary genomics of anaerobic protists. Flexibility in working hours is desired as evening and weekend work may be required, depending on the nature of the research underway.

Qualifications / Requirements:

Ph.D. degree in Biology or related area required.

Minimum 4 years of Postdoctoral experience in this field are required.

Research experience in comparative and functional genomics of anaerobic protists, transcriptomics, molecular

phylogenetics, phylogeography and population genetics required.

Strong skills in bioinformatics, demonstrated proficiency in Python and R programing languages.

Proven abilities in next generation sequencing (NGS) libraries construction and sequencing, downstream data

processing, as well as general molecular biology procedures.

Experience in experimental design and statistical analyses.

Strong communication skills (written and oral), experience working as part of a team as well as independently.

Experience in grant application writing.

Annual salary: $41,000-46,000 CAD

Application Deadline: June 27, 2016

Applicants must submit a letter of application, a statement of research interests, curriculum vitae, and the names of three references to: Wanda Danilchuk, Biochemistry & Molecular Biology, Dalhousie University, P.O. Box 15000, Halifax, Nova Scotia, B3H 4R2, CANADA. Email: wanda.danilchuk@dal.ca

Please note, only those candidates chosen to continue on through the selection process will be contacted.

Dalhousie University is committed to fostering a collegial culture grounded in diversity and inclusiveness. The university encourages applications from qualified Aboriginal people, persons with a disability, racially visible persons, women, persons of minority sexual orientations and gender identities, and all qualified candidates who would contribute to the diversity of our community. All qualified candidates are encouraged to apply; however, Canadians and permanent residents will be given priority.

Andrew.Roger@Dal.Ca

EwhaWomansU Seoul GenomeSequencing

Ewha Womans University in Seoul (South Korea)

Postdoctoral research associate position on Genome sequencing of marine animals and invertebrates

The Marine Genome 100+ Korea project, a newly initiated large scale genomics project, aims to determine the sequences of whole genomes and transcriptomes of > 100 selected marine species. The position will primarily involve the analysis of NGS (Next Generation Sequencing) data from marine animals and invertebrates and extensive study of their genomes using phylogenomics and comparative genomics approaches. We seek a highly motivated and enthusiastic person who is able to work both as part of a team and independently.

The candidate will be responsible for: * Managing NGS data and analyses; * Proactively identifying and incorporating new algorithms and technology to automate the analysis of marine genomes and to extend the features of existing analysis pipeline; * Participating in a team of scientists to offer bioinformatics, genomics, transcriptomics and other omics solutions; * Training research staffs on the use of relevant bioinformatics software and tools;

The successful candidate is required to possess the following: * Ph.D. or equivalent in Computational Biology, Bioinformatics, Genomics, Marine Biology or related field and experiences in two or more of the following areas: comparative genomics, transcriptome sequencing analysis, phylogenetic analysis, and/or genome wide association studies; * Applicants must have at least one strong first-author publication.

* Experience with bioinformatics analyses, including programming in any scripting language (e.g. PERL or Python) and ability to handle a large data set efficiently using scripts, particularly in the analysis of NGS data;

* Familiar with commercial and open-source bioinformatics tools and various public genomic databases; * Genome assembly of de novo genomes; * Knowledge of statistical software tools and packages (e.g. R);

* Evidence of excellence in research and high productivity.

The estimated start date is September 1^st, 2016 with a two year position at lea st (extensible). Salary is competitive and commensurate with experience and care er. Applicants should send a short research statement (including past, present, and future goals), CV, and the names and email addresses of at least 3 potential references as a single pdf file to Prof. Joong-Ki Park (Project PI: E-mail: jkp ark@ewha.ac.kr). Informal inquiries are also welcome.

Joong-Ki Park, PhD. Professor Division of Eco-Science Ewha Womans University Science A Building (Room# 210) 52 Ewhayeodae-gil, Seodaemun-gu Seoul 120-750, Korea Tel: (office) +82-(0)2-3277-5948; (lab.) +82-(0)2-3277-4038 CP:+82-(0)10-6431-3735 E-mail: jkpark@ewha.ac.kr E-mail: jkpyou@gmail.com http://www.ewha.ac.kr/mbs/ewhaen/index.jsp http://www.ewha.ac.kr/mbs/ewhakr/index.jsp Joong-Ki Park <jkpark@ewha.ac.kr>

FederalUParana Brazil EvolutionaryBiology

The Zoology Department of the Federal University of Paraná (UFPR), located in Curitiba, Brazil, is seeking a

Postdoctoral Research Associate to work on any project of his/her interest within the broader discipline of Zoology. Interfaces with research projects conducted by department Pis are desirable, but not mandatory.

We are looking for highly motivated individuals with strong publication record and good communication skills. A PhD in any area is acceptable, provided that the track-record demonstrates the candidate ability to publish in the areas of Ecology, Systematics and/or Evolution, with emphasis on animal-oriented systems.

Proficiency in Portuguese is not required, but candidates must be fluent in either English or Spanish. The successful applicant will be required to offer one discipline per year. Appointment renewals will be evaluated on a yearly basis up to 5 years. The scholarship is R$ 4,100.00 per month, tax free. Up to R$ 12,000/annum may be available every year to cover research expenses, depending on fund availability.

Application deadline is May 25th 2016.

Follow the links below for application instructions in Portuguese and English.

http://www.prppg.ufpr.br:8080/pgzoo/-sites/default/files/Documentos/PNPD/-2016_EDITAL_01%20_SELECAO_PNPD_Zoologia_2016.pdf http://www.prppg.ufpr.br:8080/pgzoo/node/8080/-pgzoo/sites/default/files/Documentos/PNPD/-2016_EDITAL_01%20_SELECAO_PNPD_Zoologia_2016_%20English.pdf Curitiba is a beautiful, multicultural city that ranks consistently among the top ten cities to live in Brazil. Surrounded by lush Atlantic Forest, it enjoys easy access to an international airport and it is linked by major highways to the scenic beaches of Paraná and Santa Catarina states. UFPR is a centenary institution and one of the top Brazilian research universities.

Further inquiries should be directed to Dr. Lilian Manica (lilianmanica@gmail.com) or Dr. Rodrigo Feitosa (rsmfeitosa@gmail.com).

– Marcos S. Barbeitos

Departamento de Zoologia - Sala 360 Setor de Ciências Biológicas Universidade Federal do Paraná Caixa Postal 19020 Curitiba, PR 81531-990 Brazil

Phone: (55 41) 3361-1634

Marcos Barbeitos <msbarbeitos@gmail.com>

FHCRC Seattle BayesianPhylogeneticInference

Vladimir Minin and I have an open postdoc position as part of a project to develop new methods for Bayesian phylogenetic inference. To summarize,

- collaborate with a very strong team on a challenging and important problem - integrate theory, computational experiment, and implementation - 4 years of support if it's a perfect match - live in Seattle, and work near downtown with a view of the lake

More details at http://matsen.fredhutch.org/general/-2016/04/18/altphylo-postdoc.html – Frederick "Erick" Matsen, Associate Member Fred Hutchinson Cancer Research Center http://matsen.fredhutch.org/ matsen@fredhutch.org

FieldMuseum Chicago EvolutionaryBiology

Interdisciplinary Postdoctoral Scientist Positions at the Field Museum

The Field Museum invites applications for Interdisciplinary Postdoctoral Scientists. The successful candidates will work on interdisciplinary research projects advised by one or several Field Museum curators to complement any of the ongoing research programs at the Field Museum and to collaborate with scientists outside the Field Museum. At the Field Museum, research is being pursued in the areas of Life Sciences, Social Sciences, and Earth and Planetary Sciences.

Requirements: Research proposals must be written rigorously for a general scientific audience (the review committee can consist of biologists, geologists, and anthropologists). The scientific motivation should be given in a broad context. The project must include one Field Museum curator combined with one or several other Field Museum researchers and/or one or several researchers outside of the Field Museum. Applicants are required to contact the most relevant curator prior to application; a complete application must include the curator's endorsement letter (list of curators and potential in-house collaborators at https://www.fieldmuseum.org/sponsors-visting-scholars-bass-senior-visiting-fellows-and-postdoctoral-scholars). Required format for research proposals: Limit to two letter-sized pages, 12 pt font for all text including figure captions and tables, 1-inch margin on all sides, PDF format required. A bibliographic reference list is required but does not count towards the two-page limit.

Selection: Candidates will be selected based on the scientific merit of the research proposal, its potential to augment the Field Museum's research and collections strengths, to maximize the impact and to combine expertise of Field Museum curators and outside researchers across disciplines, and the qualifications of the applicant.

Qualifications: A completed Ph.D. in a field of one of the proposed research disciplines is required before the proposed start date.

Terms: Funding is available for one to two positions with two-year terms (second year will be provided upon satisfactory performance) and one position for a one-year term. The appointments are anticipated to begin in October 2016. In addition to salary and benefits, limited funds for research and/or travel will be provided.

Requested application materials include a research proposal (see above for requirements), curriculum vitae including publications list, PDFs of three of your peer-reviewed publications and names of three referees (with e-mail addresses and phone numbers). In addition, we require a curatorial endorsement letter and at least two reference letters. We will instruct letter writers on how to submit letters. We encourage women and minorities to apply. Applications and letters need to be submitted between July 1st, 2016 and July 21st, 2016. Submission instructions will be posted end of June at https://www.fieldmuseum.org/about/careers/research-scholarships-and-grants .
rree@fieldmuseum.org

FloridaStateU ComputationalBiol

Postdoctoral Scholar - Computational Biologist Department of Scientific Computing, Florida State University

=== Qualifications === Eligible candidates must hold a PhD in computational biology, applied mathematics, statistics, or computational physics at the time of appointment. Familiarity with C, C++, and Python is required. Some knowledge of the coalescence theory and population genetics is also required. The postdoctoral scholar must have a demonstrated ability to publish papers and also to be able to not only write but also debug software codes and document the software.

=== Responsibilities === The postdoctoral scholar will - participate in theoretical/computational biology research that aims at inference of adaptation using coalescent trees. - write inference and simulator software using C/C++ and Python - publish research findings, present at conferences, mentor undergraduate and graduate students, and assist with grant proposal writing.

=== Terms === Ideally the position would start in August 2016, but start date is flexible. Initial appointment for one year with strong potential for renewal contingent on performance, appointment is maximally for 3 years. FSU offers competitive salary and excellent benefits including access to faculty insurance plan options and retirement plan. See http://opda.fsu.edu/ and http://hr.fsu.edu/ for more information.

=== How to apply === Applicants should apply at https://jobs.fsu.edu (Job ID 40327). Applicants must submit a cover letter describing their qualifications, research interests, and career goals; a CV; and names and contact information for three professional references.

**** Please forward a copy of all application materials as a single PDF to beerli@fsu.edu.****

=== Open until filled === This position will remain open until filled. Application review will begin on June 20, 2016 and applicants should submit materials no later than July 5 for primary consideration.

=== Contact information === Contact Dr. Peter Beerli at beerli@fsu.edu with any questions about the position.

An Equal Opportunity/Access/Affirmative Action/Pro Disabled & Veteran Employer. FSU's Equal Opportunity Statement can be viewed at: http://www.hr.fsu.edu/PDF/Publications/diversity/EEO_Statement.pdf "Beerli, Peter" <pbeerli@fsu.edu>

FloridaStateU GuppyEvolution

Post-doc, for up to three years: We seek a post-doc to participate in a US National Science Foundation supported project entitled “The Paradox of Coexistence: The Evolution of Ontogenetic Interactions”. This research is a continuation of an ongoing experimental study of the interactions between ecology and evolution in natural streams in the Northern Range Mountains on the island of Trinidad. Our project is built around four experimental introductions of guppies into previously guppy-free tributaries that contain only one other fish species - the killifish Rivulus hartii. Our prior research has characterized how each of these species evolves in response to the other and to the way the ecosystem changes after the guppy introduction. One discovery is that their interactions include bi-directional intra-guild predation. Theory predicts that such an interaction is very unlikely to be stable, yet it proves to be reliably stable in all four introductions and in all natural streams where these fish coexist. This apparent anomaly is the basis for an exploration of factors not included in theory that could lend to this stability, including the contemporary evolution of both participating species and how these interactions change with the age and size of individuals in both species. Our project is an integration of the development of new theory, new experiments to be performed in natural and artificial streams in Trinidad and the continued study of the four introductions in natural streams. The post-doc's home base will be with Joseph Travis (PI) at Florida State University but will include extensive periods of time in Trinidad, where he/she will execute experiments in natural and artificial streams. The successful applicant must have a completed PhD, publication record and extensive field experience. You can learn more about our project at our website <CNAS.UCR.EDU/guppy>. To apply, please send a CV and arrange to have at least three letters of reference sent to David Reznick at david.reznick@ucr.edu.

Ronald Bassar <ronald.bassar@zoo.ox.ac.uk>

HowardU EvoDevoMacroevolution

Postdoctoral Position in Anatomical Networks, Evo-Devo and Macroevolution

Hiring Organization:

Howard University

Date Posted:

2016-05-11

Position Description:

Postdoctoral Position in Anatomical Networks, Evo-Devo and Macroevolution

A Postdoctoral researcher is sought to join the Rui Diogo lab (www.ruidiogolab.com), at the Howard University College of Medicine, Department of Anatomy (Washington DC). For more details on the research done at the lab, and the papers/chapters/books published in recent years, see also:

https://www.researchgate.net/profile/Rui_Diogo Diogo's books: http://www.amazon.com/Rui-Diogo/e/B001JS2K96 We are interested in a candidate that will have the ability to combine two or more - and ideally all four - items; there is a strong competition, so please make sure you have the necessary skills and interest and drive for this position:

1) contribute to uncover evolutionary and developmental mechanisms underlying both hard tissue (cartilages and bones) and soft tissue (mainly muscles) formation and patterning during ontogeny of a wide range of vertebrate taxa. Some of the issues and broader questions in which we are particularly interested include: the parallelism between ontogeny and phylogeny, the remarkable similarity between the hard and particularly the soft tissues of the upper and lower limbs of tetrapods, the importance of evolutionary reversions/neotenic events, the study of birth defects in human and non-human primates and their implications for medicine and for the understanding of evolutionary biology, and the regeneration of hard and soft tissues in key vertebrate taxa. For more information about these subjects and about other issues being studied in the lab, please see www.ruidiogolab.com . 2) you should have good writing skills, and a profound interest in reading, as you will be expected to lead, and help write, review papers and probably books/book chapters on the broader macroevolutionary topics covered above. In turn, by doing this

you can relatively rapidly get a substantial experience in publishing in top journals and monographs.

3) you will also help build and maintain a website, so you need to have and be able to show previous skills on website design, managing, maintenance.

4) you will be mainly involved in learning, the framework of anatomical networks, and helping in anatomical network analysis, which relate directly to broader discussions on evolvability, complexity, modularity and integration

In summary, this will be a highly demanding - and expected to be a highly-demanded - position, in a very productive lab, in which there is a relatively high independence, where the drive of the postdoc is essential to make her/him more productive, taking advantage of the broader scope and numerous collaborations of the lab.

There are funds available for one year, starting fall (September) 2016, with the hypothesis of extending the position for two years, in case of excellent results and fit within the lab, i.e. the second contract depending on the productivity, interest and dedication of the candidate. There are possibilities to continue being part of the lab after the two-year period of the post-doc position. The post-doc will also have the opportunity to learn, and potentially to then become an instructor/faculty of human gross anatomy; this will further allow him/her to also postulate for faculty positions in medical schools in the DC area (including Howard University) as well as in other regions.

Interested candidates should send a CV including research interests, a list of publications and the names and contact information for three references to Rui Diogo, at rui.diogo@howard.edu. Please write “post-doc in Diogo’s lab” followed by your last name in the email subject.

Howard University is a historical University situated in the center of Washington DC, which is a beautiful, green and enjoyable city with numerous cultural and outdoor activities. The Department of Anatomy provides a prosperous, resourceful and multidisciplinary environment for biomedical research, includes faculty with a broad experience in developmental biology, paleontology, neurobiology, comparative anatomy and medicine. We have strong ties with surrounding institutions, particularly with George Washington University, and the candidate will probably have the opportunity to do part of his/her research at those institutions and thus to expand his/her knowledge and academic connections.

Qualifications/Experience:

The successful candidate will have a PhD degree with a broad experience in developmental biology (e.g., doing/using developmental techniques such as antibody staining, in situ, and cell tracing, among others)

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HowardU EvoDevoMacroevolution 2

2nd Postdoc Position in Evo-Devo and Macroevolution

Hiring Organization:

Howard University

Date Posted:

2016-05-19

Position Description:

Postdoctoral Position in Evo-Devo and Macroevolution

Apart from the position postd a few days ago, we are happy to announce that a 2nd postdoctoral researcher is sought to join the Rui Diogo lab (www.ruidiogolab.com), at the Howard University College of Medicine, Department of Anatomy (Washington DC). For more details on the research done at the lab, and the papers/chapters/books published in recent years, see also:

https://www.researchgate.net/profile/Rui_Diogo
Diogo’s books: http://www.amazon.com/Rui-Diogo/e/B001JS2K96 The main difference between this position and the one previously announced is that the position will not be related to anatomical networks nor building websites. We are therefore interested in a candidate that will have the ability to:

1) contribute to uncover evolutionary and developmental mechanisms underlying both hard tissue (cartilages and bones) and soft tissue (mainly muscles) formation and patterning during ontogeny of a wide range of vertebrate taxa. Some of the issues and broader questions in which we are particularly interested include: the parallelism between ontogeny and phylogeny, the remarkable similarity between the hard and particularly the soft tissues of the upper and lower limbs of tetrapods, the importance of evolutionary reversions/neotenic events, the study of birth defects in human and non-human primates and their implications for medicine and for

the understanding of evolutionary biology, and the regeneration of hard and soft tissues in key vertebrate taxa. For more information about these subjects and about other issues being studied in the lab, please see www.ruidiogolab.com . 2) help write review papers and books on the broader macroevolutionary topics covered above and other topics, and, by doing this you can relatively rapidly get a substantial experience in publishing in top journals and monographs.

In summary, this will be a position in a very productive lab, in which there is a relatively high independence, where the drive of the postdoc is essential to make her/him more productive, taking advantage of the broader scope and numerous collaborations of the lab. Contrary to the previously announced position, you will thus more involved in lab evo-devo research and in writing and publishing.

There are funds available for one year, starting fall (September) 2016, with the hypothesis of extending the position for two years, in case of excellent results and fit within the lab, i.e. the second contract depending on the productivity, interest and dedication of the candidate. There are possibilities to continue being part of the lab after the two-year period of the post-doc position. The post-doc will also have the opportunity to learn, and potentially to then become an instructor/faculty of human gross anatomy; this will further allow him/her to also postulate for faculty positions in medical schools in the DC area (including Howard University) as well as in other regions.

Interested candidates should send a CV including research interests, a list of publications and the names and contact information for three references to Rui Diogo, at rui.diogo@howard.edu. Please write “post-doc in Diogo’s lab” followed by your last name in the email subject.

Howard University is a historical University situated in the center of Washington DC, which is a beautiful, green and enjoyable city with numerous cultural and outdoor activities. The Department of Anatomy provides a prosperous, resourceful and multidisciplinary environment for biomedical research, includes faculty with a broad experience in developmental biology, paleontology, neurobiology, comparative anatomy and medicine. We have strong ties with surrounding institutions, particularly with George Washington University, and the candidate will probably have the opportunity to do part of his/her research at those institutions and thus to expand his/her knowledge and academic connections.

Qualifications/Experience:

The successful candidate will have a PhD degree with a broad experience in developmental biology (e.g., doing/using developmental techniques such as antibody staining, in situs, and cell tracing, among others) and/or evolutionary biology, and hopefully both, backed by publications in peer-reviewed journals, and ideally also some experience in comparative anatomy. He/She will have the skills and motivation to pursue a career in research, be interested in studying and comparing a wide range of taxa and various model organisms and in discussing various evolutionary and

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

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LoyolaUChicago Bioinformatics

Loyola University Chicago, College of Arts and Sciences, Department of Biology invites applications for a full-time postdoctoral associate, with expertise in the areas of Computational Biology and complex trait genetics. The position is for one year with the possibility of renewal, for additional years, based on performance.

This position will support research on the development of computational models and pipelines that leverage and integrate similarity in genetic, transcriptomic, or other omics-level data for complex trait prediction in the laboratory of Dr. Heather Wheeler. The postdoc will work with Dr. Wheeler and her collaborators to investigate how genetic variation leads to phenotypic variation for complex traits including disease susceptibility and drug response. This position is jointly funded by the Department of Biology, and the postdoc will teach 1-2 departmental courses each semester. This is an ideal position for candidates who are interested in gaining teaching experience while conducting cutting-edge research. For more information about the department visit http://luc.edu/biology/index.shtml . The successful candidate will be involved in data analysis, statistical modeling, software development, writing manuscripts, giving presentations, and mentoring students under the supervision of Dr. Wheeler. In addition to computational work, the postdoc will teach courses in the Department of Biology.

Applicants must have a Ph.D. in genomics, bioinformatics, computational biology, biostatistics, or a related field with a solid publication record. The ideal candidate will have strong analytical, statistical, quantitative, and computational/programming (e.g. R, Python, Linux) skills and should be comfortable with large data sets, distributed computing, and databases. High performance computing and cloud computing experience is a plus.

Applicants should submit a Cover Letter describing their research interests and availability, current Curriculum Vitae, and contact information for two references to www.careers.luc.edu/applicants/-Central?quickFindX820. The position is available immediately and will remain open until filled.

Loyola University Chicago is an Equal Opportunity/Affirmative Action employer with a strong commitment to hiring for our mission and diversifying our faculty. As a Jesuit Catholic institution of higher education, we seek candidates who will contribute to our strategic plan to deliver a Transformative Education in the Jesuit tradition. To learn more about LUC's mission, candidates should consult our website at www.luc.edu/mission/. For information about the university's focus on transformative education, they should consult our website at www.luc.edu/transformativeed . sreddy6luc@gmail.com

LundU EvolutionPhylogenyThermal Adaptation 2

Postdoc in evolution, phylogeny and thermal adaptation (Lund University, Sweden)

I have an opening for a postdoc with background and experience in phylogenetic comparative methods for a project on micro- and macroevolution of thermal adaptation and thermal plasticity (start date: October 1 2016). This is a perfect opportunity for somebody who is interested in combining phylogenetic comparative methods and experiments, theory and empirical work.

I am seeking a qualified candidate anywhere from the world, as long as (s)he fits the required qualifications and criteria and is interested to work in my lab and in a friendly, collaborative and creative international research environment in Lund (Sweden). Please do not hesitate to contact me if you have any further questions and spread the information about this position to suitable members in your lab and in your international networks.

Information about the position and application procedure can be found here: https://-lu.mynetworkglobal.com/en/what:job/jobID:99355/ Sincerely, Erik Svensson

Erik Svensson Professor Department of Biology, Evolutionary Ecology Unit Lund University SE-223 62 Lund SWEDEN Phone: +46 46 222 38 19 Fax: +46 46 222 47 16 E-mail: erik.svensson@biol.lu.se Webpage: http://www.biology.lu.se/erik-svensson Lab blog: http://exeblund.blogspot.se Researcher ID: http://www.researcherid.com/rid/E-8324-2010 New book: "The Adaptive Landscape in Evolutionary Biology" Edited by Erik Svensson and Ryan Calsbeek Available through all good bookshops, or direct from Oxford University Press at: http://-ukcatalogue.oup.com/product/9780199595389.do Erik Svensson <erik.svensson@biol.lu.se>

MaxPlanckInstitute EvolutionaryGenomics

Postdoc Position in Computational Biology and Evolutionary Genomics

The Research Group "Computational Biology and Evolutionary Genomics" in Dresden, Germany has an opening for a Computational Biology Postdoc. The computational postdoc will leverage methods developed in the lab to discover genomic differences underlying the evolution of morphological differences in mammals. Promising candidates will be tested experimentally. The Postdoc will work closely with other lab members on all computational aspects and with a group of collaborators on phenotypic and experimental aspects. Funding according to the German TVöD scale is available for at least 3 years.

Our group:

The mission of our group is to discover the differences in the genome that underlie phenotypic differences between species. Thus, we will contribute to our understanding how nature's incredible diversity evolved. To this end, we are combining computational and experimental approaches. On the computational side, we build high-quality genome alignments, develop and apply comparative methods to discover functional genomic differences, and use statistical approaches to associate genomic to phenotypic differences. On the experimental side, we sequence and assemble genomes of species with interesting phenotypes, we use approaches like RNA-seq and ATAC-seq to annotate genes and regulatory regions, and we experimentally test whether editing a discovered genomic loci in a model organism recapitulates natural phenotypic differences.

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

Requirements:

Applicants should have a background in bioinformatics or computational biology and a strong publication record. Excellent programming skills (perl, python, or C/C++) in a Linux environment as well as experience with shell scripting and Unix tools are required. Previous experience in large-scale genomic data analysis is an advantage. Applicants should also have a strong interest in the molecular biology underlying species' phenotypes.

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

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

MNHN Paris ButterflyWingVariations

Postdoctoral position on genetic basis of variations in wing colour pattern development in butterflies at the Natural History Museum in Paris

We are seeking an independent, creative and motivated post-doc to take part to a project on the evolution of butterfly wing colour patterns in Heliconius and Morpho clades. The repeated recruitment of the same genes in contrasted colour patterns from highly divergent Lepidoptera species (Nadeau et al. 2016 Nature) stimulates our research on the development of wing colour pattern variations in different clades. This project is supported by a 4-years Emergence grant, involving a research team headed by Violaine Llaurens, with focus on evolutionary biology, population genetics and evo-devo. Our lab is located at the Institute of Systematics, Evolution and Biodiversity at the National Museum of Natural History in Paris (France), where both collections and research facilities cohabit. The emergence grant can cover two years of postdoc salary and research expenses.

Postdoc projects: The postdoc will be specifically in charge of investigating molecular mechanisms underlying wing colour pattern variations, including dominance and epistasis.

A first part, for which samples and preliminary data are already available, will focus on studying expression patterns of genes underlying colour pattern variations in mimetic butterflies Heliconius numata and H. hecale. We are currently characterizing genetic variation underlying wing colour patterns in the polymorphic species Heliconius numata. In this species, variation of colour pattern is mainly controlled by a supergene, exhibiting chromosomal inversions (Joron et al. 2011 Nature). We have identified a few candidate genes controlling different aspects of wing colour patterns. However, this supergene is highly polymorphic within natural populations, maintaining high haplotype heterozygosity. By precisely quantifying wing colour pattern variation, we showed that dominance between supergene haplotypes is generally strict, preventing the expression of intermediate, non-mimetic patterns (Le Poul et al. 2014 Nature Communications). However, given the recent evidence that several genes from the supergene are expressed at different developmental stages, we question how such coordinated dominance has evolved. The postdoc will be in charge of analyzing transcriptome data from homozygotes and heterozygotes at the supergene, to identify the mechanisms underlying epistasis and dominance in this polymorphic species. He/she will also compare these mechanisms in a closely-related species, namely Heliconius hecale, to investigate the potential evolution of dominance mechanisms in the genus.

In parallel to this project on Heliconius for which a lot of genomic resources are already available, the postdoc will also investigate the genetic basis of wing colour pattern variations in three Morpho species (M. helenor, M. achilles and M. deidamia) from Peru, using both genomic and transcriptomic data. These three species exhibit similar wing colour patterns, but also similar geographical variations, questioning the similarity of the underlying genetic architecture.

This postdoc will imply mostly lab work and bioinformatics, but will also include fieldwork in tropical areas (Panama and Peru), in order to enlarge the sampling of colour pattern variations displayed in natural populations. This two-faceted project will provide ample opportunity for the postdoc to develop his/her own original research ideas.

Candidate profile: A Phd in Evo-Devo, with a strong interest in evolutionary ecology. Experiences with non-model (insect) organisms, genomics/transcriptomics and in situ hybridization, as well as fieldwork experience in Tropical countries would be appreciated.

Income and Starting Date: Net salary will be around 2000-2500 euros net per months, depending on experience. The postdoc will start as soon as possible, but dates are negotiable.

Application deadline: Applicants should send a CV and a cover letter, and the names of two references by 31st May 2016 to the following address: llaurens@mnhn.fr

More information:

http://isyeb.mnhn.fr/annuaire-et-pages-personnelles/pages-personnelles/LLAURENS-Violaine

Violaine Llaurens - CR1 CNRS

Institut de Systématique, Evolution et Biodiversité (UMR 7205 CNRS/MNHN/UPMC/EPHE) Muséum National d'Histoire Naturelle - CP50 45 rue Buffon 75005 PARIS

01 71 21 46 96

Violaine Llaurens <violaine.llaurens@mnhn.fr>

NIAB EMR England BioinformaticianPopGenet

A bioinformatician/ population geneticist is required to undertake population genomics research on perennial fruit species and their pathogens and pests. Much of the research undertaken will work towards investigating the molecular mechanisms involved in host resistance to pathogens. The successful applicant will work across multiple BBSRC funded projects to elucidate the genetic basis of disease resistance in the first instance to the oomycete pathogens Phytophthora cactorum and Phytophthora fragariae in the octopoloid strawberry Fragaria x ananassa. An interest in the evolutionary dynamics of host-pathogen interactions would be highly desirable.

Key areas of the job

* Population-level analysis of candidate resistance genes and pathogen effector genes: Familiarity with basic population genetics approaches to detect selection from nucleotide sequences either using between species data (e.g. PAML) and/or within species (e.g. McDonald-Kreitman tests, Tajima's D, haplotype tests etc.)

* Analysis of RNA-seq transcriptome time-course data in order to identify candidate host and effector genes which are implicated in host-pathogen interactions. Analysis of gene regulatory networks is an important component of this work, linking expression to genes with QTL and analysing subgenome-specific patterns of expression variation

* Quantitative genetics analysis of disease resistance using mixed modelling approaches- a working knowledge of mixed-model approaches to the analysis of quantitative trait data and genotypic data to identify genetic variants contributing to variation in complex traits

Salary:£27,099 to £37,810 with salary dependent on experience and relevant qualifications. Pay Band 5/6

25 days annual leave plus 8 days public holidays, pleasant working environment and eligibility to join an occupational pension scheme upon appointment.

Further details and an application form can be obtained from the NIAB-EMR website, www.emr.ac.uk, or by e-mail from recruitment@emr.ac.uk Please include a detailed CV with your application.

For informal enquiries please contact Dr Richard Harrison (richard.harrison@emr.ac.uk).

Interviews will be at East Malling on the 9th June.

< http://www.emr.ac.uk/vacancy/bioinformatician-population-geneticist/ >

Dr Richard Harrison Senior Group Leader | Genetics and Crop Improvement NIAB-EMR | New Road, East Malling, Kent, ME19 6BJ ' | 01732 52 3747 (| 07773 059456 +| richard.harrison@emr.ac.uk 8| http://www.emr.ac.uk/projects/harrisonlab/ richard.harrison@emr.ac.uk

Paris6U MicrobialBioinformatics

Hello,

Please find below the description of a postdoctoral position to 'Search for common 'genetic goods' in gene families and microbial communities'.

We are offering a 14 months post-doctoral position, starting on September the 1rst 2016 (see also http://

www.evol-net.fr/index.php/fr/postes-a-pourvoir).

The theory of 'genetic public goods' recently postulated that genetic sequences can be exploited in various combinations, even by distantly related or unrelated evolving entities, i.e. microbial communities benefiting from the sharing of genes between their members, such as photosynthesis genes between cyanophages and cyanobacteria, or such as drug resistance genes within multispecies biofilm. Yet, the nature, size and diversity of microbial communities sharing such 'genetic goods' remain poorly known. Moreover, the rules of gene sharing also remain to be described.

A wealth of molecular data from metagenomic, single cell metagenomic, and microbial genomes projects is now available to tackle these fundamental issues. Furthermore, sequence similarity networks offer a promising complementary niche to phylogenetic methods to exploit the complexity of these data. These graphs allow for mathematical analyses of genetic diversity and similarities over dozens of millions of sequences, providing novel ways to detect 'clubs' of genomes, which have not necessarily evolved from a single last common ancestor yet exploit some common genetic material. Likewise, these networks allows for the detection of some 'sets' of gene families that exploit common pools of genetic fragments/domains.

To further develop the detection strategies of genetic public goods, our lab is now looking for a post-doctoral fellow in bio-informatics, who will be funded for up to three years by an ERC grant (for an approximate salary of 2197 euros/ month after taxes, i.e. 57 350euro before taxes for the entire post-doc). The candidate will take advantage of graph properties and algorithms from the graph theory:

-1) to improve the identification of 'clubs' of genomes /'sets' of gene and their pool of genetic goods in complex networks with a few millions nodes and dozens of millions of edges;

- 2) to analyze domains combinations in genes and gene sharing in communities, using bipartite graphs;

-3) He/she will then analyze the functions of these 'genetic goods' and their distribution across genes and genomes to test what lifestyles favors their sharing.

The candidate will work within a consortium of friendly bioinformaticians (Philippe Lopez, Eduardo Corel), evolutionary biologists (Eric Bapteste), and graph theorists (Michel Habib, Laurent Viennot), and be hosted in the University Pierre and Marie Curie in the center of Paris, France. Ideally, the candidate should have a strong interest for evolutionary biology, microbial evolution and a good background in bio-informatics, or graph theory. The position will start by September 2016, but interested candidates are invited to apply immediately.

He/she should be early in his/her carreer (i.e. holding a PhD degree for less than 2 years).

Applicants are requested to send a detailed resume, a motivation letter, a pdf copy of their PhD thesis, and the names of two scientific referees to : eric.bapteste[at]snv.jussieu.fr

The first round of applications will be closed June 1rst, 2016.

epbapteste@gmail.com

PotsdamU EvolutionaryGenomics

Research Scientist/PostDoc position (TVL13) in Evolutionary Genomics at Potsdam University

A Research Scientist/PostDoc position (TVL 13) is available at the Unit of Evolutionary Biology/Systematic Zoology at the University of Potsdam, starting August 1^st 2016. The position will be available for 3 years, with the possibility of prolongation for a total duration up to 6 years.

The Unit of Evolutionary Biology/Systematic Biology has a strong focus on population genetic and speciation research, involving various taxonomic groups and a suite of molecular, morphological, and behavioural approaches (see http://www.uni-potsdam.de/-ibb/arbeitsgruppen/ordentliche-professuren/ev olutionsbiologie-spez-zoologie.html for recent work). The Unit runs a state-of-the-art molecular evolutionary laboratory and has access to a NGS facility.

The successful applicant is expected to run his/her own research program (including attraction of third-party funding) as well as to scientifically interact with other group members.

The position includes a teaching duty of 4 hours/week in zoology/evolutionary biology for undergraduates and graduates. Teaching can be generally performed in English, but the willingness to acquire German language skills for undergraduate teaching would be preferential.

Applicants must hold a university doctoral degree in biology or a related discipline. Familiarity with modern molecular genetic and genomics techniques (including Next Generation Sequencing) as well as in genomic data analysis is strongly preferred.

The University of Potsdam is an equal opportunity employer. If equally qualified, disabled applicants will be preferably considered. The University of Potsdam aims at increasing the number of female researchers and encourages qualified females to apply.

Potsdam is a beautiful city in close vicinity to the German capital of Berlin. Potsdam University takes an effort to assist its members in family-related issues and has repeatedly been awarded the total e-quality award.

Please send your application by email (preferably in a single pdf) before 31^st of May 2016 to: Prof. Dr. Ralph Tiedemann, University of Potsdam, Institute of Biochemistry and Biology, Evolutionary Biology/Systematic Zoology, Karl-Liebknecht-Str. 24-25, Haus 26, D-14476 Potsdam, Germany, Email: tiedeman@uni-potsdam.de

Prof. Dr. Ralph Tiedemann Unit of Evolutionary Biology/Systematic Zoology Institute of Biochemistry and Biology University of Potsdam Karl-Liebknecht-Str. 24-25, Haus 26 D-14476 Potsdam Germany Tel: +49-331-977-5249, -5253 (secretary) Fax: +49-331-977-5070 Email tiedeman@uni-potsdam.de www.uni-potsdam.de/ibb/evolution Ralph Tiedemann <tiedeman@uni-potsdam.de>

RBG Kew PlantPhylogenomics

Phylogenomics Research Fellow Royal Botanic Gardens, Kew Link: https://careers.kew.org/vacancy/-phylogenomics-research-fellow-264707.html Closing Date: 19/06/2016

We are seeking to recruit a talented, postdoc-level scientist to join a team of plant phylogenomic and evolutionary experts in Kew's Comparative Plant and Fungal Biology department. The post will provide excellent opportunities to engage with the latest advances in high-throughput DNA sequencing technologies to address both pure and applied research questions, with a focus on palm phylogenomics, conservation and seed science. The research forms part of a broader science programme "Delivering global tree conservation through seed science" at Kew funded by the Garfield Weston Foundation and is linked to Kew's Plant and Fungal Trees of Life initiative.

The project will focus on a model group of tree species, the palms. Palms are among the most economically important of all plants and, as a result, face intensified threats due to selective use by humans. Kew is a recognised global centre of excellence in palm diversity research and has a long term interest in the seed biology of the family. A family-wide synthesis of phylogenomic and seed trait data will create new opportunities to advance the conservation of this charismatic plant group and may facilitate the development of protocols for the conservation of its recalcitrant seeds.

As the research scientist on this project you will 1) generate and manipulate genomic data for all genera of palms and for species in the megadiverse Indo-Pacific tribe Areceae using high throughput sequence capture techniques, 2) use these data to reconstruct global phylogenies for palms and for tribe Areceae, 3) compile seed trait data to explore their correlations with biogeographic history, diversification and extinction risk in an evolutionary context. The project will be highly collaborative, involving numerous opportunities to interact with experts at Kew and beyond.

You will be an outstanding and inspiring scientist with a PhD and some relevant specialist experience in high-throughput sequencing, phylogenetic analysis, bioinformatics and/or comparative evolutionary biology. You will also have experience of writing and contributing to research publications (both as lead author and as part of a team), together with excellent communication skills. Experience of independently managing a discrete area of a research project with good time management skills is also essential.

How to apply: Please complete an application via the Kew jobs portal. https://careers.kew.org/vacancy/-phylogenomics-research-fellow-264707.html In addition, please upload 1) a covering letter describing your motivations and qualifications for the role (max. 2 pages) and 2) your CV, which should include a full list of your publications and grants/awards.

For informal enquiries, please contact Dr. Bill Baker w.baker@kew.org

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

W.Baker@kew.org

RoslinInstitute UK 2 ComputationalBiol

Dear All,

I would like to draw your attention to two post-doc level positions at The Roslin Institute.

Regards,

John

Research Fellow

Salary Range: 31,656 - 37,768

The Roslin Institute is a world-class centre for research on Quantitative Genetics of populations, particularly in managed populations such as livestock, companion animals, forests and crops. We have a vacancy for a Research Fellow to work with John Hickey to analyse the genome sequences, pedigrees and phenotypes of large datasets.

Working in a team of eleven computational biologists the post holder will develop tools and applications for manipulation of huge datasets and analyse such data sets to help unravel the genetic basis of quantitative traits.

The ideal candidate will be a self-motivated, proactive and autonomous individual with strong experience in a wide range of population genetic analysis on Linux platform, GWAS, genomic prediction and haplotyping. This post is for 2 years.

The post-holder will join the Division of Genetics and Genomics at the Institute which comprises 18 group leaders, both desk based and lab based scientists. The department benefits from synergies arising from academic backgrounds including DNA-chemistry, statistics, mathematics and theoretical physics in addition to genetics.

Informal enquires can be made to John Hickey at john.hickey@roslin.ed.ac.uk

Formal applications should be made via this link: http://www.roslin.ed.ac.uk/vacancies/036272/-research-fellow/ Closing Date: 01 Jun 2016

Lead Scientific Programmer

Salary Range: 31,656 - 37,768

The Roslin Institute is a world-class centre for research on Quantitative Genetics of populations, particularly in managed populations such as livestock, companion animals, forests and crops. We have a vacancy for a scientific programmer to work with John Hickey on the further development of the AlphaSuite, a collection of software packages widely used in the animal and plant breeding communities, as well in the human genetics field.

Working in a team of eleven computational biologists the post holder will lead a team on the development of tools and applications for manipulation of huge datasets and maintaining and developing software codes to required standards.

The ideal candidate will be a self-motivated with strong experience in programming in different languages (C/C++, FORTRAN), proven knowledge in scripting languages (Python and BASH) and in developing and implementing tools in parallel software architectures. The post is initially for 2 years, with the expectation of a longer term extension.

The post-holder will join the Division of Genetics and Genomics at the Institute which comprises 18 group leaders, both desk based and lab based scientists. The department benefits from synergies arising from academic backgrounds including DNA-chemistry, statistics, mathematics and theoretical physics in addition to genetics.

Informal enquires can be made to John Hickey at john.hickey@roslin.ed.ac.uk

Formal applications should be made via this link: http://www.roslin.ed.ac.uk/vacancies/036305/-lead-scientific-programmer/ Closing Date: 02 Jun 2016

HICKEY John <John.Hickey@roslin.ed.ac.uk>

SGN Germany HoloceneEvolution

Job posting - Ref. #02-16002

The Senckenberg Nature Research Society (SGN), an institution of the Leibniz Association with almost 800 employees, operates six research institutes located in seven federal states. SGN also assists the UNESCO World Heritage Site “Grube Messel”.

The Department “Marine Research” at Senckenberg in Wilhelmshaven invites application for a

Postdoctoral Position (Geoscience)

The position is part of the joint research project 'WASA - The Wadden Sea as an archive of landscape evolution, climate change and settlement history: exploration - analysis - predictive modelling' in the framework of the research initiative âüsten- und Meeresforschung in Niedersachsen' funded by the MWK (VW-Vorab). The successful candidate will be working in Subproject â' in close cooperation with the three project partners from the NIhK, NLWKN FS Küste, and the University Bremen. The subproject focusses on the sedimentology and paleoecology of coastal geoarchives to infer information to reconstruct Holocene landscape evolution as well as changes in environment and linked processes. The understanding of these processes is essential in developing models predicting potential sites of postglacial human settlement.

Your tasks: - Organisation and implementation of field surveys in the Wadden Sea area (salt marshes, tidal flats, barrier island and onboard of Research Vessels) - Acquisition of highly resolving sedimentological, benthic, and micro-paleontological data from coastal sediment cores - Analysis and interpretation of this data with respect to the evolution of landscape and ecosystems and its application for predictive models

Your profile: - PhD in geoscience (preferably geology) - profound background and knowledge in sedimentology and paleontology - excellent experience in sedimentological analytics and methods (facies analysis, sequence stratigraphy) - high motivation to work in the field in different coastal settings and onboard of research vessels - training and application in benthic and micropaleontologic methods will be expected - very good written and oral communication skills in English language - open and communicative nature for interdisciplinary teamwork is highly recommended - valid driving license

Salary and benefits are according to a public service position in Germany (TV-H E13). The contract should start around July 1st 2016 and will be restricted to three years.

The Senckenberg Research Institute supports equal opportunity of men and women and therefore strongly invites women to apply. Equally qualified handicapped applicants will be given preference. The type of handicap should not prevent work needed to conduct the research. The place of employment will be Wilhelmshaven, Germany. The employer is the Senckenberg Gesellschaft für Naturforschung.

Please send your application before May, 26th 2016, preferably by e-mail (attachment in a single pdf document), mentioning the reference of this position (Ref. #02-16002) and including a letter outlining your suitability for the post, a detailed CV, contact details of 2 references, and a list of publications to:

Senckenberg Gesellschaft für Naturforschung Senckenberganlage 25 60325 Frankfurt E-Mail: recruiting@senckenberg.de

For scientific enquiries please get in contact with Dr. Achim Wehrmann, achim.wehrmann@senckenberg.de, Tel.: 04421 / 9475 - 230

Mit freundlichen Grüßen /Best Regards

Isabell Bast Personalsachbearbeiterin

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

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

Leiterin Personal & Soziales - 1458 Loke, Uta

Stellv. Leiterin Personal & Soziales - 1319 Elsen, Carina

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

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

recruiting <recruiting@senckenberg.de>

Smith College Genome Evolution Ciliates

The Department of Biological Sciences at Smith College invites applications for a full-time, benefits-eligible, non-tenure-track postdoctoral research position focusing on characterizing germline and somatic genomes of ciliates isolated from various freshwater and marine habitats, to begin August 15, 2016 or thereafter. The position will be housed in Professor Laura Katz's laboratory in the Department of Biological Sciences (http://www.science.smith.edu/departments/Biology/lkatz/Research.htm). The initial appointment is for one year, with the possibility of extending for additional years. A Ph.D. in genome evolution or a related field is required by time of appointment.

The goal of the project is to assess intraspecific variation in both somatic macronuclei and germline micronuclei from diverse ciliates. The ideal candidate will: 1) be a productive researcher with interests in population genetics and phylogenomics of microorganisms; 2) have experience working with eukaryotic microbes and/or the bioinformatic tools required to analyze complex genome data; 3) have excellent communication and interpersonal skills; and 4) be interested in collaborating with graduate and undergraduate students in the laboratory. The project is collaborative with George McManus at the University of Connecticut (http://microzooplankton.uconn.edu/people.html).

More details on the position and application submission process can be found at http://apply.interfolio.com/35192 .

Laura A Katz <lkatz@smith.edu>

SmithsonianTropResInst 3 Microbiomes

Smithsonian Tropical Research Institute

The Smithsonian Tropical Research Institute (STRI), with generous support from the Simons Foundation, is pleased to announce a new research initiative to understand the roles played by microbiomes in tropical forests. This initiative is intended to expand dramatically our understanding of the identity, distribution, and function of tropical terrestrial microbiomes. As part of this initiative, we are accepting applications for three postdoctoral fellowships. The fellowships are for three years, and each includes a stipend, travel and research funds, and relocation expenses to Panama. Candidates should propose their own research projects related to this initiative. The proposed research should incorporate genomic and meta-genomic approaches and complement one or more existing strengths at STRI, including forest ecology, evolutionary biology of mutualisms, soil biology and biochemistry, behavioral ecology and evolution, and plant physiology [see www.stri.si.edu]. The positions will be based at STRI, and proposed research should be based primarily at facilities in Panama, although comparative studies involving other sites may be included if strongly justified.

Applications should consist of a single PDF containing a cover letter, a research proposal, a complete curriculum vitae, and the names and contact information of three referees. The research proposal should not exceed five single-spaced pages plus references and include a research budget.

Please also include up to three significant reprints as separate files. Applications should be addressed to Adriana Bilgray, Office of Academic Programs (BilgrayA@si.edu).

For inquiries contact Dr. William Wcislo, Deputy Director for Research (WcisloW@si.edu). Review of applications will begin 15 August 2016 and continue until positions are filled.

STRI is an equal opportunity employer and is committed to diversity in its workforce.

Appointments are made regardless of nationality.

"Bilgray, Adriana" <BilgrayA@si.edu>

UAntwerp EvolEcol Rodent ArenavirusModel

POSTDOC POSITION FOR TWO OR THREE YEARS - The Evolutionary Ecology Group at University of Antwerp (www.uantwerpen.be/eveco) has an open position for a postdoc for two or three years, in a project "Ecology of Lassa virus and related arenaviruses in the natural host Mastomys natalensis."

Our team in the Evolutionary Ecology Group (www.uantwerpen.be/eveco) is studying the ecology of infections in free-living populations of small mammals, mostly rodents. The pathogens we focus on include mainly viruses (hantaviruses, arenaviruses, filoviruses, poxviruses,...) and bacteria (Yersinia pestis, Leptospira, Borrelia,...). Our main research question is how the ecology and evolution of the hosts affects the transmission, ecology and evolution of the pathogens, and vice versa. We are particularly interested in the temporal and spatial dynamics of these host-pathogen systems.

We have an open position for a postdoc for 2 or 3 years, in a project "Ecology of Lassa virus and related arenaviruses in the natural host Mastomys natalensis." Arenaviruses are RNA viruses with in most cases rodents as natural host. Lassa virus causes Lassa fever, a disease that is endemic in West Africa. Control measures aiming at reducing the virus prevalence in the rodent population could reduce the risk of rodent-to-human transmission. However, the course of infection, the dynamics of virus-rodent interaction, and modes of virus transmission among the rodents are poorly understood. Therefore, a major objective of this research project is to enhance knowledge on rodent-virus ecology to develop, in future, rodent-based intervention strategies that are applicable in the endemic area. In East Africa, other arenaviruses are found in Mastomys natalensis: those are not pathogenic to humans but can be studied as a model system for Lassa virus.

The project involves both fieldwork and analyses of existing long-term data and samples. For the present position, the focus will be on the modelling work, but field activities in Africa and lab experiments in our biosafety animal facility can be included as well.

Applicants should have a strong cv and proven skills in statistical and mathematical modelling of dynamic systems, preferably in ecology or epidemiology. Field experience would be a bonus.

The successful applicant will take the daily lead of the project, develop the scientific questions and study design in collaboration with the project leader and take responsibilities in supervising M.Sc. and Ph.D. students working on the project. He/she will be expected to become involved in the general activities of the research group, which may also involve a limited amount (max. 30h) of teaching.

The position can be taken up from 1 September 2016 or soonest thereafter.

More information and application form at: https://www.uantwerpen.be/nl/jobs/vacatures/ap/2016bapfwetef142/ Prof. dr. Herwig Leirs https://www.uantwerpen.be/herwig-leirs "herwig.leirs@uantwerpen.be" <herwig.leirs@uantwerpen.be>

UBern MutationLoad

Postdoc position: Modelling and quantification of mutation load in human populations

A 2 years+ post-doc position is available from July 1st 2016 at the University of Berne to model and quantify mutation load in human populations. It has been shown that mutation load should increase in populations having gone through spatial expansions, and human populations actually show a gradient of mutation load along expansion axes out of Africa (http://www.pnas.org/content/113/4/E440.abstract).

The successful candidate will develop models of genomic evolution to find signals of mutation load in genomic data and study how load is purged after the end of an expansion. The post-doc will also study how expansion load might interfere with adaptations to new environments.

Finally, available human whole genome sequences will be used to quantify mutation load in populations having a history of range expansions and study how these signatures are spread and have evolved over the genome.

We are looking for a highly motivated candidate to join our very international lab. The ideal candidate will have a strong background in statistical or population genetics and proven abilities to work independently and in team. Previous experience in C++ and R or another high-level programming language is a plus.

The successful candidate is expected to be involved in light teaching and administrative duties. Gross salary is in the range of 80K CHF per year and follows the Swiss NSF scale. The CMPG lab offers a very stimulating research environment with access to high performance computation facilities and close connections with the Swiss Institute of Bioinformatics. Berne is ideally located in the middle of Switzerland and Europe, and provides rich cultural and outdoor activities.

Please send before May 31st 2016, an application letter, CV and contact information of two references to laurent.excoffier@iee.unibe.ch.

Further information can be requested at the same email address.

Laurent Excoffier

Computational and Molecular Population Genetics (CMPG) Institute of Ecology and Evolution, University of Bern 6, Baltzerstrasse, CH-3012 Bern, Switzerland Tel: +41 31 631 30 31 Email: laurent.excoffier@iee.unibe.ch http://cmpg.iee.unibe.ch Computational Population Genetics Swiss Institute of Bioinformatics (SIB) http://www.isb-sib.ch/groups/-Computational_Population_Genetics.htm Laurent Excoffier <laurent.excoffier@iee.unibe.ch>

UCalifornia LosAngeles 2 EvolutionaryBiol

A two-year post-doctoral position is available (start date flexible, can start as early as July, 2016) in the group of Dr. Van Savage (http://faculty.biomath.ucla.edu/-vsavage/) in the Department of Ecology and Evolutionary Biology at UCLA. This position will be supported by a recently awarded McDonnell Foundation grant (https://www.jsmf.org/grants/20150014/). Savage combines mathematical models with analysis of large datasets to uncover insights into biological systems. The overall goal is to better understand, both empirically and theoretically, higher-order interactions in biological systems that range from drug combinations that may slow antibiotic resistance to consumer-resource interactions in food webs. In this context, higher-order interactions means beyond pairwise interactions that involve three or more objects. The project has the potential to involve theory development, numerical simulations, and data analysis. Savage will mentor the postdoc in designing and conducting research projects, writing papers, giving talks, and applying for jobs.

UCLA is a major research university with the Faculty of Arts and Sciences, Medical School, and Engineering School all on the same campus, allowing access to myriad researchers and resources that could be useful to this project. UCLA is consistently in the top 5 in terms of federal research funding awarded to universities. Los Angeles is a vibrant, diverse city with outdoor activities available nearby, including beaches and mountains. L.A. also has a wide array of arts and culture, including world-class museums, theater, music, and of course, movies.

Candidates are expected to be independent, highly motivated problem solvers who communicate well and enjoy working in a collaborative environment. The ideal candidate would have a background in mathematical modeling, knowledge of either consumer-resource interactions or microbial systems, and experience with programming languages such as Matlab, R, Mathematica, C, and Python. Applicants with only a subset of these skills are encouraged to apply. Applications and any questions should be sent to vsavage@ucla.edu. The application should include a Curriculum Vitae that details education, past research, and publications. Applicants should also submit a cover letter that describes their interest in the project and the names of three references. Review of applications will begin immediately and continue until the position is filled.

UCLA is an AA/EOE that is strongly committed to diversity and excellence among its researchers.

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A two-year post-doctoral position is available (start date as early as July, 2016) in the group of Dr. Van Savage (http://faculty.biomath.ucla.edu/-vsavage/) in the Department of Ecology and Evolutionary Biology and Department of Biomathematics at UCLA. This position will be connected to an NSF CAREER grant (http://nsf.gov/awardsearch/-showAward?AWD_ID=1254159). Savage combines mathematical models with analysis of large datasets to uncover insights into biological systems. The project has the potential to involve software development, analysis of large datasets, and construction of analytical and numerical models for the vascular system. Results from this project will help lead to a deeper understanding of resource distribution networks and allometric scaling theory, which connects to physiology and ecology. Findings will also aid in identifying differences in structure and function between plants and animals, different organs, and healthy versus diseased (e.g., tumor) tissue. The postdoctoral researcher will have the opportunity to work closely with and mentor high school, undergraduate, and graduate students. Savage will mentor the postdoc in designing and conducting research projects, writing papers, giving talks, and applying for jobs.

UCLA is a major research university with the Faculty of Arts and Sciences, Medical School, and Engineering School all on the same campus, allowing access to myriad researchers and resources that could be useful to this project. UCLA is consistently in the top 5 in terms of federal research funding awarded to universities. Los Angeles is a vibrant, diverse city with outdoor activities available nearby, including beaches and mountains. L.A. also has a wide array of arts and culture, including world-class museums, theater, music, and of course, movies.

Candidates are expected to be independent, highly motivated problem solvers who communicate well and enjoy working in a collaborative environment. The ideal candidate would have a background in mathematical modeling, knowledge of vascular systems in animals and plants, and experience with C++, Matlab, R, and/or OCaml programming

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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

UCalifornia SanFrancisco EvolutionaryGenetics

UCSF.EvolutionaryGenetics

POSTDOCTORAL POSITIONS IN EVOLUTIONARY GENETICS University of California, San Francisco

The Wall lab at UCSF is searching for multiple postdocs interested in evolutionary genetics and with a strong background in statistics, programming, genetics and/or bioinformatics. Current projects in the lab include

1. New methods for imputing genotypes in a large baboon pedigree with a mixture of high-coverage and low-coverage whole genome sequence data

2. New methods for identifying recombination hotspots in closely related populations/species, and application to new primate and canid whole-genome sequence data

3. Inference of admixture between archaic hominins and modern humans

4. Analysis of thousands of human genomes from around the world as part of the GenomeAsia 100K consortium

Postdocs are expected to spend at least half of their time on either of the first 2 listed projects. Funding is available for 2-3 years, and the salary is negotiable. Candidates who wish to apply should send a cover letter, CV and the names of at least 2 references to Jeff Wall <jeff.wall@ucsf.edu>. Please write “Postdoc application” in the subject line. Informal inquiries are also welcome.

“Wall, Jeff” <Jeff.Wall@ucsf.edu>

UCambridge EvolutionCancer

Postdoc position “Evolutionary biology of cancer” in Cambridge UK

The Markowetz lab in the Cancer Research UK Cambridge Institute at the University of Cambridge is looking for outstanding candidates to work on inferring patterns of tumor evolution from genomics data.

We will analyse two types of data: (1) large cohorts of single-sample bulk sequenced tumors from the TCGA and ICGC pan-cancer projects as well as from other sources, and (2) genomes of single cells from individual tumors. We plan to adapt methods from population genetics and phylogenetics to the cancer setting. Key problems will be to compare mutation rates and selection hotspots between the genomes of cancer clones.

This position is ideal for somebody trained in evolutionary biology in model systems to make the transition to biomedical applications in cancer.

The successful applicant will have a PhD in a quantitative field like mathematics, statistics, physics, engineering, bioinformatics, or computer science. A background in evolutionary biology, molecular evolution or population genetics is highly desired. The applicant should have a good biological background and excellent computing skills. The atmosphere at CI is very collaborative and interactive; good communication skills are key.

To apply, please send your academic CV and a covering letter to Tania Smith at tania.smith@cruk.cam.ac.uk

More about the lab at http://www.markowetzlab.org More about tumor evolution at https://scientificbsides.wordpress.com/tag/intra-tumour-phylogeny-probl em

References

Beerenwinkel et al (2014) Cancer evolution: mathematical models and computational inference, Systematic Biology.

Ross and Markowetz (2016), OncoNEM: Inferring tumour evolution from single-cell sequencing data, Genome Biology, 17:69

Schwarz et al (2015), Spatial and temporal heterogeneity in high-grade serous ovarian cancer: a phylogenetic reconstruction, PLoS Med, 12(2)

Yuan et al (2015), BitPhylogeny: A probabilistic framework for reconstructing intra-tumor phylogenies, Genome Biol, 16:36

– Florian Markowetz University of Cambridge Cancer Research UK Cambridge Institute Li Ka Shing Centre Robinson Way, Cambridge, CB2 0RE, UK phone: +44 (0) 1223 769 628 fax : +44 (0) 1223 769 510 email: florian.markowetz@cruk.cam.ac.uk skype: florian.markowetz blog : http://scientificbsides.wordpress.com web : http://www.markowetzlab.org ORCID: 0000-0002-2784-5308

Florian Markowetz <Florian.Markowetz@cruk.cam.ac.uk>

UCambridge HostVirusCoevolution

We are looking for a postdoctoral researcher to work on how host-parasite coevolution can result in changes in host susceptibility to RNA viruses. The work will be carried out in the lab of Dr Frank Jiggins (University of Cambridge) in collaboration with Dr Ben Longdon (University of Exeter).

Working with several species of Drosophila and a group of naturally occurring viruses (sigma viruses), you will examine whether coevolution between hosts and parasites increases genetic variation in susceptibility to infection. The project will examine the genetic basis of disease susceptibility to further our understanding of how resistance to parasites evolves.

The work will suit a researcher who holds, or is about to be awarded, a PhD in evolutionary biology. Desirable skills include a familiarity with animal/insect husbandry, experience with molecular techniques, ideally including DNA/RNA extractions, PCR and qRT-PCR and experience of data analysis in R. Experience in host-pathogen coevolution, evolutionary biology or evolutionary genetics will be beneficial.

Fixed-term: The funds for this post are available until 10 May 2018 in the first instance.

Apply here: http://www.jobs.cam.ac.uk/job/9783/ Please contact Frank Jiggins (fmj1001@cam.ac.uk) and/or Ben Longdon (b.longdon@gen.cam.ac.uk) for further information about the project.

Ben Longdon <b.longdon@gen.cam.ac.uk>

UCologne ComputationalBiol

A postdoctoral position to work on molecular population genetics of wild populations of Danio rerio is immediately available in the labs of Thomas Wiehe (http://www.bioinf-popgen.uni-koeln.de/) and Maria Leptin (http://www.embl.de/research/units/directors_research/leptin/) at the Institute of Genetics, University of Cologne, Germany.

We are seeking a skilled computational biologist or bioinformatician with expertise in the handling and analysis of NGS data, and who ideally has experience in evolutionary biology and/or population genetics. A welcomed, but not conditional, asset is knowledge of immunology.

The aim of the project is to understand the evolutionary causes and mechanisms which have generated a large family of innate immune receptor genes (NLR family) in Danio rerio (see http://rsob.royalsocietypublishing.org/content/6/4/160009). An integral part of the project is to survey and analyze genetic diversity in these genes from several wild populations of Danio and to explore the link to ecological conditions. The project is part of a DFG-funded Priority Program to study processes of Rapid Evolutionary Adaptation (https://dfg-spp1819.uni-hohenheim.de).

The position is initially available for two years, with the perspective of prolongation, and is to be filled as soon as possible. The position is paid according to the German salary scale TVL E13, full time employment, and comes with the usual social benefit packages. Our research groups are located in the Institute of Genetics and we are members of the Collaborative Research Center SFB680 (http://www.sfb680.uni-koeln.de), of the Priority Programs SPP1590 (http://www.dfg-spp1590.de) and SPP1819 (https://dfg-spp1819.uni-hohenheim.de), and of the newly established CRC SFB1211 (“Earth-Evolution at the dry limit”).

Besides its excellent scientific environment, Cologne offers a wide range of cultural life and entertainment options.

For inquiries and further details please contact Thomas Wiehe at twiehe@uni-koeln.de. Applications should contain a concise resumee with past and planned research, and the details of two reference addresses, and should be sent as a single PDF file to the above address.

– Thomas Wiehe Universitaet zu Koeln Institut fuer Genetik Zuelpicher Stra3e 47a D-50674 Koeln Germany Tel 0049 221 470 1588

"twiehe@uni-koeln.de" <twiehe@uni-koeln.de>

UConnecticut PlantGenomics Bioinformatics

— Postdoctoral Researcher: Forest Genomics Database and Software Developer

The Plant Computational Genomics laboratory at University of Connecticut (Storrs, CT) has an opening for a database and software developer position as part of a collaborative project involving researchers from around the world. This person will take a lead role in the continued development of the TreeGenes genomics database and the CartograTree application (treegenesdb.org and cartogratree.org). These web-based resources serve vast amounts of genomic, phenotypic, and environmental data to our diverse user community. In specific, the CartograTree application provides a portal for association genetics studies of georeferenced forest trees through the implementation of web services and high performance computing resources available through the iPlant/Cyverse project (http://www.cyverse.org/). In addition, we are committed to developing mechanisms for data sharing among partner databases through Galaxy modules, the Tripal platform (http://www.tripal.info/), the GMOD project, and custom analysis/visualization platforms.

The successful candidate will work as part of a small interdisciplinary team of bioinformaticians and data curators. Tasks will include development of the existing database, developing connections to collaborating databases, improving the user experience (interface development) and implementation of novel analysis and visualization tools for comparative genomics. The Postdoctoral Scholar will be provided with training opportunities and will attend conferences to present/train users on these new tools. In addition, publications on innovative software solutions will result from this work.

The qualified applicant will have a PhD degree in Bioinformatics, Information Systems, Computer Science, or a related field. Biology/Bioinformatics experience is essential as well as previous experience with web/database development. The applicant should have strong knowledge of Java and JavaScript (jQuery). Experience with Linux/Unix, scripting languages (Python), and relational databases.

Interested applicants, please send the following THREE documents: cover letter, research statement, and CV to: Jill Wegrzyn at jill.wegrzyn@uconn.edu—

Applications will be accepted until June 10th or until the position is filled.

"jill.wegrzyn@uconn.edu" <jill.wegrzyn@uconn.edu>

UEssex ComputationalGenomics

POSTDOCTORAL POSITION IN COMPUTATIONAL GENOMICS

== Deadline on the 1st of June, 2016 We are looking for an enthusiastic postdoctoral researcher to work in microRNA computational genomics, in the group of Antonio Marco (http://amarco.net/) at the University of Essex.

THE PROJECT: MicroRNAs are gene regulators that bind to gene transcripts by pairwise complementarity. MicroRNA target sites are often conserved and subject to purifying selection. Recently, we found that selection against target sites is prevalent (doi:10.1534/g3.115.019497). The current project aims to explore the impact of this type of selection in humans, and its application to understand regulatory networks of complex diseases.

WHAT WE EXPECT: The postdoc will contribute to the development of new methods and software to analyse human polymorphisms at microRNA target sites. The postdoc will also analyse extensive collections of human variation data and explore complex-disease gene networks in collaboration with experimental scientists.

WHAT WE PROVIDE: The project is funded by a grant from the Wellcome Trust and will cover the salary of the successful applicant for two years (pounds 31,655 per annum). We provide a vibrant and stimulating environment, mentoring schemes, advanced training programmes, and support for travelling to conferences and workshops. Our recently established Genomics Group at the University of Essex is form by seven labs with diverse interests and expertises (http://genomics.essex.ac.uk/). We have state-of-the art labs (both dry and wet), a sequencing machine and a high-performance computer cluster.

ABOUT ESSEX: The School of Biological Sciences at University of Essex has a broad-based structure, providing a strong multidisciplinary environment. Colchester campus is located at Wivenhoe Park, a picturesque and historic 200 acres parkland. It is a vibrant and international campus, hosting more than 9,000 students from more than 130 different nationalities. The campus is only two miles from the historic centre of Colchester - England's oldest recorded town, and just one hour from London.

APPLICATION: Closing date for applications: 1st June 2016 Interviews for sortlisted candidates: Week of the 20th June 2016 Expected start date: 1st September 2016

Please include in your application a cover letter (PDF, 1 page), a CV (PDF, 2-pages maximum) and contact details for three references.

For any question regarding this application please contact Antonio Marco (amarco@essex.ac.uk; amarco.bio@gmail.com).

Apply to this position from the University of Essex jobs webpage: https://jobs.essex.ac.uk/fe/-tpl_essex01.asp?s=4A515F4E5A565B1A&jobid=-86428,1212614836 amarco.bio@gmail.com

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UExeter SexualAntagonism

Dear all,

We are looking to recruit a postdoc to study the genetics of sexual antagonism and sex chromosome evolution in the Trinidadian guppy (Poecilia reticulata). This is an ERC funded post, which is part of a larger multi-institute project led by Professor Deborah Charlesworth (University of Edinburgh), and is available from August 1 2016 for 48 months. The post will be based in the Centre for Ecology and Conservation at the University of Exeter's Cornwall campus in the group of Dr Alastair Wilson, while collaborating with Professors Darren Croft (Exeter, Streatham) and Deborah Charlesworth (Edinburgh).

The successful applicant will be running breeding experiments using fish derived from wild guppy populations, and subsequently collecting phenotypic and genetic data for analysis. Phenotypes targeted will include male colour and pattern traits, but also aspects of life history and behaviour. The project will also include a targeted field component with sampling and live fish collection from Trinidad during the first year. Genetic approaches to be used will include pedigree-based quantitative genetic analyses, molecular pedigree analysis, and mapping of putatively sexually antagonistic loci using genomic data (e.g. from RAD-Seq). Through close collaboration with Edinburgh-based researchers the project will map colour and pattern genes to test the role of sexually antagonistic selection in driving sex chromosome evolution. A comparative approach, in which fish from paired populations differing in selective regime are used, also provides opportunities to explore the role of sexual antagonism in shaping patterns of genetic variation and generating intra-locus conflict within and among-populations.

The post will include setting up and maintaining fish colonies for breeding experiments (with support from technical staff), phenotypic data collection, sample preparation (for outsourced sequencing), and bioinformatics/data analysis. The successful applicant will be able to develop research objectives, projects and proposals; prepare manuscripts for publication in the peer reviewed literature; and present at conferences and other events.

Applicants will possess a PhD (or be nearing completion) in a relevant area of evolutionary biology or genetics. They should have specialist knowledge and skills in at least one quantitative aspect of the project (e.g., quantitative genetic modelling, bioinformatics, genomics) and research experience working with live fish would be advantageous. The successful applicant will be capable of working independently when needed but must also be a good collaborator, with strong interpersonal skills to liaise with external partners and supervise others locally in the lab. Applicants will also be able to demonstrate a strong track record of seeing projects through to publication.

For further information please contact Alastair Wilson (a.wilson@ex.ac.uk)

Application is online at https://-jobs.exeter.ac.uk/hrpr_webrecruitment/wrd/-run/ETREC107GF.open?VACANCY_ID=-470125EoA2&WVID=3817591jNg&LANG=USA Closing date is 12th June 2016.

"A.Wilson@exeter.ac.uk" <A.Wilson@exeter.ac.uk>

UHawaii Manoa FlyEvolutionSystematics

Postdoc in Tephritid fruit fly evolution, systematics and taxonomy

The Insect Biodiversity and Systematics lab at the University of Hawaii Manoa has funding for a Junior Researcher (Postdoc) to work on the taxonomy and systematics of pest fruit flies as part of an ongoing effort to develop an evolutionary framework for the group.

The research project combines traditional taxonomy with collaborators at UH and USDA using genomic approaches to improve detection and identification of tephritid pests. Most of the work for this position involves identification of Tephritid flies and description of new species using both classical morphology and taxonomy in concert with Sanger and genome-wide analysis techniques. A core goal of this project will be a broad and deep phylogeny for several genera of Tephritid fruit flies. Intensive curation of specimens and supervision of graduate and undergraduate researchers are also part of the position. There is the opportunity to participate in the development of the genomics data, though the morphology is the primary focus of this position.

The applicant will be expected to work independently and

supervise students, as well as work well as part of a larger research team, including collaborators off campus. Prior experience in insect morphology and taxonomy, preferably dipteran, as demonstrated through publications is required. Specific background in insect taxonomy and the use of morphological characters for species identification and description is required. Participation in the University of Hawaii Insect Museum is an aspect of this position.

Experience in wet-lab molecular biology, genetics, and strong interpersonal skills are desirable. The resources of the University of Hawaii Insect Museum are available, including multiple high-end dissecting scopes and cameras for dissection and species descriptions, workspace for morphological work, and one of the best Tephritid collections in the country, including dozens of paratypes and holotypes. The Rubinoff lab is a fully functional Molecular Systematics facility with personnel actively engaged in a wide variety of research questions pertaining to insect evolution, ecology and conservation.

Salary is ~$~60,000/yr,

Minimum PhD in entomology, or comparable field is required. If interested,

please contact Prof Dan Rubinoff rubinoff@hawaii.edu. To apply,submit CV and contact information for at least 3 references. Review of applicants will begin immediately; for full consideration, apply by August 1^st, 2016. Position to begin on or about October 1, 2016. Funding is for one year, with the possibility of continuation based on productivity and continued success of the research program.

The University of Hawaii is a major U.S. research institution based in the Manoa district of Honolulu, up against the gorgeous Koolau Mountains. The Hawaiian archipelago is made up of six main high islands and twice that many smaller ones. The island of Oahu is home to almost one million people and the state capital, Honolulu, a cosmopolitan subtropical city with a diverse and vibrant culture of Polynesian, Asian and, to a large extent, North American influences. Oahu is 596 square miles (1545sq km), and hosts two mountain ranges, including a peak over 4,000 feet (1220m) tall. The State contains almost of the climate zones on the planet, including 4,000 meter elevation alpine stone deserts, montane and lowland rainforests, deserts and dry forests. Annual rainfall regularly varies over an order of magnitude on the same island making this a rish and interesting place to study evolution.

Daniel Rubinoff <rubinoff@hawaii.edu>

UIllinois Chicago TeachingResearch

Postdoctoral Research Associate in Biological Sciences:

The Department of Biological Sciences in the UIC College of Liberal Arts & Sciences seeks applications for a postdoctoral research associate starting Fall 2016 and extending through Spring 2019. The successful candidate will contribute 50% effort toward instruction of undergraduate biology courses and 50% effort toward research with a Biological Sciences faculty member (http://bios.uic.edu/). We are seeking a coordinator / instructor for laboratory courses in genetics. There may also be opportunities to teach lecture courses in genetics or other biology courses. The position provides a new PhD with an exceptional opportunity to gain teaching and research experience under the mentorship of Biological Sciences faculty, in preparation for applying for tenure-track jobs, especially at an institution that values teaching. UIC boasts a strong and flourishing undergraduate Biological Sciences major, a large, interdisciplinary faculty with ties to the medical campus and all the resources associated with a first-rate research institution situated in an attractive, metropolitan environment.

For fullest consideration, please submit an on-line application at *https://jobs.uic.edu* by June 1st, 2016 and upload (a) a cover letter addressing the candidate's teaching and mentoring experiences, as well as research interests that could be pursued at UIC, (b) curriculum vitae, (c) three letters of recommendation (d) syllabi and teaching evaluations from classes taught as primary instructor or teaching assistant. Please contact Suzanne Harrison (suzanne7@uic.edu) with any questions regarding the position.

The successful candidate must earn the PhD before August 1, 2016. The University may conduct background checks on all job candidates upon acceptance of a contingent offer. Background checks will be conducted in compliance with the Fair Credit Reporting Act. The University of Illinois at Chicago is an affirmative action/equal opportunity employer, dedicated to the goal of building a culturally diverse pluralistic faculty and staff committed to teaching in a multicultural environment. We strongly encourage applications from women, minorities, individuals with disabilities and covered veterans.

"millern@uic.edu" <millern@uic.edu>

UJohannesburg MarineGenomics

Postdoc: Postdoctoral fellowships in marine genomics, University of Johannesburg

Topic: Various new and ongoing projects; deadline: May 30, 2016

[Please note that this is a modified version of an earlier post; the position is no longer limited to previously disadvantaged female South Africans as none have applied]

The Molecular Zoology Laboratory at the University of Johannesburg (Auckland Park, South Africa; https://sites.google.com/site/drpeterteske/) invites applications for postdoctoral positions to investigate population structure, demographic changes, systematics and environmental adaptation in various marine organisms. The positions are funded for at least 2 years, and will commence no later than September 30, 2016.

The exact type of work to be done is flexible, and applicants may be involved in multiple projects and collaborate with postgraduate students. Target taxa include sharks, teleosts, crustaceans, mollusks and plants. Collaboration with previous host institutions is encouraged.

All projects will use genomic tools to study marine populations. Such methods are expected to replace traditional genetic approaches (e.g. mitochondrial DNA sequencing and microsatellite analyses) in the near future. Applicants should have at least 2 of the following skills:

1. Development of next-generation sequencing libraries (ddRAD, ezRAD etc.) or comparable laboratory skills (e.g. microsat library development)

2. Analysis of genomic/transcriptomic data by means of unix-based software, or experience with comparable ("user-unfriendly") software

3. Good scientific writing skills and an adequate track record in publishing scientific papers in ISI-listed journals

4. Good inter-personal skills and the ability to work well in a team, but also independently

Successful candidates will initially apply for financial support through the National Research Foundation's SANCOR Postdoctoral Fellowship Call (application deadline: May 30, 2016; commencement of research: between July 1 and September 30, 2016; remuneration: R 120 000 p.a. + R30 000 for running expenses; http://www.nrf.ac.za/content/sancor-postdoctoral-fellowships-call-2016). The option exists to upgrade at a later stage to a University of Johannesburg Global Excellence and Stature fellowship (R 220 000, details to follow).

Interested candidates should please contact Prof. Peter Teske: pteske101@gmail.com. In your application, please include

a) a full CV, including publications, software experience and laboratory skills;

b) contact information of 3 academic referees, and

c) a personal statement describing research experience, interests and career goals (500 words maximum).

Prof. Peter Teske *Molecular Zoology LabDepartment of ZoologyUniversity of Johannesburg, Kingsway CampusAuckland Park 2006South AfricaTel +27 (0)11 559 3373*

For courier shipments: D3 LAB 339 (D LAB building on the far right (seen from D RING), two floors up, turn right through the glass door, last entrance on the left) Department of Zoology University of Johannesburg, Kingsway Campus (APK) Corner Kingsway and University Rd. Auckland Park 2092 Email: pteske101@gmail.com Tel.: 011 559 3373

*Molecular Zoology Lab: http://sites.google.com/site/drpeterteske/ *Flinders University Molecular Ecology Lab: http://www.molecularecology.flinders.edu.au pteske101@gmail.com

ULausanne SexDeterminationAmphibians

Applications are invited for a Postdoctoral position in the research group of Nicolas Perrin (Department of Ecology and Evolution, University of Lausanne).

Sex determination in common frogs (Rana temporaria) already raised interest in the 1930s with the description of "sex races" that differ in the patterns of gonadal development, distributed along climatic gradients. Our recent studies suggest that sex races also differ both in the extent of sex chromosome differentiation and in the amount of non-genetic contribution to sex determination, in association with a polymorphism at the candidate sex-determining gene Dmrt1 (references below).

During this project we will analyze families from different geographic origins and sex races for Y-haplotype differentiation, with a focus on Dmrt1. Practical work will involve the sampling/rearing of frogs and wetlab analyses (including microsats and RADseq).

The position is available for two years, with starting date summer 2016 (negotiable). The Department of Ecology and Evolution is large and thriving, and provides excellent facilities for research and training (see http://www.unil.ch/dee/).

Informal enquiries and applications should be sent to Nicolas.Perrin@unil.ch. Applications should include a cover letter with a statement of research interests and qualifications for the position, complete CV with publication list, and contact details of three referees, embedded in a single pdf file.

We will start reviewing the applications on June 1st 2016, but will continue to consider incoming applications until the position is filled.

Nicolas Perrin (Nicolas.Perrin@unil.ch)

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References

Ma WJ, Rodrigues N, Sermier R, Brelsford A, Perrin N. 2016. Dmrt1 polymorphism covaries with sex-determination patterns in Rana temporaria. Ecology & Evolution. In Press

Rodrigues N, Vuille Y, Brelsford A, Merila J, Perrin N. 2016. The genetic contribution to sex determination and number of sex chromosomes vary among populations of common frogs (Rana temporaria). Heredity. In Press.

Brelsford A, Rodrigues N, Perrin N. 2016. High-density linkage maps fail to detect any genetic component to sex determination in a Rana temporaria family. J. Evol. Biol. 29 : 220-225.

Rodrigues N, Vuille Y, Loman J, Perrin N. 2015. Sex-chromosome differentiation and 'sex races' in the common frog (Rana temporaria). P Roy Soc B 282 : 20142726.

Rodrigues N, Merila J, Patrelle C, Perrin N. 2014. Geographic variation in sex-chromosome differentiation in the common frog (Rana temporaria). Mol Ecol 23 : 3409-3418.

Rodrigues N, Betto-Colliard C, Jourdan-Pineau H, Perrin N. 2013. Within-population polymorphism of sex-determination systems in the common frog (Rana temporaria). J Evol Biol 26 : 1569-1577.

Nicolas Perrin <Nicolas.Perrin@unil.ch>

UMassachusetts Amherst EvolutionaryGenetics

POSTDOCTORAL POSITION IN DEVELOPMENTAL AND EVOLUTIONARY GENETICS, University of Massachusetts Amherst

The Albertson Lab at the University of Massachusetts Amherst (UMass, Amherst) seeks a Postdoctoral Research Associate to perform research on the development, plasticity and evolution of the skeletal system in fishes under the guidance and supervision of the Principle Investigator (Dr. Craig Albertson) and co-PI (Dr. Rolf Karlstrom). The successful candidate is expected to establish some independence in research design and execution, and to publish his/her work as appropriate in collaboration with the principle investigators.

This is a benefited, full-time Postdoctoral Research Associate position. Initial appointment is for one year;

reappointment beyond the first year is contingent upon availability of funding and job performance. Primary responsibilities will include, but are not limited to, in situ analysis of gene expression in zebrafish and cichlid larvae and juveniles, generation of stable mutant lines via CRISPR/cas9 system, light and electron microscopic analysis of different mutant phenotypes, use of different transgenic zebrafish lines to conditionally regulate gene expression, landmark-based morphometric analysis of craniofacial bone shape, maintenance of zebrafish and cichlid stocks, training of lab personnel in various molecular biology techniques.

The successful candidate is required to have a Ph.D. in biology or related field by the start of the position. Highly desirable qualifications include 2-3 years experience in the field of developmental genetics, experience with CRISPR and/or TALEN mediated mutagenesis, and experience and/or strong interest in evo-devo. Inquiries about the position can be directed to Craig Albertson, albertson@bio.umass.edu.

Postdoctoral Research Associates at the University of Massachusetts are unionized and receive standard salary and benefits, depending on experience. Salary is subject to bargaining unit contract.

Candidates must apply online by submitting a cover letter, CV, summary of research interests, and the contact details of three references willing to provide letters of recommendation to:

http://umass.interviewexchange.com/-jobofferdetails.jsp?JOBID=3D72111 Review of applications will begin June 13, 2016 and continue until the position is filled. Applications received by June 13th will be given priority consideration.

The University of Massachusetts Amherst is an Affirmative Action/Equal Opportunity Employer of women, minorities, protected veterans, and individuals with disabilities and encourages applications from these and other protected group members.

– Lisa Barry Biology Department Morrill Science Center South, Room 348 611 North Pleasant Street University of Massachusetts Amherst, MA 01003

Phone: 413-545-2602 Fax: 413-545-3243

Lisa Barry <lisak@bio.umass.edu>

UNAMexico Comparative Genomic of bats and birds

We are seeking for two postdoctoral research associates to study and analyze the genome of bats and birds (especially hummingbirds) using an evolutionary and comparative approach.

The study is funded by a generous grant from the program Frontiers in Science (CONACYT) awarded to Dr. Luis Eguiarte and his team at the Institute of Ecology at UNAM (Mexican National University), in beautiful and lively Mexico City. The salaries are competitive and good for living in the city.

We are looking for highly motivated individuals, with experience in evolution and informatics, which have obtained their PhD within the last five years before 21 May 2015. Speaking Spanish is useful, but it is not a requirement.

Those interested, please contact Luis Eguiarte: fruns@unam.mx

Dr. Luis E. Eguiarte

Investigador titular C de TC

Laboratorio de Evolución Molecular y Experimental,

Departamento de Ecología Evolutiva,

Instituto de Ecología,

Universidad Nacional Autónoma de México.

fruns@unam.mx

Jonas Aguirre <jonas_aguirre@hotmail.com>

UNebraska 2 PlantMicrobes

Postdoctoral Researchers - Two Positions in Plant-Microbe Interactions. Two postdoctoral research positions are available in plant and microbial biology in the laboratories of Dr. Sabrina Russo (http://-russolab.unl.edu/) and Dr. Karrie Weber (https:/-/sites.google.com/site/ microbialbiogeochemistry/) at the University of Nebraska - Lincoln. These positions are part of a multi-PI NSF-funded project investigating plant-microbe rhizosphere interactions in natural and agricultural systems. We are seeking two postdoctoral fellows with complementary expertise to work collaboratively with each other, Russo and Weber, and other project investigators on field, greenhouse, and lab-based research to identify how microbial community structure and function influence plant phenotypes using stable-isotope probing, metagenomics, and proteomics. The postdoctoral fellows will also have the opportunity to develop independent projects. We are looking for creative, independent scientists with expertise in the following or related areas: plant or microbial ecology and physiology, community and ecosystem ecology, bioinformatics, or molecular biology or -omics approaches. Qualified candidates will have a PhD in biology, ecology, microbiology, plant physiology, biochemistry, or related disciplines, as well as a demonstrated track record of scientific publication. Interested candidates should send a single PDF document with a cover letter explaining their interests and experience and a CV listing the names and contact information of three references to both Dr. Russo (srusso2@unl.edu) and Dr. Weber (kweber@unl.edu) with the subject line, "Postdoctoral Position". For the full ad, see: http://biosci.unl.edu/employment-opportunities-0 Sabrina E. Russo Associate Professor School of Biological Sciences | 208 Manter Hall | 1104 T Street University of Nebraska - Lincoln | Lincoln, NE 68588-0118 USA (1) 402-472-8387 (voice) | (1) 402-472-2083 (FAX) srusso2@unl.edu | http://russolab.unl.edu "srusso2@unl.edu" <srusso2@unl.edu>

UNorthCarolina Charlotte Bioinformatics

Multiple postdoctoral opportunities in Charlotte North Carolina at UNC.

We are a new dynamic department of Bioinformatics and Genomics with all the latest tools and staff to invent new ones.

You are someone who can come in and hit the ground running to do interesting things in terms of evolution, genetics, and geography of pathogens.

Send me a cv and set of ideas and we will discuss details.

Thanks Dan Janies

unccpostdoc@gmail.com

UOsnabrueck TheoreticalEcolEvolution

Postdoctoral scientist position in Theoretical Ecology and Evolution (Salary level 13 TV-L, 100 %)

in the newly established Department of Ecology and Evolution in the School of Biology/Chemistry of the University of Osnabrück.

Initially for 3 years with extensions possible thereafter

Starting at the earliest possible date.

Area of work:

The successful candidate should have a profound interest in I) evolution of cooperation, II) bacterial multicellurarity/individuality, III) metabolic network modelling, and/or IV) ecology and evolution of bacterial interactions. The position provides the opportunity to collaborate with experimental biologists working in the above fields. Within the 5-years timeframe, the candidate shall develop an innovative research agenda and start an independent research group. In addition, the candidate will be involved in the teaching activities of the group at the Bachelor- or Master-level (4 hours per week).

Required Qualifications:

– University degree and PhD in biology, physics, or (bio-) informatics within one of the research fields listed above – Demonstrated ability to conduct research independently – Excellent knowledge of (individual-based) modelling, analysing and modelling of metabolic networks, and/or evolutionary genomics

Special Requirements:

– Previous postdoctoral experience (ideally abroad) – Demonstrated ability to attract third-party funding – Interest in interdisciplinary collaboration – Experience in teaching students and supervising BSc and MSc projects

We offer:

– The contract will be initially issued for 3 years, but can be extended – The successful candidate will be based in the newly established Department of Ecology and Evolution, where we combine approaches of experimental evolution, synthetic ecology, quantitative microbiology, and analytical chemistry to address fundamental ecological and evolutionary questions – Vibrant and stimulating working environment with many possibilities to interact synergistically – Laboratories that are equipped with state-of-the-art analytical instrumentation

The position is available on a full-time basis.

Osnabrück University has been certified as a family-friendly university committed to helping working/studying parents and carers balance their family and work life.

The university aspires to ensure equal opportunities for men and women and strives to work towards a gender balance in schools or departments where new appointments are made.

If equally qualified candidates apply, preference will be given to those with special needs.

Applications

Applications should include a letter of motivation (2 pages max.), CV, publication list, copies of certificates, names, and contact details of 2-3 referees that are familiar with the applicants work.

Deadline for submission is

1 July 2016

Please send your application docuemnts as a single pdf-document via Email to the dean of the School of Biology Prof. Dr. Achim Paululat (bewerbung@biologie.uni-osnabrueck.de).

For further information please contact Dr. Christian Kost (christiankost@gmail.com).

Dr. Christian Kost

Head of the VW Research group Experimental Ecology and Evolution Max Planck Institute for Chemical Ecology Beutenberg Campus, Hans-Knöll-Straße 8 07745 Jena, Germany Tel.: ++49 (0)3641 57 1212 Fax.: ++49 (0)3641 57 1202

Starting 1.08.2016

Professor for Ecology and Evolution School of Biology/ Chemistry University of Osnabrück Barbarastrasse 13 49076 Osnabrück, Germany Tel.: ++49 (0)541 969 2853 Fax.: ++49 (0)541 969 12836

Christian Kost <christiankost@gmail.com>

UTuebingen Germany Evolutionary Genomics of Behavior

University of Tübingen, Institute of Evolution and Ecology, Group of Comparative Zoology

We have an open position (2 years) for a PostDoc with a strong interest in the genetic/genomic basis of phenotypic traits. In a project related to the genetic basis of behavior, we will use already available phenotypic data on personality and cognitive traits from a captive population of European harvest mice to search for genetic variation that correlates with behavioral profiles. We seek a candidate with strong molecular lab skills, including Sanger and next generation sequencing, and strong bioinformatics skills, preferably with training in genome wide association studies. A theoretical background in the evolutionary genetics of behavior would be an asset.

Tübingen University offers a large community of researchers working in the field of evolution and ecology of model and non-model systems, joined together in the Institute for Evolution and Ecology (https://www.uni-tuebingen.de/en/faculties/faculty-of-science/departments/bi ologie/institute/evolutionecology.html). The successful candidate will join the Comparative Zoology group of Katharina Foerster. We offer molecular lab facilities within the group and through collaborations with the Max Planck Institute Tübingen. Further lab support and computational facilities are available through the Quantitative Biology Center on campus (http://www.uni-tuebingen.de/en/facilities/zentrale-einrichtungen/quantitati ve-biology-center-qbic.html).

The working language in the group is English. However, for teaching and everyday life at the University and in Tübingen, some knowledge of German or the willingness to learn the language will be advantageous.

Founded in 1477, Tübingen University has influenced the historical town significantly. Tübingen today remains a place of research and teaching. In addition to the 85.500 inhabitants, there are some 28.300 German and international students. 450 professors and 4.400 other academic staff teach at the University's seven faculties. Tübingen offers a lively mix of shops, bars, and restaurants. Urban parks, nearby nature reserves, as well as the Swabian Jura and the Black Forest offer outdoor recreation. Tübingen is well connected via bus and local trains to Stuttgart and its airport. The Welcome Center of the university provides service and support for international researchers: https://www.uni-tuebingen.de/en/international/international-scholars.html . Applications are accepted beginning immediately and official review will begin June 6, 2016, and will continue until the position is filled. Intended starting date is September 1, 2016. Applications should include a current CV (specifying training in relevant methods and applications), along with a cover letter that provides a short statement of research interests (maximum three pages) and contact information for three references.

Applications should be submitted by email as a single file attachment to henri.thomassen@uni-tuebingen.de, with the subject line: Postdoc. Informal inquiries can be sent to katharina.foerster@uni-tuebingen.de.

Henri A. Thomassen, Ph.D. Institute of Evolution and Ecology University of Tübingen Auf der Morgenstelle 28 D-72076 Tübingen Germany Email: henri.thomassen@uni-tuebingen.de Phone: +49 7071 29 76 947

"henri.thomassen@uni-tuebingen.de"

UUtah SolanaceaeSystematics

A NSF-funded postdoctoral position at the University of Utah in Salt Lake City is available in the area of plant systematics. The project focuses on the systematics and phylogeny of the genera Capsicum and Lycianthes in the Solanaceae. Capsicum is a New World genus of about 40 species that includes the bell, chili, and paprika peppers. Lycianthes is its sister genus, with ca. 200 species distributed in Asia and throughout the Neotropics. The project will examine the species level taxonomy of these genera and distribute monographic information on our Solanaceae Source webpage (solanaceaesource.org). We will also use next-generation sequencing techniques to generate phylogenies for the group and its component clades. This project will provide opportunities for field work, student mentoring, public outreach, and collaboration with our partner institution at the University of California-Davis.

Candidates should have a Ph.D. and experience in plant systematics; experience with Solanaceae is preferred but not required. Expertise in molecular phylogenetics and data analysis is also required and familiarity with next-gen methods is a plus. The position is available immediately; review of applications will begin on May 15, 2016 and continue until the position is filled. The initial appointment is for one year, renewable for a second year upon mutual agreement and satisfactory progress.

Applicants should submit a statement of interest and description of past experience, a CV, and contact information of three references to Lynn Bohs (bohs@biology.utah.edu).

Information on the Biology Department at the University of Utah is available at www.biology.utah.edu The University of Utah is an Equal Opportunity Employer.

Thanks,

Lynn

Lynn Bohs Biology Department 257 South 1400 East University of Utah Salt Lake City, UT 84112

office: 801-585-0380 lab: 801-585-0420 fax: 801-581-4668

Solanaceae Source: www.solanaceaesource.org Bohs lab: http://biologylabs.utah.edu/bohs/ Lynn Bohs <bohs@biology.utah.edu>

WashingtonStateU EvolutionaryGenomics

Postdoc Position: Evolutionary Genomics at Washington State University

A postdoctoral position is available in the laboratory of Dr. Joanna Kelley, in the School of Biological Sciences at Washington State University in Pullman, WA (labs.wsu.edu/genomes). The research goals of the laboratory are to use genomic and computational methods to understand the genomic basis of adaptation to extreme environments. We are interested in understanding how genetic and environmental variation interact to drive population differentiation and adaptive evolution. The School of Biological Sciences at Washington State University has a strong research presence in evolution and ecology research and there are many opportunities for interaction and collaboration. The postdoctoral position is a computational genomics position studying phenotypic plasticity in the mangrove rivulus, Kryptolebias marmoratus. The candidate will lead an exciting research project studying genome, transcriptome and phenotypic data from many lineages of this primarily self-fertilizing hermaphroditic fish.

The ideal candidates will have recently completed or be completing a PhD degree in Genetics, Genomics, Computational Biology or related disciplines. We welcome applications from candidates with diverse backgrounds. Applicants must have at least one strong first-author publication. A computing background is desired, especially experience with Linux, and knowledge in at least one programming language. Prior experience with handling large-scale data and with the use of bioinformatics and statistical tools would be an advantage. Candidates should have strong organizational, written, and oral communication skills; and be able to work both independently and as part of a collaborative team. Applicants will be encouraged to develop and lead independent projects.

The appointment is for two years. Salary is competitive and commensurate with experience, and benefits are included. Applicants should email Joanna Kelley at joanna.l.kelley@wsu.edu and include a (i) cover letter that includes a statement of research interests that explicitly describes your professional qualifications for the position, (ii) curriculum vitae, and (iii) contact information for three references. Applications will be accepted through May 15th. The desired start date is August 2016.

Joanna L. Kelley, PhD Assistant Professor, School of Biological Sciences Member, Center for Reproductive Biology Washington State University joanna.l.kelley@wsu.edu http://labs.wsu.edu/genomes Phone: 509-335-0037

"Kelley, Joanna.l" <joanna.l.kelley@wsu.edu>

WorkshopsCourses

Asilomar California ConservationAndGeneExpression Sep19-23

Workshop in Conservation and Gene Expression. September 19-23, 2016, Asilomar, CA

Genomic variation has been a recent focus in conservation of rare and endangered species. However, the immediate response to environmental challenges will likely be determined by gene expression, which will constrain the efficacy of response and the likelihood of population persistence. Nonetheless, gene expression has been poorly studied in natural populations facing environmental and anthropogenic threats. This 5-day workshop at Asilomar, a resort on the central California coast, will focus on providing an overview of the general approaches to studying gene expression as well as the molecular and analytical tools needed to initiate and complete a field study. We will be oriented toward questions regarding the conservation of biodiversity, but the tools and approaches can be applied to a wide variety of questions. The topics covered will include: 1) RNA sampling, preservation, extraction and quantification; 2) library construction and sequencing (RNA-Seq and reduced representation bisulphite sequencing (RRBS)); 3) filtering, quality control, mapping of reads to transcriptomes and genomes; and 4) statistical analysis, mixed linear model, WGCNA, GO analysis, TOA and TCA (for whole blood samples) and other inference techniques; and 5) interpretation of results and functional analysis.

See examples:

Charruau et al. (2016) Pervasive effects of aging on gene expression in wild wolves. Mol Biol Evol.

Koch et al. (2016) The concerted impact of domestication and transposon insertions on methylation patterns between dogs and gray wolves. Mol Ecol.

The workshop will not be restricted to taxonomic groups; it will include examples from plants, invertebrates, and vertebrates. Applications from University of California graduate and post-graduate community will receive higher priority as funding is partly due to a UC president's office catalyst award. However, all applications will be considered. There will be some special fellowship support for UC students. The $600 registration includes housing and all meals. Please apply online below. Space will be limited to 25 students.

Lecturers (two talks from each on a research topic) Robert Wayne, Matteo Pellegrini, Steve Cole (UCLA), Beth Shapiro (UCSC), Jenny Tung (Duke U), Steve Palumbi (Stanford U), Bridgett vonHoldt (Princeton U), Zac Cheveron (U Montana) and Christina Richards (U South Florida).

Workshop Instructors Rachel Johnson, Tiffany Armenta, Alice Mouton, Devaughn Fraser, Gabriela Pinto, Annabel Beichman, Adam Freedman, and Amanda Lee.

Apply to the Workshop in Conservation and Gene Expression here:

https://ucconservationgenomics.eeb.ucla.edu/-workshops/ Rachel Meyer <rm181@nyu.edu>

Barcelona PhylogeneticAnalysisUsingR Mar6-10

DearColleague,

Registrationis open for the fourth edition of the course PHYLOGENETIC ANALYSIS USINGR, March 6th-10th, 2017.

INSTRUCTORS:Dr. Emmanuel Paradis (Institut de Recherche pour le Développement, France)and Dr. Klaus Schliep (University of Massachusetts, USA).

Moreinformation: http://-www.transmittingscience.org/courses/phylogeny/-phylogenetic-analysis-using-r/ Thiscourse is for biologists dealing with the analysis of multiple molecular sequencesat several levels: Populations, species, clades, communities. These biologistsaddress questions relative to the evolutionary relationships among thesesequences, as well as the evolutionary forces structuring biodiversity at differentscales. The objectives are: (i) to learn the theorical bases phylogeneticanalysis, (ii) to know how to choose a strategy of molecular data analysisat the interÂ©\ or intraspecific levels, (iii) to be able to initiate a phylogeneticanalysis starting from the files of molecular sequences until the interpretationof the results and the graphics. The software used for this coursewill be centered on the R language for statistics. This will include the useof specialized packages particularly ape, phangorn, and adegenet.

Requeriments:Knowledge of multivariate statistics, phylogenetics and molecular evolution.User level of R.

PLACE: Facilities of the Centre of RestauraciÂÂ i InterpretaciÂÂ Paleontologica, ElsHostalets de Pierola, Barcelona (Spain).

Organizedby: Transmitting Science, the Institut CatalÂÂ de Paleontologia M. Crusafontand the Centre de RestauraciÂÂ i InterpretaciÂÂ Paleontologica de Els Hostaletsde Pierola.

Placesare limited and will be covered by strict registration order.

Withbest regards

Sole

SoledadDe Esteban-Trivigno, PhD. ScientificDirector TransmittingScience www.transmittingscience.org soledad.esteban@transmittingscience.org

Lisbon Portugal Biodiversity Lichens

Subject: Portugal-cE3c-Course: two advanced courses with deadlines May 2016 cE3c - Centre for Ecology, Evolution and Environmental Changes is organizing several Advanced Courses: see below the two with closer deadlines.

Additional informations at: http://-ce3c.ciencias.ulisboa.pt/training/?cat=1 cE3c - Centre for Ecology, Evolution and Environmental Changes Advanced Course Natural History Collections and Biodiversity taught by Maria Judite Alves, Raquel Barata, Cristiane Bastos-Silveira et al. | May 30 - June

3 @ Lisbon, Portugal

Objectives Natural history museums are privileged spaces for seminal research on different subjects of biological sciences such as biodiversity, evolution, ecology, biogeography and taxonomy. This crucial role is due to the fact that they represent biological diversity repositories becoming huge libraries of information on Earth living organisms. The long-term sampling through various decades renders to natural history collections an historic perspective that allows reconstructing a "memory", sometimes secular, of natural patterns and processes. This aspect gains particular relevance nowadays because of the increasing rate of species extinctions and biodiversity decrease. This course aims to: - evidence the importance of natural history collections for the study of biodiversity. - show new tools and approaches to extract and disseminate biodiversity data from natural history collections - increase awareness of young researchers for the scientific and culture value of Natural History Museums.

Course coordinator Maria Judite Alves (mjalves@fc.ul.pt) Researcher at the Centre for Ecology, Evolution and Environmental Changes (cE3c), Faculty of Sciences of the University of Lisbon (http://ce3c.ciencias.ulisboa.pt/teams/user/?id=211)

Intended audience This five days intensive course will be open to a maximum number of 16 participants, being directed to PhD or MSc students in Biology, Evolution, Ecology or related areas, and postdocs and other professionals working in related topics. Minimum formation: Bachelor in Biology or related area.

The course is free for 1st year PhD students in the Doctoral programme in Biology (FCUL), Biodiversity, Genetics and Evolution (UL; UP) and Biology and Ecology of Global Changes (UL, UA). For information of fees for other participants see the programme details (access link below).

Deadline for applications: May 9, 2016

Candidates should send a short CV and motivation letter to Maria Judite Alves (mjalves@fc.ul.pt)

For additional details about the course and to know how to register, click here: http://ce3c.ciencias.ulisboa.pt/training/ver.php?id For more information about the course, please contact by email: Maria Judite Alves (mjalves@fc.ul.pt)

cE3c - Centre for Ecology, Evolution and Environmental Changes Advanced Course Lichens as a tool for interpretation of environmental changes taught by Cristina Maguas, Cristina Branquinho, Sofia Augusto et al.| July 11-15 2016 @ Lisbon, Portugal

Objectives: With this course, we aim at providing the participants with the basics of lichen biology and ecology, biomonitoring and data analysis methods to allow the use of lichens for the interpretation of the environmental conditions and the development of a responsible scientific-based environmental management.

Course coordinator Cristina Maguas (cmhanson@fc.ul.pt) Associate Professor at the Faculty of Sciences of the University of Lisbon, Researcher at the Centre for Ecology, Evolution and Environmental Changes (cE3c) (http://ce3c.ciencias.ulisboa.pt/teams/user/?id=145)

Intended audience This course will be open to a maximum number of 18 participants, being directed to PhD or MSc students in Ecology, Environmental Studies, Geography or related areas, and postdocs and other professionals working in related topics. Minimum formation: Bachelor in Biology, Natural Science or related areas.

The course is free for 1st year PhD students in the Doctoral programme in Biology (FCUL), Biodiversity, Genetics and Evolution (UL; UP) and Biology and Ecology of Global Changes (UL, UA). For information of fees for other participants see the programme details (access link below)

Deadline for applications: May 13, 2016

Candidates should send a short CV and motivation letter to lichenscourse@fc.ul.pt

For additional details about the course and to know how to register, click here: http://ce3c.ciencias.ulisboa.pt/training/ver.php?id For more information about the course, please contact by email: Cristina Máguas (cmhanson@fc.ul.pt)

Margarida Matos, PhD Associate Professor

Researcher ID: K-2365-2012

— / —

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

MDIBL Maine EnvironmentalGenomics Jul30-Aug6

Next-Generation Summer Course in Environmental Genomics at the Mount Desert Island Biological Lab

A technical course to guide research into how environmental conditions affect gene responses and the fitness of organisms

Date: July 30 to August 6, 2016. Number of participants: Restricted to 25. Only $300 registration fee!

We are pleased to announce that this course is now supported by the National Institutes of Health through the Big Data To Knowledge (BD2K) Program. Therefore, scholarships are available for US citizens or permanent residents, including room and board.

https://mdibl.org/course/envgen-2016/ The faculty at MDIBL is pleased to again offer a training course in Environmental Genomics, aiming to better understand technologies and approaches used to discover how gene function is influenced by environmental conditions while accounting for variation that exists within and among natural populations. This course is built on the paradigm that the research field will most effectively grow by properly designing large-scale experiments enabled by drastically increased sample-throughput and lower sequencing costs. Most importantly, the bioinformatics challenges of manipulating and analysing population-level genomics data must be addressed.â€â€

This course is designed to train the next-generation of environmental scientists, which have included in past years: university professors, postdoctoral researchers, doctoral students and government scientists, representing institutions from North America and Europe. Most responded in the departure survey that the course curriculum, choice of technologies, and effectiveness provided sufficient training to either begin or enlarge an environmental genomics project in their own laboratories. All reported that they would recommend this course to a colleague.

This course trains researchers to design studies, and to collect and analyse RNA-Seq gene expression data. Daphnia is used for training because of its growing use as a model system for environmental genomics and for improving environmental health protection, yet the skills learned during the course will be applicable to all study systems with maturing genomics resources. Much time is devoted to guiding the current and future projects of attendees.

Ultimately, participants will be better positioned to incorporate these technologies into their own research laboratories, while better understanding how functional genomics and automation can be applied to ecology, evolution and environmental toxicology.â€

Mount Desert Island Biological Laboratory Old Bar Harbor Rd., Salisbury Cove, ME 04672 MDIBL - http://www.mdibl.or j.k.colbourne@bham.ac.uk

Montana ConservationGenetics Sep5-10

We are pleased to invite you to attend the ConGen-2 course & workshop (see http://www.umt.edu/sell/cps/congen/)!

ConGen-2: Landscape Genomics & Genetic Monitoring Course:

“Applications of Next Gen Sequencing Data to Understand Population Connectivity, Adaptation, and Environmental Influences on Genomic Variation”

September 5-10, 2016, Flathead Lake Biological Station, Montana

Early bird registration before the 15th of June 2015

Instructors include: Fred Allendorf, Tiago Antao, Brian Hand, Paul Hohenlohe, Marty Kardos, Tabatha Graves, Gordon Luikart, Garret McKinney, Mike Miller, Mike Schwartz, Robin Waples, Diane Whited, and more.

[dinner at McD (Large)]

ConGen 2013 - dinner by the lake

Objective: To provide training in conceptual and practical aspects of data analysis for the population and evolutionary genomics of natural and managed populations. Emphasis will be on next generation sequence data analysis (RADs, exon capture, and whole genome sequence analyses) and interpretation of output from recent novel statistical approaches and software programs. The course also will allow daily discussions among young researchers (student participants) and >10 leaders in population genomics (instructors) to help develop the next generation of conservation and evolutionary geneticists. We will identify and discuss developments needed to improve data analysis approaches. This course will cover analysis methods including the coalescent, Bayesian, approximate Bayesian, and likelihood-based approaches. Most the material and activities will be different from ConGen 2015 including an emphasis on monitoring diversity, effective size and connectivity, as well as landscape genomics, and detecting effects of environmental variation on genomics variation (http://onlinelibrary.wiley.com/doi/10.1111/mec.13647/full ; and see: Andrews and Luikart 2014, Molecular Ecology, 23:1661-7. doi: 10.1111/mec.12686).

Who should apply: Advanced undergrads, graduate students, post-docs, faculty, and population biologists with a background of at least one semester university-level course in population genetics and a course in population ecology. Applicants must have a basic background in population genetic data analysis, including testing for Hardy-Weinberg proportions and gametic disequilibrium. Participation will be limited to 25-30 people allowing efficient instruction with hands-on computer exercises during the course. Priority will be given to persons with their own data to analyze.

"Luikart, Gordon" <gordon.luikart@mso.umt.edu>

Montana ConservationGenetics Sep5-10 2

Landscape Genomics & Genetic Monitoring Course: ConGen-2: "Applications of Next Gen Sequencing Data

to Understand Population Connectivity, Local Adaptation, and Environmental Influences on Genomic Variation"

September 5-10, 2016, Flathead Lake Biological Station, Montana; Early bird registration before the June 15th

14 Instructors include: Fred Allendorf, Tiago Antao, Brian Hand, Paul Hohenlohe, Marty Kardos, Tabatha Graves,

Jeff Good, Gordon Luikart, Garret McKinney, Mike Miller, Mike Schwartz, Robin Waples, Diane Whited, and more.

[dinner at McD (Large)]

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The course also will allow daily discussions among young researchers (student participants) and >12 leaders in population genomics (instructors) to help develop the next generation of conservation and evolutionary geneticists.

Most material will be different from ConGen 2015 including an emphasis on monitoring diversity and effective size (& Nb), connectivity & landscape genomics to detect effects of environmental variation on genomics variation, linkage mapping to help detect selection, simulations & power analysis for study design, WGS vs RADs for quantifying runs of homozygosity (RoH), filtering reads (the F-word!) & calling haplotype from RAD data (http://onlinelibrary.wiley.com/doi/10.1111/mec.13647/full ; and see: Andrews and Luikart 2014, Molecular Ecology, 23:1661-7. doi: 10.1111/mec.12686).

Who should apply: Advanced Undergrads, Ph.D. students, post-docs, faculty, and population biologists with a background of at least one semester university-level course in population genetics and a course in population ecology. Applicants must have a basic background in population genetic data analysis, including testing for Hardy-Weinberg proportions and gametic disequilibrium. Participation will be limited to 25-30 people allowing efficient instruction with hands-on computer exercises during the course. Priority will be given to persons with their own data to analyze.

For detailed information (on instructors etc.) see http://www.umt.edu/sell/cps/congen/ "Luikart, Gordon" <gordon.luikart@mso.umt.edu>

Scotland BioinformaticsUsingLINUX Aug15-19

Course: Introduction to Bioinformatics using LINUX

Instructor: Dr. Martin Jones

There are still a few places left on this courses scheduled for the 15th - 19th August 2016 at SCENE (the Scottish Centre for Ecology and the Natural Environment), Loch Lomond National Park, Glasgow.

Course overview: Most high-throughput bioinformatics work these days takes place on the Linux command line. The programs which do the majority of the computational heavy lifting â€genome assemblers, read mappers, and annotation tools â€are designed to work best when used with a command-line interface. Because the command line can be an intimidating environment, many biologists learn the bare minimum needed to get their analysis tools working. This means that they miss out on the power of Linux to customize their environment and automate many parts of the bioinformatics workflow. This course will introduce the Linux command line environment from scratch and teach students how to make the most of its tools to achieve a high level of productivity when working with biological data.

Availability: 15 places total.

Course programme

Monday 15th - Classes from 09:00 to 17:00 (approximately) • Session 1 - The design of Linux In the first session we briefly cover the design of Linux: how is it different from Windows/OSX and how is it best used? We'll then jump straight onto the command line and learn about the layout of the Linux filesystem and how to navigate it. We'll describe Linux's file permission system (which often trips up beginners), how paths work, and how we actually run programs on the command line. We'll learn a few tricks for using the command line more efficiently, and how to deal with programs that are misbehaving. We'll finish this session by looking at the built in help system and how to read and interpret manual pages.

• Session 2 - System management We'll first look at a few command line tools for monitoring the status of the system and keeping track of what's happening to processor power, memory, and disk space. We'll go over the process of installing new software from the built in repositories (which is easy) and from source code downloads (which is trickier). We'll also introduce some tools for benchmarking software (measuring the time/memory requirements of processing large datasets).

Tuesday 16th - Classes from 09:00 to 17:00 (approximately) • Session 3 - Manipulating tabular data Many data types we want to work with in bioinformatics are stored as tabular plain text files, and here we learn all about manipulating tabular data on the command line. We'll start with simple things like extracting columns, filtering and sorting, searching for text before moving on to more complex tasks like searching for duplicated values, summarizing large files, and combining simple tools into long commands.

• Session 4 - Constructing pipelines In this session we will look at the various tools Linux has for constructing pipelines out of individual commands. Aliases, shell redirection, pipes, and shell scripting will all be introduced here. We'll also look at a couple of specific tools to help with running tools on multiple processors, and for monitoring the progress of long running tasks.

Wednesday 17th - Classes from 09:00 to 17:00 (approximately) • Session 5 - EMBOSS EMBOSS is a suite of bioinformatics command-line tools explicitly designed to work in the Linux paradigm. We'll get an overview of the different sequence data formats that we might expect to work with, and put what we learned about shell scripting to biological use by building a pipeline to compare codon usage across two collections of DNA sequences.

• Session 6 - Using a Linux server Often in bioinformatics we'll be working on a Linux server rather than our own computerâ€typically because we need access to more computing power, or to specialized tools and datasets. In this session we'll learn how to connect to a Linux server and how to manage sessions. We'll also consider the various ways of moving data to and from a server from your own computer, and finish with a discussion of the considerations we have to make when working on a shared computer.

Thursday 18th - Classes from 09:00 to 17:00 (approximately) • Session 7 - Combining methods In the next two sessions â€i.e. one full day â€we'll put everything we have learned together and implement a workflow for next-gen sequence analysis. In this first session we'll carry out quality control on some paired-end Illumina data and map these reads to a reference genome. We'll then look at various approaches to automating this pipeline, allowing us to quickly do the same for a second dataset. • Session 8 - Combining methods The second part of the next-gen workflow is to call variants to identify

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SwissAlps Social Decisions Jul19-22

In this workshop we are very much interested in the evolutionary mechanisms behind social behavior and we will specifically concentrate on sensory constrains. Consequently, we would greatly appreciate the participation of evolutionary biologists.

THE ROLE OF SENSORY ECOLOGY AND COGNITION IN SOCIAL DECISIONS

When? 19-22 July 2016 Where? Arolla (Swiss Alps), Switzerland This workshop is organized by Prof. MichaÃ«l Taborsky and Dr. Karin Schneeberger from the University of Bern (CH).

Invited speakers: Prof. Lars Chittka, University of London (UK) Prof. Rui Oliveira, Universidade de Lisboa (PT) Prof. Kevin Laland, University of St. Andrews (UK) Prof. Douglas Chivers, University of Saskatchewan (CA) Prof. Maud Ferrari, Prof. University of Saskatchewan (CA) Prof. Tecumseh Fitch, University of Vienna (AT) Prof. David Stephens, University of Minnesota (US)

DESCRIPTION: The program of the workshop will consist of a combination of plenary talks by invited speakers and work performed in small groups, in which the participants will discuss a particular theme together with one of the invited speakers. The results of these small-group sessions willl be presented to the plenum by student participants, followed by a general discussion.

Social interactions are often assumed to require advanced cognitive abilities, as social behaviour typically happens among a large network of individuals, across different contexts, and over extended time periods. This is at variance with the observation that complex social behaviour can be observed in a wide range of animals, both in the laboratory and field. We think that rather simple cognitive mechanisms can generate complex social responses.

The aim of this workshop is to discuss sensory and cognitive abilities and limitations of animals in the context of the evolution of social behaviour. Topics discussed in the workshop will include, for instance: -â how social cues and signals are perceived by individuals -â how they are used for decision making - the role of memory for behavioural responses in repeated social interactions - the significance of different sensory modalities for communication in the contexts of conflict and cooperation.

These topics are of great interest to students and scientists from different disciplines, such as evolutionary and behavioural ecology, neurobiology, cognitive sciences, and psychology. Interaction between different fields will identify open questions and directions for future interdisciplinary research

For more info and registration: http://www.cuso.ch/-activity/?p=1128&uid=3033 Queries: ecologie-evolution@cuso.ch

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UExeter PoreCamp Aug15-19

PoreCamp is a hands-on training course based around Oxford Nanopore MinON sequencing technology. This is the second Porecamp to be run. t is organised and run by researchers for researchers and is the next installment in the PoreCamp series of courses. The last installment was run in December 2015< http://porecamp.github.io/-index.html > at the University of Birmingham, UK.

The aim is to provide practical, hands-on experience of the technology to enable any researcher with basic molecular biology expertise to perform their own sequencing experiments and learn from some of the leading experts in the field.

Date: Monday 15th August - Friday 19th August 2016

Location: Penryn Campus, Cornwall, University of Exeter, U.K.

Learning objectives:

* Preparing high quality MinON sequencing libraries * MinON operation * Custom scripts to maximise sequencer throughput * nitial QC and analysis of MinON output * Downstream analysis involving de-novo assembly and remapping * Production of a dataset for several fungal genomes as part of the 1000 fungal genomes project< http://1000.fungalgenomes.org/home/ >.

DNA will be provided for those who would like work on the 1000 fungal genomes project. Users will also be able to bring their own DNA samples but we cannot guarantee data will be generated from these - please do not rely on this event to generate data for your work. Further guidance will be provided on this to successful applicants.

More information on course content can be found here: http://sequencing.exeter.ac.uk/porecamp/ J.R.Paris@exeter.ac.uk

UGothenburg MetageneticBioinformaticPipelines Nov7-11

Dear all,

Please find below the preliminary schedule and general aims of the course, "An introduction to bioinformatic tools for population genomic and metagenetic data analysis", offered November 7-11 2016 at the Sven Loven Centre for Marine Sciences on the island of Tjärnö outside of Strömstad on the Swedish West Coast (http://-loven.gu.se/english/about_the_loven_centre/tjarno).

There is no course fee. Accommodation and meals for students are provided by the Royal Academy of Sciences of Sweden. Students will need to provide their own means of transportation to and from the course, however.

The course will be open to a maximum of 18 students, as large parts of the course will consist of hands-on exercises. The aim is a broad mix of students both from the University of Gothenburg and from the outside, mainly PhD students but postdocs are also welcome to apply.

Knowledge of general molecular biology and genetics is necessary, as is some previous experience with command-line interfaces. Previous experience working on a remote server will also be beneficial. No previous bioinformatics skills are needed, however.

For more information and registration, please visit the course web site at: https://sites.google.com/site/-bioinformaticpipelines2016/ Deadline for registration is September 15th 2016.

Please note that ALL students must bring their own computers.

Best wishes,

Pierre De Wit Sarah Bourlat

An introduction to bioinformatic tools for population genomic and metagenetic data analysis, 2.5 higher education credits Third Cycle

Faculty of Science; Department of Marine Sciences

The Swedish Royal Academy of Sciences

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1 Confirmation

The syllabus was confirmed by the Steering Committee of the Department of Marine Sciences 200X-XX-XX, 200X-XX-XX.

Discipline: Natural Science Responsible department: Department of Marine Sciences Main fields of study: Bioinformatics

2. Position in the educational system

Elective course; third-cycle education.

3. Entry requirements

Admitted to third cycle education.

4. Course content

This course aims at detailed understanding and hands-on experience of using state of the art bioinformatics pipelines for one"s own biological research questions. An important aspect of the course is to show how genomic data can be applied to address and answer research questions in the fields of genetics, ecology, population biology, biodiversity monitoring and conservation. The students will be trained in the latest bioinformatic methods to analyze high throughput sequencing data, which is present in many research projects. The course will cover basic computing tools required to run command line applications, processing high throughput sequencing data of the CO1 gene from environmental samples to reveal biodiversity and analysis of sequencing data from whole genome scans for population genomic studies.

The first part of the course introduces general computing tools for beginners such as the UNIX command line environment, bash commands, data formatting using regular expressions and basic scripting in the unix shell with a series of examples and exercises. The course introduces bioinformatics software for analysis of sequence data from metagenetics (The high-throughput sequencing of a molecular marker from an ecosystem or a community of organisms, used for large-scale analyses of biodiversity), through a series of live demonstrations (AmpliconNoise, TaxAssign, QIIME). The course also introduces basic and advanced concepts of population genomics data analysis such as genome/transcriptome assembly, annotation (BLAST), alignment/mapping, differential Gene expression, functional enrichment tests, SNP genotyping, PCA, outlier tests. The course corresponds to 1 week of full time studies and and is composed of lectures, demonstrations and computer labs.

5. Outcomes

1. Knowledge and understanding 1a. Demonstrate advanced knowledge of experimental strategies, applications and tools of DNA barcoding/metabarcoding and

population genomics. 1b. Demonstrate advanced knowledge of the potential of genomics approaches to answer ecosystem-wide questions, in particular for biodiversity monitoring.

2. Skills and abilities 2a. Ability to use basic commands in the Unix command line environment (reformatting data with regular expressions, basic scripting, running python scripts from the unix shell)

2b. Ability to use metagenetics software tools to analyse sequence data from environmental samples (data cleaning steps, clustering of reads into operational taxonomic units (OTUs) and taxonomic assignment through hidden markov models and database matching (BLAST, barcode of life database).

2c. Ability to use population genomics software tools to assemble and

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

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.